

Tue May 4 14:34:49 2004

us-10-644-187-6.rai

Page 2

Db 241 FEFPPDMLSVRSQTKPLFTVGEWMSYDINKLHNYITKTGIMSLEFPAFLNKFTYASK 300
QY 301 SGGAEDMRLTMTNTLMKQPTLAFTVFNHDEPGQALQSWDPWFKPLAFAFILTRQEG 360
Db 301 SGGAEDMRLTMTNTLMKQPTLAFTVFNHDEPGQALQSWDPWFKPLAFAFILTRQEG 360
QY 361 YPCVFYGDYVGIPOYNIPLSKIDPLLIARDYAVGTQHDYLDSDIIGWTRGGTEKP 420
Db 361 YPCVFYGDYVGIPOYNIPLSKIDPLLIARDYAVGTQHDYLDSDIIGWTRGGTEKP 420
QY 421 GSGLAALITDGGGSKMAYVGHQAGKVFYDLTGNRSDVTITNSDGMGEFKNQGSVSW 480
Db 421 GSGLAALITDGGGSKMAYVGHQAGKVFYDLTGNRSDVTITNSDGMGEFKNQGSVSW 480
QY 481 VPKTTVSTIARPIITRPWTGFEVWTEPRLYAM 514
Db 481 VPKTTVSTIARPIITRPWTGFEVWTEPRLYAM 514

RESULT 2
US-09-264-097-8
Sequence 8, Application US/09264097
Patent No. 6287826
GENERAL INFORMATION:
APPLICANT: Hendriksen, Barrie Edmund
APPLICANT: Hendriksen, Hanne Vang
TITLE OF INVENTION: Enzymatic Preparation of Glucose Syrup
FILE REFERENCE: 5278.200-US
CURRENT APPLICATION NUMBER: US/09/264,097
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: PA 0321/98
EARLIER FILING DATE: 1998-03-09
EARLIER APPLICATION NUMBER: 60/079,209
EARLIER FILING DATE: 1998-03-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 8
LENGTH: 514
TYPE: PRF
ORGANISM: Bacillus
US-09-264-097-8

Query Match 100.0%; Score 2847; DB 3; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.6e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFGTMMQYFEWYLPDDGTLMTKVAENANNLSIGITLWLPAYKGTSSSDVGYGY 60
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Db 61 DLYDLGEFNOKGVTATKYGKAYLOAIQAHAAGQYADVFEHKGADGTEWDAVE 120
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Db 121 VNSPDRNOEISGTYYQIOAWTKFDPGKNTYSSFKRWYHFGVWMDSESKLSRIYKFRG 180
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Db 181 IGRAMDVEVTENGNDYLMYADLMDHDEVTTELKMGKMYNTNIDGFLDAVKHAK 240
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QY 421 GSGLAALITDGGGSKMAYVGHQAGKVFYDLTGNRSDVTITNSDGMGEFKNQGSVSW 480
Db 421 GSGLAALITDGGGSKMAYVGHQAGKVFYDLTGNRSDVTITNSDGMGEFKNQGSVSW 480
QY 481 VPKTTVSTIARPIITRPWTGFEVWTEPRLYAM 514
Db 481 VPKTTVSTIARPIITRPWTGFEVWTEPRLYAM 514

RESULT 3
US-09-672-459-6
Sequence 6, Application US/09672459
Patent No. 643688
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/672,459
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 6
LENGTH: 514
TYPE: PRF
ORGANISM: Bacillus stearothermophilus
US-09-672-459-6

Query Match 100.0%; Score 2847; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.6e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 DLYDLGEFNOKGVTATKYGKAYLOAIQAHAAGQYADVFEHKGADGTEWDAVE 120
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Db 361 YPCVFYGDYVGIPOYNIPLSKIDPLLIARDYAVGTQHDYLDSDIIGWTRGGTEKP 420

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Page 3

QY 421 GSGLAALITDGGGSKMYVGVKQKAGKVFYDLTGNRSDVTITNSDGWGEFKVNGGSVSW 480
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QY 481 VPRKTTVSTIARPIITTRPMTGFEFVMTBRLVAM 514
DB 481 VPRKTTVSTIARPIITTRPMTGFEFVMTBRLVAM 514

RESULT 4
US-10-186-042-6
Sequence 6, Application US/10186042
Patent No. 6642044
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Friantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/186,042
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 514
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-10-186-042-6

Query Match 100.0%; Score 2847; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.6e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPNGTMQVFEWYLPDDGTLMTKYANEANNLSLIGITALLMPPAYKGTSRSDVGYGY 60
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DB 61 DLYDGEFNOKGIVRTKGTGKAYLOAIQAAHAGQVADVPFHKGADGTEWDAVE 120
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DB 121 VNPSDRNOEISGTYQIOAWTKFDPFGKNTYSSFKRWYHFDGVMDSEKLSRIYKFRG 180
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DB 181 IGAAMDVEVDTEGNVDYLMYADLDMDHPEVTELKNMGKMYNTNIDGFRDLDAVGHK 240
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DB 241 FSEFPDWLSYVRSGTKPLFTVGEYWSYDINKLHNYITKTGTMSLFDAPLHNKFTYASK 300
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DB 361 YPCVFGDYGYGIPQYNIPLSKSKIDPELLARADYAGTQHDYLDHSDIIGWREGGTEKP 420

QY 421 GSGLAALITDGGGSKMYVGVKQKAGKVFYDLTGNRSDVTITNSDGWGEFKVNGGSVSW 480
DB 421 GSGLAALITDGGGSKMYVGVKQKAGKVFYDLTGNRSDVTITNSDGWGEFKVNGGSVSW 480
QY 481 VPRKTTVSTIARPIITTRPMTGFEFVMTBRLVAM 514
DB 481 VPRKTTVSTIARPIITTRPMTGFEFVMTBRLVAM 514

RESULT 5
US-09-291-023A-17
Sequence 17, Application US/09291023A
Patent No. 6309871
GENERAL INFORMATION:
APPLICANT: Oultup, Helle
APPLICANT: Borchert, Torben
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Vibeke
TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
FILE REFERENCE: 5821.010-US
CURRENT APPLICATION NUMBER: US/09/291,023A
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: DK 1999 00438
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
SEQ ID NO 17
LENGTH: 515
TYPE: PRT
ORGANISM: Bacillus
US-09-291-023A-17

Query Match 100.0%; Score 2847; DB 4; Length 515;
Best Local Similarity 100.0%; Pred. No. 1.6e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 DLYDGEFNOKGIVRTKGTGKAYLOAIQAAHAGQVADVPFHKGADGTEWDAVE 120
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DB 181 IGAAMDVEVDTEGNVDYLMYADLDMDHPEVTELKNMGKMYNTNIDGFRDLDAVGHK 240
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DB 361 YPCVFGDYGYGIPQYNIPLSKSKIDPELLARADYAGTQHDYLDHSDIIGWREGGTEKP 420
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QY 481 VPRKTTVSTIARPIITTRPMTGFEFVMTBRLVAM 514
DB 481 VPRKTTVSTIARPIITTRPMTGFEFVMTBRLVAM 514

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us-10-644-187-6.ra1

Page 4

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RESULT 6
US-09-537-168-8
; Sequence 8, Application US/09537168
; Patent No. 6410295
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/09/537,168
; CURRENT FILING DATE: 2000-03-29
; EARLIER APPLICATION NUMBER: PA 1999 00437
; EARLIER FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: 60/127,427
; EARLIER FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 515
; TYPE: PR
; ORGANISM: Bacillus stearothermophilus
US-09-537-168-8
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Query Match      100.0%; Score 2847; DB 4; Length 515;
Best Local Similarity 100.0%; Pred. No. 1,66-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 DLYDGEFNQKGTVRKTKYKAQYLQALQAAHAGQYADVDFPHKGGADTEWDAVE 120
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DB 121 VNPSDRNOISGTYOIQAMTKFDPGRGNTYSSFKRWYHFGVWMDSRKLSRYKFRG 180
QY 122 VAPSPNDEISGTYOIQAMTKFDPGRGNTYSSFKRWYHFGVWMDSRKLSRYKFRG 180
DB 122 VAPSPNDEISGTYOIQAMTKFDPGRGNTYSSFKRWYHFGVWMDSRKLSRYKFRG 180
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DB 421 GSGLAALITDGPGGSKMYTVGKQHAGKVFYDLTGNRSDVTITNSDGMGEFKYNGGSVSW 480
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DB 481 VPKRTVSTIARPIITRRPWTGEFVWTEPRLVAM 514
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RESULT 7
US-09-540-715A-17
; Sequence 17, Application US/09540715A
; Patent No. 6623948
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; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/540,715A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/291,023
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 515
; TYPE: PR
; ORGANISM: Bacillus
US-09-540-715A-17

Query Match      100.0%; Score 2847; DB 4; Length 515;
Best Local Similarity 100.0%; Pred. No. 1,66-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 DLYDGEFNQKGTVRKTKYKAQYLQALQAAHAGQYADVDFPHKGGADTEWDAVE 120
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QY 481 VPKRTVSTIARPIITRRPWTGEFVWTEPRLVAM 514
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RESULT 8
US-08-720-899-6
; Sequence 6, Application US/08720899
; Patent No. 5753460
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
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NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57534600 No. 5753460disk of No. 5753460th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,899
FILING DATE: 10-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowrey Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054, 214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-899-6

Query Match 100.0%; Score 2847; DB 1; Length 549;
Best Local Similarity 100.0%; Pred. No. 1,7e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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275 BSFFPDMLSYRSQSGKPLFTVGEWYSYDINKLHNYITKIDGTMSLFPAFLHNKFTYASK 334
301 SGGAEDMRLMTNTLMKQOPTLAVTFVNDHTEPGQALQSWDPMFKELAYAFILTRQEG 360
335 SGGAEDMRLMTNTLMKQOPTLAVTFVNDHTEPGQALQSWDPMFKELAYAFILTRQEG 394
361 YECVPGYGVYGIPOYNIPELKSIDPLIARDYAYGQHDYLDSDIIGMREGSEKXP 420
395 YECVPGYGVYGIPOYNIPELKSIDPLIARDYAYGQHDYLDSDIIGMREGSEKXP 454
421 GSGALALITDGGSGKMTYVGRQHAKYVYDITGNRSDVTIINSQWGEFKNVGGSVSW 480
455 GSGALALITDGGSGKMTYVGRQHAKYVYDITGNRSDVTIINSQWGEFKNVGGSVSW 514
481 VPKTTVSTIARPIITRPWTGEFVWTERLVAM 514

DB 515 VPKTTVSTIARPIITRPWTGEFVWTERLVAM 548
RESULT 9
US-08-459-610-6
Sequence 6, Application US/08459610
Patent No. 5801043
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Bercher, Torden Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58010430 No. 5801043disk of No. 5801043th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,610
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowrey Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054, 214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-610-6

Query Match 100.0%; Score 2847; DB 1; Length 549;
Best Local Similarity 100.0%; Pred. No. 1,7e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 AAPFGTMMQYFEWYLPDDGTMTKVAANEANNLSIGITALLMPPAYKSTSSDVGYGY 60
35 AAPFGTMMQYFEWYLPDDGTMTKVAANEANNLSIGITALLMPPAYKSTSSDVGYGY 94
61 DLYDGEFNQKGTVRKYGTKAQYLOAIQAABAAGQYADVVFEDKGGADGTEWDAVE 120
95 DLYDGEFNQKGTVRKYGTKAQYLOAIQAABAAGQYADVVFEDKGGADGTEWDAVE 154
121 VNPSDRNOEISGTQYIOAWTKFDPGRGNTYSSFKRWYHFDGVDMDSRKLRIYKFRG 180
155 VNPSDRNOEISGTQYIOAWTKFDPGRGNTYSSFKRWYHFDGVDMDSRKLRIYKFRG 214
181 IGAAMDWEVDTEENGYDYLKADLMDHBEVVTLEKMGKMYNTNIDGFRLDAYKIK 240
215 IGAAMDWEVDTEENGYDYLKADLMDHBEVVTLEKMGKMYNTNIDGFRLDAYKIK 274
241 BSFFPDMLSYRSQSGKPLFTVGEWYSYDINKLHNYITKIDGTMSLFPAFLHNKFTYASK 300
275 BSFFPDMLSYRSQSGKPLFTVGEWYSYDINKLHNYITKIDGTMSLFPAFLHNKFTYASK 334

QY 301 SGGAFAKRTLTMTNTLMKQPTLAVTFVNDHTEPQALQSVWDPWFKEFLAYAFILTRQEG 360
DB 335 SGGAFAKRTLTMTNTLMKQPTLAVTFVNDHTEPQALQSVWDPWFKEFLAYAFILTRQEG 394
QY 361 YPCVFYGDYVGIPOYNIPSLKSKIDPLLIARDYAVGTQHDYLDHSDIIGWTRGGTEKP 420
DB 395 YPCVFYGDYVGIPOYNIPSLKSKIDPLLIARDYAVGTQHDYLDHSDIIGWTRGGTEKP 454
QY 421 GSGLAALITDGPGGSKMWTYVKGQAKVFDLTGNSRSDVTITNSDGEFFKVGSGSVW 480
DB 455 GSGLAALITDGPGGSKMWTYVKGQAKVFDLTGNSRSDVTITNSDGEFFKVGSGSVW 514
QY 481 VPKRTVSTIARPIITRPWTGFEFVWTEPRLVAM 514
DB 515 VPKRTVSTIARPIITRPWTGFEFVWTEPRLVAM 548

RESULT 10

US-08-343-804-6
Sequence 6, Application US/08343804

Patent No. 5830837

GENERAL INFORMATION:

APPLICANT: Bisgaard-Frantzen, Henrik

APPLICANT: Borchert, Torben Vedel

APPLICANT: Sverdsen, Allan

APPLICANT: Thellersen, Marianne

APPLICANT: Van der Zee, Pia

TITLE OF INVENTION: AMYLASE VARIANTS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESSES:

ADDRESSSEE: No. 5830837, disk of No. 5830837, th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/343,804

FILING DATE: 22-NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lowney Dr., Karen A.

REGISTRATION NUMBER: 31,274

REFERENCE/DOCKET NUMBER: 4054.214-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 549 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-343-804-6

Query Match 100.0%; Score 2847; DB 2; Length 549;

Best Local Similarity 100.0%; Pred. No. 1.7e-245;

Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFNGTMMQVREMYPDGCTMTKYANRANLSSIGTALMLPAPYAGTSSDVGYVY 60
DB 35 AAPFNGTMMQVREMYPDGCTMTKYANRANLSSIGTALMLPAPYAGTSSDVGYVY 94
QY 61 DLYDLGEFNQKGVTRTKYGTAKQVYLQALQAAHAGQVYADVDPHKGAGDTEWVDAVE 120
DB 95 DLYDLGEFNQKGVTRTKYGTAKQVYLQALQAAHAGQVYADVDPHKGAGDTEWVDAVE 154
QY 121 VNPSDNRNEISGTVOIQAWTKFDPFGKNTYSSFKRWYHFGVGMDESKLSRIYKRG 180

DB 155 VNPSDNRNEISGTVOIQAWTKFDPFGKNTYSSFKRWYHFGVGMDESKLSRIYKRG 214
QY 181 ICKAMDWEVDTENGVYDYLNTADLDMDHEVYVTELRKMGKRYVNTTINDGRDLAVGHIX 240
DB 215 ICKAMDWEVDTENGVYDYLNTADLDMDHEVYVTELRKMGKRYVNTTINDGRDLAVGHIX 274
QY 241 RSFPEDMLSYRSQSGKFLFTVGEYSYDINKLHNYITKTDGMSLFDPAPLNKFEYTSK 300
DB 275 RSFPEDMLSYRSQSGKFLFTVGEYSYDINKLHNYITKTDGMSLFDPAPLNKFEYTSK 334
QY 301 SGGAFAKRTLTMTNTLMKQPTLAVTFVNDHTEPQALQSVWDPWFKEFLAYAFILTRQEG 360
DB 335 SGGAFAKRTLTMTNTLMKQPTLAVTFVNDHTEPQALQSVWDPWFKEFLAYAFILTRQEG 394
QY 361 YPCVFYGDYVGIPOYNIPSLKSKIDPLLIARDYAVGTQHDYLDHSDIIGWTRGGTEKP 420
DB 395 YPCVFYGDYVGIPOYNIPSLKSKIDPLLIARDYAVGTQHDYLDHSDIIGWTRGGTEKP 454
QY 421 GSGLAALITDGPGGSKMWTYVKGQAKVFDLTGNSRSDVTITNSDGEFFKVGSGSVW 480
DB 455 GSGLAALITDGPGGSKMWTYVKGQAKVFDLTGNSRSDVTITNSDGEFFKVGSGSVW 514
QY 481 VPKRTVSTIARPIITRPWTGFEFVWTEPRLVAM 514
DB 515 VPKRTVSTIARPIITRPWTGFEFVWTEPRLVAM 548

RESULT 11

US-08-687-399-6
Sequence 6, Application US/08687399

Patent No. 5928381

GENERAL INFORMATION:

APPLICANT: Toft, Annette H.

APPLICANT: Marcher, Dorte

APPLICANT: Pedersen, Hanne H.

APPLICANT: Nilsen, Thomas E.

TITLE OF INVENTION: A Combined Desizing and Bleaching

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESSES:

ADDRESSSEE: No. 5928381, disk of No. 5928381, th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/687,399

FILING DATE:

CLASSIFICATION: 008

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 4127.204-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 549 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-687-399-6

Query Match 100.0%; Score 2847; DB 2; Length 549;

Best Local Similarity 100.0%; Pred. No. 1.7e-245;

Tue May 4 14:34:49 2004

us-10-644-187-6.ra1

Page 7

Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AAPNGTMMQYFEMWLPDDGTLMTKYANFANNLSIGITATMLPPAYKGTSSSDVGYV 60
DB 35 AAPNGTMMQYFEMWLPDDGTLMTKYANFANNLSIGITATMLPPAYKGTSSSDVGYV 94
QY 61 DLYDLGEFNQKGTVRTKYGTAQYLOAIQAAHAGQVADVFDDHKGADGTEWDAVE 120
DB 95 DLYDLGEFNQKGTVRTKYGTAQYLOAIQAAHAGQVADVFDDHKGADGTEWDAVE 154
QY 121 VNPSDRNOEISGTYYQIQAMTKFDPGRGNTYSSFKRWYHFDGVDMDESKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTYYQIQAMTKFDPGRGNTYSSFKRWYHFDGVDMDESKLSRIYKFRG 214
QY 181 IGRAMDMEVDTEGNNDYLYADLDMDHPEVTELKMGKMYVNTNIDGFRLDAYKHK 240
DB 215 IGRAMDMEVDTEGNNDYLYADLDMDHPEVTELKMGKMYVNTNIDGFRLDAYKHK 274
QY 241 FSPFPDMLSYRSQGTGKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLNKFFY7ASK 300
DB 275 FSPFPDMLSYRSQGTGKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLNKFFY7ASK 334
QY 301 SGCAFDMRTMTNTLTKKDOPTLATVFDNHDTEPGALQSWDPMFKPLAYAFILTRQEG 360
DB 335 SGCAFDMRTMTNTLTKKDOPTLATVFDNHDTEPGALQSWDPMFKPLAYAFILTRQEG 394
QY 361 YPCVFYGDYGIPIQYNIPLSKSKIDPLLIARDYAGTQHDYLDHSDIIGMTREGGTEK 420
DB 395 YPCVFYGDYGIPIQYNIPLSKSKIDPLLIARDYAGTQHDYLDHSDIIGMTREGGTEK 454
QY 421 GSGLAALITDGPGGSKMYGKQHAGKVFYDLGNRSDVTYINSDDGGEFKVNGGSVSVW 480
DB 455 GSGLAALITDGPGGSKMYGKQHAGKVFYDLGNRSDVTYINSDDGGEFKVNGGSVSVW 514
QY 481 VPRKTVSTIARPIITRPWTGEFVRWTEBRLVAM 514
DB 515 VPRKTVSTIARPIITRPWTGEFVRWTEBRLVAM 548
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RESULT 12

US-08-600-908A-6
Sequence 6, Application US/08600908A

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Franzen, Henrik
APPLICANT: Borchert, Torden Vedel
TITLE OF INVENTION: '-Amylase Mutants'
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59891690 No. 5989169disk of No. 5989169th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,908A

FILING DATE: 13-FEB-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza

REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394,204-US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-600-908A-6

Query Match 100.0%; Score 2847; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.7e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AAPNGTMMQYFEMWLPDDGTLMTKYANFANNLSIGITATMLPPAYKGTSSSDVGYV 60
DB 35 AAPNGTMMQYFEMWLPDDGTLMTKYANFANNLSIGITATMLPPAYKGTSSSDVGYV 94
QY 61 DLYDLGEFNQKGTVRTKYGTAQYLOAIQAAHAGQVADVFDDHKGADGTEWDAVE 120
DB 95 DLYDLGEFNQKGTVRTKYGTAQYLOAIQAAHAGQVADVFDDHKGADGTEWDAVE 154
QY 121 VNPSDRNOEISGTYYQIQAMTKFDPGRGNTYSSFKRWYHFDGVDMDESKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTYYQIQAMTKFDPGRGNTYSSFKRWYHFDGVDMDESKLSRIYKFRG 214
QY 181 IGRAMDMEVDTEGNNDYLYADLDMDHPEVTELKMGKMYVNTNIDGFRLDAYKHK 240
DB 215 IGRAMDMEVDTEGNNDYLYADLDMDHPEVTELKMGKMYVNTNIDGFRLDAYKHK 274
QY 241 FSPFPDMLSYRSQGTGKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLNKFFY7ASK 300
DB 275 FSPFPDMLSYRSQGTGKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLNKFFY7ASK 334
QY 301 SGCAFDMRTMTNTLTKKDOPTLATVFDNHDTEPGALQSWDPMFKPLAYAFILTRQEG 360
DB 335 SGCAFDMRTMTNTLTKKDOPTLATVFDNHDTEPGALQSWDPMFKPLAYAFILTRQEG 394
QY 361 YPCVFYGDYGIPIQYNIPLSKSKIDPLLIARDYAGTQHDYLDHSDIIGMTREGGTEK 420
DB 395 YPCVFYGDYGIPIQYNIPLSKSKIDPLLIARDYAGTQHDYLDHSDIIGMTREGGTEK 454
QY 421 GSGLAALITDGPGGSKMYGKQHAGKVFYDLGNRSDVTYINSDDGGEFKVNGGSVSVW 480
DB 455 GSGLAALITDGPGGSKMYGKQHAGKVFYDLGNRSDVTYINSDDGGEFKVNGGSVSVW 514
QY 481 VPRKTVSTIARPIITRPWTGEFVRWTEBRLVAM 514
DB 515 VPRKTVSTIARPIITRPWTGEFVRWTEBRLVAM 548
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RESULT 13

US-08-683-838A-6
Sequence 6, Application US/08683838A

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Franzen, Henrik
APPLICANT: Borchert, Torden Vedel
TITLE OF INVENTION: '-Amylase Mutants'
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60227240 No. 6022724disk of No. 6022724th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,838A
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/600,908
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394, 204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-683-838A-6

Query Match 100.0%; Score 2847; DB 3; Length 549;
Best Local Similarity 100.0%; Pred. No. 1,7e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AAFPGTMMQYFENWLPDDGTLMTKVAANEANLSIGITLMLPPAYKGTSRSDVGYGY 60
DB 35 AAFPGTMMQYFENWLPDDGTLMTKVAANEANLSIGITLMLPPAYKGTSRSDVGYGY 94
QY 61 DLYDGEFNQKGTATKTKGTAKQYLOAIQAAHAAQYVADVPDHKGADGTEWDAVE 120
DB 95 DLYDGEFNQKGTATKTKGTAKQYLOAIQAAHAAQYVADVPDHKGADGTEWDAVE 154
QY 121 VNPSDRNOEISGTIOIOMTKFDPFGKNTYSSFKRWYHFDGVDWDSRLSLRYKRG 180
DB 155 VNPSDRNOEISGTIOIOMTKFDPFGKNTYSSFKRWYHFDGVDWDSRLSLRYKRG 214
QY 181 IGRANDMEVDTEENGNYDYLMADLMDHPEVYTELKNGKMYVNTNIDGRDLDAVKAHK 240
DB 215 IGRANDMEVDTEENGNYDYLMADLMDHPEVYTELKNGKMYVNTNIDGRDLDAVKAHK 274
QY 241 PSFEPDMISYRSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFPAPLHNRKYTASK 300
DB 275 PSFEPDMISYRSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFPAPLHNRKYTASK 334
QY 301 SGGAFDMRTLMTNTLMKQDPTLAVTFVNDHTEPQALQSWDVPFKFLAFAFILTRQEG 360
DB 335 SGGAFDMRTLMTNTLMKQDPTLAVTFVNDHTEPQALQSWDVPFKFLAFAFILTRQEG 394
QY 361 YPCVEFYGDYGGIPQYNIPSLKSKIDPLIARDVAYGTOHDYLDHSDIIGWTRREGTEKP 420
DB 395 YPCVEFYGDYGGIPQYNIPSLKSKIDPLIARDVAYGTOHDYLDHSDIIGWTRREGTEKP 454
QY 421 GSGLAALITDGGGSKMYVKGQHAGKYFYDLTGNRSDTVTINSQWGEFFVNGGSVSW 480
DB 455 GSGLAALITDGGGSKMYVKGQHAGKYFYDLTGNRSDTVTINSQWGEFFVNGGSVSW 514
QY 481 VPKTTVSTIARPIITRPWTGFEFVWTEPRIVAM 514
DB 515 VPKTTVSTIARPIITRPWTGFEFVWTEPRIVAM 548
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RESULT 14

US-09-636-252A-6
Sequence 6, Application US/09636252A
Patent No. 6440716
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borcherdt, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/09/636,252A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/683,838

PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 549
TYPE: PRT
ORGANISM: B. stearothermophilus
US-09-636-252A-6

Query Match 100.0%; Score 2847; DB 4; Length 549;
Best Local Similarity 100.0%; Pred. No. 1,7e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AAFPGTMMQYFENWLPDDGTLMTKVAANEANLSIGITLMLPPAYKGTSRSDVGYGY 60
DB 35 AAFPGTMMQYFENWLPDDGTLMTKVAANEANLSIGITLMLPPAYKGTSRSDVGYGY 94
QY 61 DLYDGEFNQKGTATKTKGTAKQYLOAIQAAHAAQYVADVPDHKGADGTEWDAVE 120
DB 95 DLYDGEFNQKGTATKTKGTAKQYLOAIQAAHAAQYVADVPDHKGADGTEWDAVE 154
QY 121 VNPSDRNOEISGTIOIOMTKFDPFGKNTYSSFKRWYHFDGVDWDSRLSLRYKRG 180
DB 155 VNPSDRNOEISGTIOIOMTKFDPFGKNTYSSFKRWYHFDGVDWDSRLSLRYKRG 214
QY 181 IGRANDMEVDTEENGNYDYLMADLMDHPEVYTELKNGKMYVNTNIDGRDLDAVKAHK 240
DB 215 IGRANDMEVDTEENGNYDYLMADLMDHPEVYTELKNGKMYVNTNIDGRDLDAVKAHK 274
QY 241 PSFEPDMISYRSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFPAPLHNRKYTASK 300
DB 275 PSFEPDMISYRSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFPAPLHNRKYTASK 334
QY 301 SGGAFDMRTLMTNTLMKQDPTLAVTFVNDHTEPQALQSWDVPFKFLAFAFILTRQEG 360
DB 335 SGGAFDMRTLMTNTLMKQDPTLAVTFVNDHTEPQALQSWDVPFKFLAFAFILTRQEG 394
QY 361 YPCVEFYGDYGGIPQYNIPSLKSKIDPLIARDVAYGTOHDYLDHSDIIGWTRREGTEKP 420
DB 395 YPCVEFYGDYGGIPQYNIPSLKSKIDPLIARDVAYGTOHDYLDHSDIIGWTRREGTEKP 454
QY 421 GSGLAALITDGGGSKMYVKGQHAGKYFYDLTGNRSDTVTINSQWGEFFVNGGSVSW 480
DB 455 GSGLAALITDGGGSKMYVKGQHAGKYFYDLTGNRSDTVTINSQWGEFFVNGGSVSW 514
QY 481 VPKTTVSTIARPIITRPWTGFEFVWTEPRIVAM 514
DB 515 VPKTTVSTIARPIITRPWTGFEFVWTEPRIVAM 548
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RESULT 15

US-09-381-687-7
Sequence 7, Application US/09381687
Patent No. 6486113
GENERAL INFORMATION:
APPLICANT: HARADA, Yuji
APPLICANT: IKAMA, Kaori
APPLICANT: ITO, Susumu
APPLICANT: IGARASHI, Kazuaki
APPLICANT: HAGIHARA, Hiroshi
APPLICANT: HAYASHI, Yasuhiko
APPLICANT: ARAKI, Hiroyuki
TITLE OF INVENTION: MUTANT ALPHA-AMYLASES
FILE REFERENCE: 2173-0115P
CURRENT APPLICATION NUMBER: US/09/381,687
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 515
TYPE: PRT
ORGANISM: B. stearothermophilus

Tue May 4 14:34:49 2004

us-10-644-187-6.rai

US-09-381-687-7

Query Match 98.5%; Score 2805; DB 4; Length 515;
Best Local Similarity 98.8%; Pred. No. 8,9e-242;
Matches 508; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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QY 1 AAFENGIMMOYFEMYLPPDGLTMTKVANEANNTSLGITTALMLPPAYKGTISRSDVGYGVY 60
DB 1 AAFENGIMMOYFEMYLPPDGLTMTKVANEANNTSLGITTALMLPPAYKGTISRSDVGYGVY 60
QY 61 DLYDGEFNQKGTVTXKGTQAYQYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAY 120
DB 61 DLYDGEFNQKGTVTXKGTQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAY 120
QY 121 VNPSDRNOEISGTQYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAY 180
DB 121 VNPSDRNOEISGTQYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAYQAY 180
QY 181 IGAANDMEVDTEENGNYDILMADLMDHPEVYTELKMGKMYVNTNIDGFRDLAVKHK 240
DB 181 IGAANDMEVDTEENGNYDILMADLMDHPEVYTELKMGKMYVNTNIDGFRDLAVKHK 240
QY 241 FSFFPDWLSYVRSQTKPLFTVGEYMSYDINKLHNYITKTDGMSLFDAPLHNKFTASK 300
DB 241 FSFFPDWLSYVRSQTKPLFTVGEYMSYDINKLHNYITKTDGMSLFDAPLHNKFTASK 300
QY 301 SGGAFTDMRTLMTNTLMKQOPLAVTFVNDHTEPGQALQSWVDPWFKPLAYAFILTRQEG 360
DB 301 SGGAFTDMRTLMTNTLMKQOPLAVTFVNDHTEPGQALQSWVDPWFKPLAYAFILTRQEG 360
QY 361 YPCVFYGDYGGIPOXNIPSLKSKIDPLIARRDYAVGTQHDYLDHSDIIGWTREGTEKP 420
DB 361 YPCVFYGDYGGIPOXNIPSLKSKIDPLIARRDYAVGTQHDYLDHSDIIGWTREGTEKP 420
QY 421 GSGLAALITDGGGSKMTVGKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQ 480
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QY 481 VPRKTVSTIARPIITRRPWTGEFVWTEBRLVAM 514
DB 481 VPRKTVSTIARPIITRRPWTGEFVWTEBRLVAM 514
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Search completed: May 3, 2004, 20:35:57
Job time : 18.4001 secs

Tue May 4 14:34:49 2004

us-10-644-187-6.rapb

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:33:58 ; Search time 40.0203 Seconds

(without alignments)
3560.078 Million cell updates/sec

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Perfect score: 2847
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2847	100.0	514	14	US-10-186-042-6
3	2847	100.0	515	9	US-09-854-346-6
4	2847	100.0	515	9	US-09-918-543-6
5	2847	100.0	515	10	US-09-925-576C-6
6	2847	100.0	515	14	US-10-146-327-8
7	2847	100.0	515	14	US-10-184-771-6
8	2847	100.0	515	14	US-10-081-872-104
9	2829	99.4	549	14	US-10-385-305-104
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11	2825	99.2	549	14	US-10-081-872-92
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ALIGNMENTS

RESULT 1
US-10-644-187-6
Sequence 6, Application US/10644187
Publication No. US20040048351A1
GENERAL INFORMATION:
APPLICANT: Svedsen, Allan
APPLICANT: Borcherdt, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/644,187
CURRENT FILING DATE: 2003-08-20
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 514
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-10-644-187-6

Query Match 100.0%; Score 2847; DB 12; Length 514;
Best Local Similarity 100.0%; Pred. No. 5e-256;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AAPFNGTMQYFEWYLPDDGTLTKVANEANNLSLITLWLPAPKGRSRVGYGVY 60

QY 61 DLYDGEFNQKGTARTKTKGTAKQYLQAIQAHAAGMÖVYADVDFHKGADGTEWDAVE 120
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QY 121 VNPSDRNOEISGTYOIQAMTKFDFPGRGNTYSSFKMWYHFDGVDMDSRSLRIYKFRG 180
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DB 181 IKGAMDEVDTEENGNVYDIAMADLMDHPEVYTELKMWGKRYVNTTINDGRLDAVGHK 240
QY 241 FSPFPDWLSYVRSGTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNFYTAASK 300
DB 241 FSPFPDWLSYVRSGTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNFYTAASK 300
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DB 421 GSGLAALITDGPQSKMNYVKGQAHGKVFYDLTGNSRSDVTITNSDGEFRVNGGSVW 480
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RESULT 2

US-10-186-042-6
Sequence 6, Application US/10186042
Publication No. US20030171236A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgaard-Franzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/186.042
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/672.459
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182.859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 514
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-10-186-042-6

Query Match 100.0%; Score 2847; DB 14; Length 514;
Best Local Similarity 100.0%; Pred. No. 5e-256;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-09-854-346-6
Sequence 6, Application US/09854346
Patent No. US2002068352A1
GENERAL INFORMATION:
APPLICANT: No. US2002068352A1ozymes A/S
APPLICANT: Svendsen, Allan
APPLICANT: Corjensen, Christel Thea
APPLICANT: Nielsen, Bjarne Ronfeldt
TITLE OF INVENTION: Alpha-amylase variants with altered i.6 activity
FILE REFERENCE: 6140.200-US
CURRENT APPLICATION NUMBER: US/09/854.346
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 515
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-09-854-346-6

Query Match 100.0%; Score 2847; DB 9; Length 515;
Best Local Similarity 100.0%; Pred. No. 5e-256;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Page 3

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RESULT 4
US-09-918-543-6
Sequence 6, Application US/09918543
Patent No. US2002015574A1
GENERAL INFORMATION:
APPLICANT: NO. US2002015574A1ozymes A/S
APPLICANT: Thisted, Thomas
APPLICANT: Kjaerulff, Soren
APPLICANT: Andersen, Carsten
APPLICANT: Fugleang, Claus Cione
TITLE OF INVENTION: Alpha-amylase mutants with altered properties
FILE REFERENCE: 10062.200-US
CURRENT APPLICATION NUMBER: US/09/918,543
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 515
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-09-918-543-6

Query Match 100.0%; Score 2847; DB 9; Length 515;
Best Local Similarity 100.0%; Pred. No. 5e-256;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AAPFNGTMMQVFEWYLPDDGTLMTKVAEANNLSSIGITATLWLPAYKGTSRSDVGYGY 60
QY 61 DLYDLGEFNQKGTVRKTYGTAQYLOAIOAABAAGQVYADVFDHKGADGTEWDAVE 120
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QY 181 IGAAMDVEVDTEGNANDYLMYADLDMDHPEVTELKMGKMYVNTNIDGFRIDAVKHIK 240
DB 181 IGAAMDVEVDTEGNANDYLMYADLDMDHPEVTELKMGKMYVNTNIDGFRIDAVKHIK 240
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DB 421 GSGLAALITDGP GSKMVTYVGHQAGKVFYDLTGNRSDVTITNSDGMGEFKVNGSVSVW 480
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DB 481 VPKRTVSTIARPIITTRPWTGEFVRWTEBRLVAM 514

RESULT 5
US-09-925-576C-6
Sequence 6, Application US/09925576C
Publication No. US20030129718A1
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Borchert, Torben Vedel
APPLICANT: Nielsen, Bjarne Romfeldt
TITLE OF INVENTION: Amylase Variants
FILE REFERENCE: 10004.204-US
CURRENT APPLICATION NUMBER: US/09/925,576C
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 515
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-09-925-576C-6

Query Match 100.0%; Score 2847; DB 10; Length 515;
Best Local Similarity 100.0%; Pred. No. 5e-256;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AAPFNGTMMQVFEWYLPDDGTLMTKVAEANNLSSIGITATLWLPAYKGTSRSDVGYGY 60
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DB 61 DLYDLGEFNQKGTVRKTYGTAQYLOAIOAABAAGQVYADVFDHKGADGTEWDAVE 120
QY 121 VNPSDRNOEISGYIOQAWTKFDPGRGNTYSEFKRWYHFDGVMDSESKLSRIYKFRG 180
DB 121 VNPSDRNOEISGYIOQAWTKFDPGRGNTYSEFKRWYHFDGVMDSESKLSRIYKFRG 180
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DB 181 IGAAMDVEVDTEGNANDYLMYADLDMDHPEVTELKMGKMYVNTNIDGFRIDAVKHIK 240
QY 241 FSEFPDMLSVRSQNGKPLFTVGEVWSYDINKLHNVTIKTDGTMSLPDAPIANKFYTASK 300
DB 241 FSEFPDMLSVRSQNGKPLFTVGEVWSYDINKLHNVTIKTDGTMSLPDAPIANKFYTASK 300
QY 301 SGGA FDMRTIMNTLMKQOPTLA VTFVDNHDTEPGQALQSWDPMFKPLAVAFILTRQEG 360
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QY 421 GSGLAALITDGP GSKMVTYVGHQAGKVFYDLTGNRSDVTITNSDGMGEFKVNGSVSVW 480
DB 421 GSGLAALITDGP GSKMVTYVGHQAGKVFYDLTGNRSDVTITNSDGMGEFKVNGSVSVW 480
QY 481 VPKRTVSTIARPIITTRPWTGEFVRWTEBRLVAM 514
DB 481 VPKRTVSTIARPIITTRPWTGEFVRWTEBRLVAM 514

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us-10-644-187-6.rapb

Page 4

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RESULT 6
US-10-146-327-8
; Sequence 8, Application US/10146327
; Publication No. US20030044954A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/10/146,327
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US/09/537,168
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: PA 1999 00437
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/127,427
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 515
; TYPE: PR
; ORGANISM: Bacillus stearothermophilus
US-10-146-327-8
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Query Match 100.0%; Score 2847; DB 14; Length 515;
Best Local Similarity 100.0%; Pred. No. 5e-256;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AAFNGTMMQYFEMWLPDDGTLMTKYANEANNLSLIGITALMLPPAYKTSRSDVGYGVY 60
DB 1 AAFNGTMMQYFEMWLPDDGTLMTKYANEANNLSLIGITALMLPPAYKTSRSDVGYGVY 60
QY 61 DLYDGEFNQKGVTRKYGTAQYLOAIOAHAGQYADVPFHKGAGDTEWDAVE 120
DB 61 DLYDGEFNQKGVTRKYGTAQYLOAIOAHAGQYADVPFHKGAGDTEWDAVE 120
QY 121 VNPSDNOEISGTQYQOAWTKEDFPGKNTYSSFKRWYHFGVMDSESRKLSRIYKFRG 180
DB 121 VNPSDNOEISGTQYQOAWTKEDFPGKNTYSSFKRWYHFGVMDSESRKLSRIYKFRG 180
QY 181 IGAAMDWEVDTEGNADYLMYADLMDHDEVTTELKMGKMYVNTNIDGFLDAVKHIX 240
DB 181 IGAAMDWEVDTEGNADYLMYADLMDHDEVTTELKMGKMYVNTNIDGFLDAVKHIX 240
QY 241 FSEFPDMLSVRSQTSKPLFTVGEWYSYDINKLHNYITTDGMSLFDAPLNKFEYTASK 300
DB 241 FSEFPDMLSVRSQTSKPLFTVGEWYSYDINKLHNYITTDGMSLFDAPLNKFEYTASK 300
QY 301 SGGAFFMRITLMTNTLTKKQPTLAVTFVDNHDTEPGALOSWVDPFKPLAYAFILTRQSG 360
DB 301 SGGAFFMRITLMTNTLTKKQPTLAVTFVDNHDTEPGALOSWVDPFKPLAYAFILTRQSG 360
QY 361 YPCVFYGDYGYIGQYNIPLSKSKIDPLIARRDYAGTGHDIYDHSDDIIGWREGTEKRP 420
DB 361 YPCVFYGDYGYIGQYNIPLSKSKIDPLIARRDYAGTGHDIYDHSDDIIGWREGTEKRP 420
QY 421 GSGIAALITDGPSSKMYVYGKQAHGKVFYDLTGNSSDTVTINSDDGGEFKVNGGSVSW 480
DB 421 GSGIAALITDGPSSKMYVYGKQAHGKVFYDLTGNSSDTVTINSDDGGEFKVNGGSVSW 480
QY 481 VPKTIVSTIARPIITTRPWTGEFVRWTEPRLVAM 514
DB 481 VPKTIVSTIARPIITTRPWTGEFVRWTEPRLVAM 514
```

```
RESULT 7
US-10-184-771-6
; Sequence 6, Application US/10184771
; Publication No. US20030170769A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 549
; TYPE: PR
; ORGANISM: B. stearothermophilus
US-10-184-771-6
```

```
Query Match 100.0%; Score 2847; DB 14; Length 549;
Best Local Similarity 100.0%; Pred. No. 5.5e-256;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AAFNGTMMQYFEMWLPDDGTLMTKYANEANNLSLIGITALMLPPAYKTSRSDVGYGVY 60
DB 35 AAFNGTMMQYFEMWLPDDGTLMTKYANEANNLSLIGITALMLPPAYKTSRSDVGYGVY 94
QY 61 DLYDGEFNQKGVTRKYGTAQYLOAIOAHAGQYADVPFHKGAGDTEWDAVE 120
DB 95 DLYDGEFNQKGVTRKYGTAQYLOAIOAHAGQYADVPFHKGAGDTEWDAVE 154
QY 121 VNPSDNOEISGTQYQOAWTKEDFPGKNTYSSFKRWYHFGVMDSESRKLSRIYKFRG 180
DB 155 VNPSDNOEISGTQYQOAWTKEDFPGKNTYSSFKRWYHFGVMDSESRKLSRIYKFRG 214
QY 181 IGAAMDWEVDTEGNADYLMYADLMDHDEVTTELKMGKMYVNTNIDGFLDAVKHIX 240
DB 215 IGAAMDWEVDTEGNADYLMYADLMDHDEVTTELKMGKMYVNTNIDGFLDAVKHIX 274
QY 241 FSEFPDMLSVRSQTSKPLFTVGEWYSYDINKLHNYITTDGMSLFDAPLNKFEYTASK 300
DB 275 FSEFPDMLSVRSQTSKPLFTVGEWYSYDINKLHNYITTDGMSLFDAPLNKFEYTASK 334
QY 301 SGGAFFMRITLMTNTLTKKQPTLAVTFVDNHDTEPGALOSWVDPFKPLAYAFILTRQSG 360
DB 335 SGGAFFMRITLMTNTLTKKQPTLAVTFVDNHDTEPGALOSWVDPFKPLAYAFILTRQSG 394
QY 361 YPCVFYGDYGYIGQYNIPLSKSKIDPLIARRDYAGTGHDIYDHSDDIIGWREGTEKRP 420
DB 395 YPCVFYGDYGYIGQYNIPLSKSKIDPLIARRDYAGTGHDIYDHSDDIIGWREGTEKRP 454
QY 421 GSGIAALITDGPSSKMYVYGKQAHGKVFYDLTGNSSDTVTINSDDGGEFKVNGGSVSW 480
DB 455 GSGIAALITDGPSSKMYVYGKQAHGKVFYDLTGNSSDTVTINSDDGGEFKVNGGSVSW 514
QY 481 VPKTIVSTIARPIITTRPWTGEFVRWTEPRLVAM 514
DB 515 VPKTIVSTIARPIITTRPWTGEFVRWTEPRLVAM 548
```

```
RESULT 8
US-10-081-872-104
; Sequence 104, Application US/10081872
; Publication No. US20030125534A1
; GENERAL INFORMATION:
; APPLICANT: Callen, Walter
; APPLICANT: Richardson, Toby
; APPLICANT: Frey, Gerhard
; APPLICANT: Short, Jay M.
; APPLICANT: Machur, Eric J.
; APPLICANT: Gray, Kevin A.
; APPLICANT: Kerovuo, Janne S.
```

```
APPLICANT: Slupska, Malgorzata
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
FILE REFERENCE: 09010-108001
CURRENT APPLICATION NUMBER: US/10/081,872
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/270,495
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/291,122
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 321
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 104
LENGTH: 549
TYPE: PRT
ORGANISM: Environmental
US-10-081-872-104
```

```
Query Match          99.4%; Score 2829; DB 14; Length 549;
Best Local Similarity 99.4%; Pred. No. 2.6e-254;
Matches 511; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 AAFNGTMMQYFEMWLPDDGTLMTKVAANEANNTLSLIGTALMLPAYKGTSSSDVGYGY 60
DB 35 AAFNGTMMQYFEMWLPDDGTLMTKVAANEANNTLSLIGTALMLPAYKGTSSSDVGYGY 94
QY 61 DLYDGEFNQKGVTRKTKGTAKQYLOAIOAAHAGQYADVPFHKGAGDTEWDAVE 120
DB 95 DLYDGEFNQKGVTRKTKGTAKQYLOAIOAAHAGQYADVPFHKGAGDTEWDAVE 154
QY 121 VNPSDRNOEISGTQYIOAWTKDFPGRGNTYSSFKRWYHFDGVWDSESKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTQYIOAWTKDFPGRGNTYSSFKRWYHFDGVWDSESKLSRIYKFRG 214
QY 181 IGAAMDWEVDTENGNDYDLYMADLMDHPEVTELKMGKMYVNTNIDGRLDAVXHIX 240
DB 215 IGAAMDWEVDTENGNDYDLYMADLMDHPEVTELKMGKMYVNTNIDGRLDAVXHIX 274
QY 241 FSFFPDMLSYVSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHKKFYTASK 300
DB 275 FSFFPDMLSYVSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHKKFYTASK 334
QY 301 SGGAEDMTLMTNTLMKQOPTLAATFVNHDTEPGQALQSWDPMFKPLAFAFLTROEG 360
DB 335 SGGAEDMTLMTNTLMKQOPTLAATFVNHDTEPGQALQSWDPMFKPLAFAFLTROEG 394
QY 361 YPCVFYGDYVGIPOYNIPLSKSIDPLLIARDVAYGTHDYLDSDIIGWREGGTEKP 420
DB 395 YPCVFYGDYVGIPOYNIPLSKSIDPLLIARDVAYGTHDYLDSDIIGWREGGTEKP 454
QY 421 GSGLAALITDGGGSKMYVQKQAGKVFYDLTGKRSPTVTINSOGWGEFFKYNAGSVSW 480
DB 455 GSGLAALITDGGGSKMYVQKQAGKVFYDLTGKRSPTVTINSOGWGEFFKYNAGSVSW 514
QY 481 VPKRTVSTIARPIITRPWTGFEFVWTEPRLVAM 514
DB 515 VPKRTVSTIARPIITRPWTGFEFVWTEPRLVAM 548
```

```
RESULT 9
US-10-385-305-104
; Sequence 104, Application US/10385305
; Publication No. US20040018607A1
; GENERAL INFORMATION:
; APPLICANT: Callen, Walter
; APPLICANT: Richardson, Toby
; APPLICANT: Frey, Gerhard
; APPLICANT: Short, Jay M.
; APPLICANT: Mathur, Eric J.
; APPLICANT: Gray, Kevin A.
; APPLICANT: Kerovuo, Janne S.
```

```
APPLICANT: Slupska, Malgorzata
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
FILE REFERENCE: 09010-108001
CURRENT APPLICATION NUMBER: US/10/385,305
CURRENT FILING DATE: 2003-03-06
PRIOR APPLICATION NUMBER: US/10/081,872
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/270,495
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/291,122
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 321
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 104
LENGTH: 549
TYPE: PRT
ORGANISM: Environmental
US-10-385-305-104
```

```
Query Match          99.4%; Score 2829; DB 15; Length 549;
Best Local Similarity 99.4%; Pred. No. 2.6e-254;
Matches 511; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 AAFNGTMMQYFEMWLPDDGTLMTKVAANEANNTLSLIGTALMLPAYKGTSSSDVGYGY 60
DB 35 AAFNGTMMQYFEMWLPDDGTLMTKVAANEANNTLSLIGTALMLPAYKGTSSSDVGYGY 94
QY 61 DLYDGEFNQKGVTRKTKGTAKQYLOAIOAAHAGQYADVPFHKGAGDTEWDAVE 120
DB 95 DLYDGEFNQKGVTRKTKGTAKQYLOAIOAAHAGQYADVPFHKGAGDTEWDAVE 154
QY 121 VNPSDRNOEISGTQYIOAWTKDFPGRGNTYSSFKRWYHFDGVWDSESKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTQYIOAWTKDFPGRGNTYSSFKRWYHFDGVWDSESKLSRIYKFRG 214
QY 181 IGAAMDWEVDTENGNDYDLYMADLMDHPEVTELKMGKMYVNTNIDGRLDAVXHIX 240
DB 215 IGAAMDWEVDTENGNDYDLYMADLMDHPEVTELKMGKMYVNTNIDGRLDAVXHIX 274
QY 241 FSFFPDMLSYVSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHKKFYTASK 300
DB 275 FSFFPDMLSYVSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHKKFYTASK 334
QY 301 SGGAEDMTLMTNTLMKQOPTLAATFVNHDTEPGQALQSWDPMFKPLAFAFLTROEG 360
DB 335 SGGAEDMTLMTNTLMKQOPTLAATFVNHDTEPGQALQSWDPMFKPLAFAFLTROEG 394
QY 361 YPCVFYGDYVGIPOYNIPLSKSIDPLLIARDVAYGTHDYLDSDIIGWREGGTEKP 420
DB 395 YPCVFYGDYVGIPOYNIPLSKSIDPLLIARDVAYGTHDYLDSDIIGWREGGTEKP 454
QY 421 GSGLAALITDGGGSKMYVQKQAGKVFYDLTGKRSPTVTINSOGWGEFFKYNAGSVSW 480
DB 455 GSGLAALITDGGGSKMYVQKQAGKVFYDLTGKRSPTVTINSOGWGEFFKYNAGSVSW 514
QY 481 VPKRTVSTIARPIITRPWTGFEFVWTEPRLVAM 514
DB 515 VPKRTVSTIARPIITRPWTGFEFVWTEPRLVAM 548
```

```
RESULT 10
US-10-081-872-92
; Sequence 92, Application US/10081872
; Publication No. US20030125534A1
; GENERAL INFORMATION:
; APPLICANT: Callen, Walter
; APPLICANT: Richardson, Toby
; APPLICANT: Frey, Gerhard
; APPLICANT: Short, Jay M.
; APPLICANT: Mathur, Eric J.
```

```

; APPLICANT: Gray, Kevin A.
; APPLICANT: Kerovuo, Janne S.
; APPLICANT: Slupeka, Malgorzata
; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
; FILE REFERENCE: 09010-108001
; CURRENT APPLICATION NUMBER: US/10/081,872
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/270,495
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/270,496
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/291,122
; PRIOR FILING DATE: 2001-05-14
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 321
; SEQ ID NO 92
; LENGTH: 549
; TYPE: PRF
; ORGANISM: Bacterial
; US-10-081-872-92

Query Match          99.2%; Score 2825; DB 14; Length 549;
Best Local Similarity 99.4%; Pred. No. 6.1e-254;
Matches 511; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 1 AAFNGTMMQYFEMWYIPDDGTMTKYANBANNLSIGITAMLPAYKTSRSDVGYGY 60
DB 35 AAFNGTMMQYFEMWYIPDDGTMTKYANBANNLSIGITAMLPAYKTSRSDVGYGY 94
QY 61 DLYDLGEFNQKGVKRYKGYKQYLOAIOAAHAGQYADVFPKHGAGDTEWDAVE 120
DB 95 DLYDLGEFNQKGVKRYKGYKQYLOAIOAAHAGQYADVFPKHGAGDTEWDAVE 154
QY 121 VNPSDRNOEISGTYYQIOAWTKFDPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTYYQIOAWTKFDPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 214
QY 181 IGRAMDEVDTEGNVDYLMYADLDMDHPEVYTELKNMKWYVNTNIDGFLDAVKHK 240
DB 215 IGRAMDEVDTEGNVDYLMYADLDMDHPEVYTELKNMKWYVNTNIDGFLDAVKHK 274
QY 241 FSEFFPDLSTYRSQTKRPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLNKRYTAS 300
DB 275 FSEFFPDLSTYRSQTKRPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLNKRYTAS 334
QY 301 SGGAFFMRITMTNTLMKDOPTLAFTVDNHDTEPGQALOSWDPMFKPLAFAFILTRREG 360
DB 335 SGGAFFMRITMTNTLMKDOPTLAFTVDNHDTEPGQALOSWDPMFKPLAFAFILTRREG 394
QY 361 YPCVFYGDYVGIPOYNIPLSKSIDPLLIARRDYAGTQHDYLDHSDIIGWREGGTERP 420
DB 395 YPCVFYGDYVGIPOYNIPLSKSIDPLLIARRDYAGTQHDYLDHSDIIGWREGGTERP 454
QY 421 GSGIALIITDGPQSGSKMYVKGQAKGVYDILGNRSDVTYINSQMGSEFKWNGSVSW 480
DB 455 GSGIALIITDGPQSGSKMYVKGQAKGVYDILGNRSDVTYINSQMGSEFKWNGSVSW 514
QY 481 VPRKTIYSTIARPIITRPWTGEFVRWTEBRLVAM 514
DB 515 VPRKTIYSTIARPIITRPWTGEFVRWTEBRLVAM 548
```

```

RESULT 11
; US-10-385-305-92
; Sequence 92, Application US/10385305
; Publication No. US20040018607A1
; GENERAL INFORMATION:
; APPLICANT: Callen, Walter
; APPLICANT: Richardson, Toby
; APPLICANT: Frey, Gerhard
; APPLICANT: Short, Jay M.
; APPLICANT: Mathur, Eric J.
```

```

; APPLICANT: Gray, Kevin A.
; APPLICANT: Kerovuo, Janne S.
; APPLICANT: Slupeka, Malgorzata
; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
; FILE REFERENCE: 09010-108001
; CURRENT APPLICATION NUMBER: US/10/385,305
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US/10/081,872
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/270,495
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/270,496
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/291,122
; PRIOR FILING DATE: 2001-05-14
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 321
; SEQ ID NO 92
; LENGTH: 549
; TYPE: PRF
; ORGANISM: Bacterial
; US-10-385-305-92

Query Match          99.2%; Score 2825; DB 15; Length 549;
Best Local Similarity 99.4%; Pred. No. 6.1e-254;
Matches 511; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 1 AAFNGTMMQYFEMWYIPDDGTMTKYANBANNLSIGITAMLPAYKTSRSDVGYGY 60
DB 35 AAFNGTMMQYFEMWYIPDDGTMTKYANBANNLSIGITAMLPAYKTSRSDVGYGY 94
QY 61 DLYDLGEFNQKGVKRYKGYKQYLOAIOAAHAGQYADVFPKHGAGDTEWDAVE 120
DB 95 DLYDLGEFNQKGVKRYKGYKQYLOAIOAAHAGQYADVFPKHGAGDTEWDAVE 154
QY 121 VNPSDRNOEISGTYYQIOAWTKFDPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTYYQIOAWTKFDPGRGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 214
QY 181 IGRAMDEVDTEGNVDYLMYADLDMDHPEVYTELKNMKWYVNTNIDGFLDAVKHK 240
DB 215 IGRAMDEVDTEGNVDYLMYADLDMDHPEVYTELKNMKWYVNTNIDGFLDAVKHK 274
QY 241 FSEFFPDLSTYRSQTKRPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLNKRYTAS 300
DB 275 FSEFFPDLSTYRSQTKRPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLNKRYTAS 334
QY 301 SGGAFFMRITMTNTLMKDOPTLAFTVDNHDTEPGQALOSWDPMFKPLAFAFILTRREG 360
DB 335 SGGAFFMRITMTNTLMKDOPTLAFTVDNHDTEPGQALOSWDPMFKPLAFAFILTRREG 394
QY 361 YPCVFYGDYVGIPOYNIPLSKSIDPLLIARRDYAGTQHDYLDHSDIIGWREGGTERP 420
DB 395 YPCVFYGDYVGIPOYNIPLSKSIDPLLIARRDYAGTQHDYLDHSDIIGWREGGTERP 454
QY 421 GSGIALIITDGPQSGSKMYVKGQAKGVYDILGNRSDVTYINSQMGSEFKWNGSVSW 480
DB 455 GSGIALIITDGPQSGSKMYVKGQAKGVYDILGNRSDVTYINSQMGSEFKWNGSVSW 514
QY 481 VPRKTIYSTIARPIITRPWTGEFVRWTEBRLVAM 514
DB 515 VPRKTIYSTIARPIITRPWTGEFVRWTEBRLVAM 548
```

```

RESULT 12
; US-09-769-864-3
; Sequence 3, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
```

Tue May 4 14:34:49 2004

us-10-644-187-6.rapb

Page 7

APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Torden L.
APPLICANT: Kjaerulff, Soren
TITLE OF INVENTION: Alpha-Amulase Mutants
FILE REFERENCES: 5368-200-US
CURRENT APPLICATION NUMBER: US/09/769,864
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 514
TYPE: PR
ORGANISM: Bacillus stearothermophilus
US-09-769-864-3

Query Match 97.6%; Score 2780; DB 9; Length 514;
Best Local Similarity 98.1%; Pred. No. 8.6e-250;
Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

1 AAFNGTMMQYFEMVLPDDGTLMTKVNANNNLSLIGITALMPPAYKTSRSDVGYGY 60
1 AAFNGTMMQYFEMVLPDDGTLMTKVNANNNLSLIGITALMPPAYKTSRSDVGYGY 60
61 DLYDLGEFNQKGVTRTKYGAQYLAQIAAAGQYADVFDHKGADGTEWDAVE 120
61 DLYDLGEFNQKGVTRTKYGAQYLAQIAAAGQYADVFDHKGADGTEWDAVE 120
121 VNPSDRNOEISGTYQIOAWTKFDPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
121 VNPSDRNOEISGTYQIOAWTKFDPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
121 VNPSDRNOEISGTYQIOAWTKFDPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
121 VNPSDRNOEISGTYQIOAWTKFDPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
181 IGAAMDWEVDTEGNANDYLAADLMDHPEVYTELKMGKMYNTNINIGFRDAVGHK 240
181 IGAAMDWEVDTEGNANDYLAADLMDHPEVYTELKMGKMYNTNINIGFRDAVGHK 240
181 IGAAMDWEVDTEGNANDYLAADLMDHPEVYTELKMGKMYNTNINIGFRDAVGHK 240
241 FSEFPDMLSVRSQGTGKPLFTVGEYWSYDINKLHNYITKTGTMSPDAPLHKKFYTASK 300
241 FSEFPDMLSVRSQGTGKPLFTVGEYWSYDINKLHNYITKTGTMSPDAPLHKKFYTASK 300
301 SGGAPDMRILMTNTLMKQDPTLAVTFVNDHTEBPGALQSWDPWFKPLAVAFILTRQEG 360
301 SGGAPDMRILMTNTLMKQDPTLAVTFVNDHTEBPGALQSWDPWFKPLAVAFILTRQEG 360
301 SGGAPDMRILMTNTLMKQDPTLAVTFVNDHTEBPGALQSWDPWFKPLAVAFILTRQEG 360
361 YPCVFYGYGIPQYNIPSLKSKIDPLLIARDYAGTQHDYLDHSDIIGWTEEGTEKP 420
361 YPCVFYGYGIPQYNIPSLKSKIDPLLIARDYAGTQHDYLDHSDIIGWTEEGTEKP 420
421 GSGIALITDGGGSKMYVKGQAHGKVFYDLTGNSDPTTINSDCGGEKXVNGSVVW 480
421 GSGIALITDGGGSKMYVKGQAHGKVFYDLTGNSDPTTINSDCGGEKXVNGSVVW 480
421 GSGIALITDGGGSKMYVKGQAHGKVFYDLTGNSDPTTINSDCGGEKXVNGSVVW 480
481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514
481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514

RESULT 13
US-09-902-188A-3
Sequence 3, Application US/09902188A
Patent No. US2002009896A1

GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
Svendsen, Allan
Borchert, Torden Vedel
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. US2002009896A10 No. US2002009896A1disk of No. US200200989
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York

COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/902,188A
FILING DATE: 10-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/354,191
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-902-188A-3

Query Match 97.6%; Score 2780; DB 9; Length 514;
Best Local Similarity 98.1%; Pred. No. 8.6e-250;
Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

1 AAFNGTMMQYFEMVLPDDGTLMTKVNANNNLSLIGITALMPPAYKTSRSDVGYGY 60
1 AAFNGTMMQYFEMVLPDDGTLMTKVNANNNLSLIGITALMPPAYKTSRSDVGYGY 60
61 DLYDLGEFNQKGVTRTKYGAQYLAQIAAAGQYADVFDHKGADGTEWDAVE 120
61 DLYDLGEFNQKGVTRTKYGAQYLAQIAAAGQYADVFDHKGADGTEWDAVE 120
121 VNPSDRNOEISGTYQIOAWTKFDPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
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121 VNPSDRNOEISGTYQIOAWTKFDPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
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181 IGAAMDWEVDTEGNANDYLAADLMDHPEVYTELKMGKMYNTNINIGFRDAVGHK 240
181 IGAAMDWEVDTEGNANDYLAADLMDHPEVYTELKMGKMYNTNINIGFRDAVGHK 240
181 IGAAMDWEVDTEGNANDYLAADLMDHPEVYTELKMGKMYNTNINIGFRDAVGHK 240
241 FSEFPDMLSVRSQGTGKPLFTVGEYWSYDINKLHNYITKTGTMSPDAPLHKKFYTASK 300
241 FSEFPDMLSVRSQGTGKPLFTVGEYWSYDINKLHNYITKTGTMSPDAPLHKKFYTASK 300
301 SGGAPDMRILMTNTLMKQDPTLAVTFVNDHTEBPGALQSWDPWFKPLAVAFILTRQEG 360
301 SGGAPDMRILMTNTLMKQDPTLAVTFVNDHTEBPGALQSWDPWFKPLAVAFILTRQEG 360
361 YPCVFYGYGIPQYNIPSLKSKIDPLLIARDYAGTQHDYLDHSDIIGWTEEGTEKP 420
361 YPCVFYGYGIPQYNIPSLKSKIDPLLIARDYAGTQHDYLDHSDIIGWTEEGTEKP 420
421 GSGIALITDGGGSKMYVKGQAHGKVFYDLTGNSDPTTINSDCGGEKXVNGSVVW 480
421 GSGIALITDGGGSKMYVKGQAHGKVFYDLTGNSDPTTINSDCGGEKXVNGSVVW 480
421 GSGIALITDGGGSKMYVKGQAHGKVFYDLTGNSDPTTINSDCGGEKXVNGSVVW 480
481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514
481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514

RESULT 14

US-10-665-667-3
Sequence 3, Application US/1065667
Publication No. US20040038368A1
GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nissen, Torben L.
APPLICANT: Kjaerulf, Soren
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 5368, 200-US
CURRENT APPLICATION NUMBER: US/10/665,667
CURRENT FILING DATE: 2003-09-19
PRIOR APPLICATION NUMBER: US/09/769,864
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 3
LENGTH: 514
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-10-665-667-3

Query Match 97.6%; Score 2780; DB 12; Length 514;
Best Local Similarity 98.1%; Pred. No. 8.6e-250;
Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 1 AAPNGTMMQYFEWYLPDDGTLMTKVANEANNLSLIGITLMLPYPAYKGTSRSDVGQVY 60
DB 1 AAPNGTMMQYFEWYLPDDGTLMTKVANEANNLSLIGITLMLPYPAYKGTSRSDVGQVY 60
QY 61 DLYDGEFNOKGTVTKTKGTAQYLOAIQAAHAAQVYADVDFHKGADGTEWDAVE 120
DB 61 DLYDGEFNOKGAVTKTKGTAQYLOAIQAAHAAQVYADVDFHKGADGTEWDAVE 120
QY 121 VNPSDRNOEISGTQYIOAWTKFDPFGKNTYSSFFKRWYHFDGVDMDESKLSRIYKFRG 180
DB 121 VNPSDRNOEISGTQYIOAWTKFDPFGKNTYSSFFKRWYHFDGVDMDESKLSRIYKFRG 180
QY 181 IGAAMDMEVDTENGNYDYLMATADLMDHPEVYTELKSGKMYVNTNIDGRDLDAVGHK 240
DB 181 IGAAMDMEVDTENGNYDYLMATADLMDHPEVYTELKSGKMYVNTNIDGRDLDAVGHK 240
QY 241 FSEFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTGNTSLFDPAPLHNFYTSK 300
DB 241 FSEFPDMLSDVRSQTKPLFTVGEYWSYDINKLHNYITKTGNTSLFDPAPLHNFYTSK 300
QY 301 SGGAFDMRTLMTNTLMKQPTLAFTVFNHDTPEGOALQSWDVPFKPLAYAFILTRQEG 360
DB 301 SGGAFDMRTLMTNTLMKQPTLAFTVFNHDTPEGOALQSWDVPFKPLAYAFILTRQEG 360
QY 361 YPCVFYGYGYIPQVNIPLSKSKIDPLIARRDYAVGTHDYSIDIGWTRREGVTEKP 420
DB 361 YPCVFYGYGYIPQVNIPLSKSKIDPLIARRDYAVGTHDYSIDIGWTRREGVTEKP 420
QY 421 GSGALALITDPGSGKMYVKGQAHGKVFYDLTGKRSPTVTINSDGWGEFKNQGSVSVW 480
DB 421 GSGALALITDPGSGKMYVKGQAHGKVFYDLTGKRSPTVTINSDGWGEFKNQGSVSVW 480
QY 481 VPRKTVSTIARPIITTRPWTGEPFRWTEPRLVAM 514
DB 481 VPRKTVSTIARPIITTRPWTGEPFRWTEPRLVAM 514

RESULT 15
US-10-025-648-3
Sequence 3, Application US/10025648
Publication No. US20030064908A1
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik

Svendsen, Allan
Borchert, Torben Vedel
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EFO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/025,648
FILING DATE: 19-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/600,656
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lambilife, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318, 204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-025-648-3

Query Match 97.6%; Score 2780; DB 12; Length 514;
Best Local Similarity 98.1%; Pred. No. 8.6e-250;
Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 1 AAPNGTMMQYFEWYLPDDGTLMTKVANEANNLSLIGITLMLPYPAYKGTSRSDVGQVY 60
DB 1 AAPNGTMMQYFEWYLPDDGTLMTKVANEANNLSLIGITLMLPYPAYKGTSRSDVGQVY 60
QY 61 DLYDGEFNOKGTVTKTKGTAQYLOAIQAAHAAQVYADVDFHKGADGTEWDAVE 120
DB 61 DLYDGEFNOKGAVTKTKGTAQYLOAIQAAHAAQVYADVDFHKGADGTEWDAVE 120
QY 121 VNPSDRNOEISGTQYIOAWTKFDPFGKNTYSSFFKRWYHFDGVDMDESKLSRIYKFRG 180
DB 121 VNPSDRNOEISGTQYIOAWTKFDPFGKNTYSSFFKRWYHFDGVDMDESKLSRIYKFRG 180
QY 181 IGAAMDMEVDTENGNYDYLMATADLMDHPEVYTELKSGKMYVNTNIDGRDLDAVGHK 240
DB 181 IGAAMDMEVDTENGNYDYLMATADLMDHPEVYTELKSGKMYVNTNIDGRDLDAVGHK 240
QY 241 FSEFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTGNTSLFDPAPLHNFYTSK 300
DB 241 FSEFPDMLSDVRSQTKPLFTVGEYWSYDINKLHNYITKTGNTSLFDPAPLHNFYTSK 300
QY 301 SGGAFDMRTLMTNTLMKQPTLAFTVFNHDTPEGOALQSWDVPFKPLAYAFILTRQEG 360
DB 301 SGGAFDMRTLMTNTLMKQPTLAFTVFNHDTPEGOALQSWDVPFKPLAYAFILTRQEG 360
QY 361 YPCVFYGYGYIPQVNIPLSKSKIDPLIARRDYAVGTHDYSIDIGWTRREGVTEKP 420
DB 361 YPCVFYGYGYIPQVNIPLSKSKIDPLIARRDYAVGTHDYSIDIGWTRREGVTEKP 420
QY 421 GSGALALITDPGSGKMYVKGQAHGKVFYDLTGKRSPTVTINSDGWGEFKNQGSVSVW 480

Tue May 4 14:34:49 2004

us-10-644-187-6.rapb

Page 9

Db 421 GSGLAALITDGPQSKMYGKHQKVFYDLTGNSDPTTINSDDGGEFKVNGGSVSW 480
Cy 481 VPRKTVSTIARPIITRPMTGSEVWTEPRLVAM 514
Db 481 VPRKTVSTIAMSITTRPMTDEFWWTEPRLVAM 514

Search completed: May 3, 2004, 20:47:47
Job time : 41.0203 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:45:43 ; Search time 14.6161 Seconds
(without alignments)
3382.735 Million cell updates/sec

Title: US-10-644-187-6

Perfect score: 2847
Sequence: 1 AAPNGTMMQYFEMWLPDDG.....TTRPWTGEPVAKWTEPRLVAM 514

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96391526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2847	100.0	549	1 A54541	alpha-amylose (EC
2	2805	98.5	549	1 A24549	alpha-amylose (EC
3	2780	97.6	549	1 A24436	alpha-amylose (EC
4	2720.5	95.6	548	1 A185P	alpha-amylose (EC
5	1874.5	65.8	518	1 A27705	alpha-amylose (EC
6	1794.5	63.0	512	1 A185L	alpha-amylose (EC
7	1773.5	62.3	514	1 A185N	alpha-amylose (EC
8	1345.5	47.3	492	2 A2079	alpha-amylose (EC
9	1315	46.0	484	2 F98026	alpha-amylose (EC
10	1311	46.0	484	2 F98026	alpha-amylose (EC
11	1278.5	44.9	493	2 S15713	alpha-amylose (EC
12	1229	43.2	491	2 C66781	alpha-amylose (EC
13	1112.5	39.1	494	1 B45738	alpha-amylose (EC
14	1101.5	38.7	494	2 AD0751	alpha-amylose (EC
15	1078.5	37.9	495	2 AD3038	alpha-amylose (EC
16	1078.5	37.9	506	2 G98247	alpha-amylose (EC
17	1074.5	37.7	495	1 A45738	alpha-amylose (EC
18	1074.5	37.7	495	2 B90962	alpha-amylose (EC
19	1054.5	37.1	495	2 B85810	alpha-amylose (EC
20	354.5	12.5	217	2 A19506	alpha-amylose (EC
21	326.5	11.5	482	2 S31478	alpha-amylose (EC
22	313	11.0	713	1 A185G	alpha-amylose (EC
23	307	10.8	826	2 E96720	alpha-amylose (EC
24	307	10.8	1196	2 A29130	alpha-amylose (EC
25	302.5	10.6	440	2 S14958	alpha-amylose (EC
26	302	10.6	440	2 S09196	alpha-amylose (EC
27	300	10.5	713	2 A58800	alpha-amylose (EC
28	286	10.4	423	2 T09942	alpha-amylose (EC
29	295	10.4	428	2 T05521	alpha-amylose (EC

30	286.5	10.1	712	1 A185G3	cyclomalto-dextrin
31	286	10.0	718	1 A185M	cyclomalto-dextrin
32	284.5	10.0	713	1 A185G1	cyclomalto-dextrin
33	283	9.9	421	2 S10514	alpha-amylose (EC
34	282	9.9	718	1 A185G6	cyclomalto-dextrin
35	280	9.8	413	1 A185T3	alpha-amylose (EC
36	279.5	9.8	504	2 A55861	alpha-amylose (EC
37	278	9.8	718	1 A185G	cyclomalto-dextrin
38	277.5	9.7	439	2 T02956	alpha-amylose (EC
39	275.5	9.7	564	2 T41503	alpha-amylose (EC
40	274.5	9.6	438	2 S14957	alpha-amylose (EC
41	274.5	9.6	528	1 A185K	alpha-amylose (EC
42	273	9.6	710	2 S63598	cyclomalto-dextrin
43	272.5	9.6	428	2 S10013	alpha-amylose (EC
44	272.5	9.6	434	2 S12775	alpha-amylose (EC
45	271.5	9.5	437	2 S14956	alpha-amylose (EC

ALIGNMENTS

RESULT 1
A54541
alpha-amylose (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DN1792)
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Bacillus stearothermophilus
C:Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
C:Accession: A54541
R:Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
FEMS Microbiol. Lett. 77, 271-276, 1991
A:Title: Cloning of a chromosomal alpha-amylose gene from Bacillus stearothermophilus.
A:Reference number: A54541
A:Accession: A54541
A:Molecule type: DNA
A:Residues: 1-549 <OR>
A:Cross-references: GB:X59476
A:Experimental source: chromosomal DNA of strain DN1792
C:Comment: Alpha-amylose genes have been found on plasmids and in multiple copies on the C:Genetics:
A:Start codon: GTG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylose, amyloliquefaciens type: alpha-amylose core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F:1-34/Domain: signal sequence #status predicted <Sig>
F:35-549/Product: alpha-amylose #status predicted <Mat>
F:125-368/Domain: alpha-amylose core homology <Mat>
F:119/237/272/Binding site: calcium (Asp, Asp, His) #status predicted
F:266/298/365/Active site: Asp, Glu, Asp #status predicted
Query Match 100.0%; Score 2847; DB 1; Length 549;
Best local similarity 100.0%; Pred. No. 5.5e-198;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 AAPNGTMMQYFEMWLPDDGTLMTKYANEANNISGITLMLPPAYKTSRDVGYY 60
Db 35 AAPNGTMMQYFEMWLPDDGTLMTKYANEANNISGITLMLPPAYKTSRDVGYY 94
Cy 61 DLYDLGFNKGTVRTYGTGAQYLOAIQAAHAAGQVADVDFDKGADGTEWDAVE 120
Db 95 DLYDLGFNKGTVRTYGTGAQYLOAIQAAHAAGQVADVDFDKGADGTEWDAVE 154
Cy 121 VNSPDRNOEISGTYOIAQWTFPPGNGNTYSSFKRMVTFDGVMDDESKLSRIYFRG 180
Db 155 VNSPDRNOEISGTYOIAQWTFPPGNGNTYSSFKRMVTFDGVMDDESKLSRIYFRG 214
Cy 181 IGKAMDVEVDTEGNTYDLYADLMDHPEVVTLEKNKGKMYNTNTNIDGFRLDAYKHK 240
Db 215 IGKAMDVEVDTEGNTYDLYADLMDHPEVVTLEKNKGKMYNTNTNIDGFRLDAYKHK 274
Cy 241 FSPFPDLSTYRSQTKELFTVGEYWSYDINKLHANYTTKTGDMSLFDPALHKFTASK 300

Db 275 FSFPDMLSYRSQGRKPLFTVGEYMSYDINKLHNYITKTGDSLFDAPLHNKFTYASK 334
Qy 301 SGGAFFDMRTMTNTLMKDQPTLAATFVNDHDEPGQALQSVWDPWFKPLAYAFILTRQEG 360
Db 335 SGGAFFDMRTMTNTLMKDQPTLAATFVNDHDEPGQALQSVWDPWFKPLAYAFILTRQEG 394
Qy 361 YPCVFYGDYVGIPOYNIPSLKSKIDPLLIARDVAYGTQHDYLDHSDIIGWTRBGTEKP 420
Db 395 YPCVFYGDYVGIPOYNIPSLKSKIDPLLIARDVAYGTQHDYLDHSDIIGWTRBGTEKP 454
Qy 421 GSGALALITDGGSGKMMYVKGQKAGKVFYDLTGNSDPTVINSDGWGEFKVNGGSYSVW 480
Db 455 GSGALALITDGGSGKMMYVKGQKAGKVFYDLTGNSDPTVINSDGWGEFKVNGGSYSVW 514
Qy 481 VPRKTVSTIARPIITRPMTGEFVWTEPRLVAM 514
Db 515 VPRKTVSTIARPIITRPMTGEFVWTEPRLVAM 548

RESULT 2

A24549
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain NZ-3)
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Bacillus stearothermophilus
C>Date: 30-Jun-1988 #sequence revision 18-Aug-1995 #text_change 18-Jun-1999
C:Accession: A24549; 139501; 139770
R:Gray, G.L.; Mainzer, S.B.; Rey, M.W.; Jamsa, M.H.; Kindle, K.L.; Carmona, C.; Reguadt,
J. Bacteriol. 166, 635-643, 1986
A>Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearother
A:Reference number: A91817; MUID:86195857; PMID:3009417
A:Accession: A24549
A:Molecule type: DNA
A:Residues: 1-549 <GR>
A:Cross-references: GB:M13255; NID:G142512; PIDN:AAA22241.1; PID:G142513
A:Experimental source: genomic DNA of strain NZ-3
J:Satoh, H.; Nishida, H.; Isono, K.
J. Bacteriol. 170, 1034-1040, 1988
A>Title: Evidence for movement of the alpha-amylase gene into two phylogenetically dista
A:Reference number: 139501; MUID:86139156; PMID:3257753
A:Accession: 139501
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 536-549 <RS>
A:Cross-references: GB:M29577; NID:G142476; PIDN:AAA22225.1; PID:G142478
A:Experimental source: strain DY-5
A:Accession: 139770
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 536-549 <RE2>
A:Cross-references: GB:M29578; NID:G142484; PIDN:AAA22228.1; PID:G142486
A:Experimental source: strain 799
C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C:Genetics:
A:Start codon: GTG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F:1-34/Domain: signal sequence #status predicted <Sig>
F:35-549/Product: alpha-amylase #status predicted <AMV>
F:235-368/Domain: alpha-amylase core homology <AMY>
F:139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F:1268,298,365/Active site: Asp, Glu, Asp #status predicted

Qy 61 DLYDGEFNQGYTRKTKGYAQLQALQAAHAGMOYADVFVDHKGADGTEWDAVE 120
Db 95 DLYDGEFNQGYTRKTKGYAQLQALQAAHAGMOYADVFVDHKGADGTEWDAVE 154
Qy 121 VNPSDRNOISGTYOIAMTFKDFPGKNTYSSEFKMEWHEFDGVDWDSRKLSTIRYERG 180
Db 155 VNPSDRNOISGTYOIAMTFKDFPGKNTYSSEFKMEWHEFDGVDWDSRKLSTIRYERG 214
Qy 181 ICKAMPWEVDTENGNYDYLMYADLMDHPEVYTELKMGKRYVNTNIDGRDLAVGRIK 240
Db 215 ICKAMPWEVDTENGNYDYLMYADLMDHPEVYTELKMGKRYVNTNIDGRDLAVGRIK 274
Qy 241 FSFPDMLSYRSQGRKPLFTVGEYMSYDINKLHNYITKTGDSLFDAPLHNKFTYASK 300
Db 275 FSFPDMLSYRSQGRKPLFTVGEYMSYDINKLHNYITKTGDSLFDAPLHNKFTYASK 334
Qy 301 SGGAFFDMRTMTNTLMKDQPTLAATFVNDHDEPGQALQSVWDPWFKPLAYAFILTRQEG 360
Db 335 SGGAFFDMRTMTNTLMKDQPTLAATFVNDHDEPGQALQSVWDPWFKPLAYAFILTRQEG 394
Qy 361 YPCVFYGDYVGIPOYNIPSLKSKIDPLLIARDVAYGTQHDYLDHSDIIGWTRBGTEKP 420
Db 395 YPCVFYGDYVGIPOYNIPSLKSKIDPLLIARDVAYGTQHDYLDHSDIIGWTRBGTEKP 454
Qy 421 GSGALALITDGGSGKMMYVKGQKAGKVFYDLTGNSDPTVINSDGWGEFKVNGGSYSVW 480
Db 455 GSGALALITDGGSGKMMYVKGQKAGKVFYDLTGNSDPTVINSDGWGEFKVNGGSYSVW 514
Qy 481 VPRKTVSTIARPIITRPMTGEFVWTEPRLVAM 514
Db 515 VPRKTVSTIARPIITRPMTGEFVWTEPRLVAM 548

RESULT 3

A24436
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid pAT5
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Bacillus stearothermophilus
C>Date: 05-Jun-1987 #sequence revision 18-Aug-1995 #text_change 18-Jun-1999
C:Accession: A24436; 139777
R:Nakajima, R.; Imanaka, T.; Aiba, S.
J. Bacteriol. 163, 401-406, 1985
A:Reference number: A24436; MUID:85234394; PMID:3924897
A:Accession: A24436
A:Molecule type: DNA
A:Residues: 1-549 <NA>
A:Cross-references: GB:M11450
A:Experimental source: plasmid pAT5
A:Note: amino end of the mature protein also determined
R:Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Didrichsen, B.
Gene 96, 37-41, 1990
A>Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con
A:Reference number: 139772; MUID:91092499; PMID:2265757
A:Accession: 139777
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-45 <RS>
A:Cross-references: GB:M62638; NID:G142514; PIDN:AAA22242.1; PID:G142515
C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C:Genetics:
A:Gene: amys
A:Genome: Plasmid
A:Start codon: GTG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F:1-34/Domain: signal sequence #status predicted <Sig>
F:35-549/Product: alpha-amylase #status experimental <MAT>
F:235-368/Domain: alpha-amylase core homology <AMY>
F:139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F:1268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 97.6%; Score 2780; DB 1; Length 549;
 Best Local Similarity 98.1%; Pred. No. 3.8e-193;
 Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAPNGTMMQYFENYLPDDGTLMTKVANEANNLSLGLTALMLPPAYKTSRSDVGVGY 60
 DB 35 AAPNGTMMQYFENYLPDDGTLMTKVANEANNLSLGLTALMLPPAYKTSRSDVGVGY 94
 QY 61 DLYDGEFNQKGTATKTKGTAQYLOAIOAAHAAQMVYADVDFDKGADGTEWDAVE 120
 DB 95 DLYDGEFNQKGTATKTKGTAQYLOAIOAAHAAQMVYADVDFDKGADGTEWDAVE 154
 QY 121 VNBSDRNOEISGTQIOAWTKFDFPGRGNTYSSFKRWYHFDGVDMDSRKLRIYKRG 180
 DB 155 VNPSDRNOEISGTQIOAWTKFDFPGRGNTYSSFKRWYHFDGVDMDSRKLRIYKRG 214
 QY 181 IGRAMDMEVDTENGNYDYLMYADLMDHPEVYTELKNMGKYYVNTNIDGFRDLDAVGHK 240
 DB 215 IGRAMDMEVDTENGNYDYLMYADLMDHPEVYTELKNMGKYYVNTNIDGFRDLDAVGHK 274
 QY 241 FSFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITTKDGTSLFDAPLHKKFYTAK 300
 DB 275 FSFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITTKDGTSLFDAPLHKKFYTAK 334
 QY 301 SGAFPMRMTLMTNTLMKQOPTLAVTFVNDHTEPGALQSWVDPFMRPLAVAFILTRQEG 360
 DB 335 SGAFPMRMTLMTNTLMKQOPTLAVTFVNDHTEPGALQSWVDPFMRPLAVAFILTRQEG 394
 QY 361 YPCVFYGDYGIPOYNIPSLKSKIDPLIARDAVYGTQHDYLDHSDIIGWREGTEK 420
 DB 395 YPCVFYGDYGIPOYNIPSLKSKIDPLIARDAVYGTQHDYLDHSDIIGWREGTEK 454
 QY 421 GSGIALITDGPQSGKMYVQKHAKVYDITGNRSDVTITNSDGWGFKNQGSVSVW 480
 DB 455 GSGIALITDGPQSGKMYVQKHAKVYDITGNRSDVTITNSDGWGFKNQGSVSVW 514
 QY 481 VPKTIVSTIARPIITRPWTGEFVWTEPRLVAM 514
 DB 515 VPKTIVSTIARPIITRPWTGEFVWTEPRLVAM 548

RESULT 4

ALBSF alpha-amyase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DY-5) plasmid
 N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C/Species: Bacillus stearothermophilus
 C/Date: 30-Jun-1987 #sequence revision 30-Jun-1987 #text_change 16-Feb-1997
 C/Accession: A21999; B91999; A91804; A00845
 R/Author: H. Sasaki, T. Tsudoi, A. Yamagata, H.; Tsukagoshi, N.; Ueda, S.
 J. Biochem. 98, 95-103, 1985
 A/Title: Complete nucleotide sequence of a thermophilic alpha-amyase gene: homology bet
 A/Reference number: A91999; MUID:86008166; PMID:3876333
 A/Accession: A91999
 A/Molecule type: DNA
 A/Residues: 1-548 <1H>
 A/Cross-references: GB:X02769
 A/Experimental source: plasmid PH1300 from strain DY-5
 A/Accession: B91999
 A/Molecule type: protein
 A/Residues: 35-48 <1H2>
 R/Experimental source: strain DY-5
 R/Author: N. Tritant, S. Sasaki, T.; Takemura, T.; Ihara, H.; Idota, Y.; Yamagata,
 U. Biochem. 164, 1182-1187, 1985
 A/Title: Efficient synthesis and secretion of a thermophilic alpha-amyase by protein-pr
 A/Reference number: A91804; MUID:86059211; PMID:299073
 A/Accession: PBAM101
 A/Contents: PBAM101
 A/Molecule type: DNA
 A/Residues: 1-29, 'C', 31-75, 'W', 77-122 <TSU>
 C/Comment: Alpha-amyase genes have been found on plasmids and in multiple copies on the
 C/Genetics:
 A/Genome: plasmid

A/Start codon: GTG

C/Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A/Pathway: glycoen/starch degradation
 C/Superfamily: alpha-amyase, amyloliquefactins type; alpha-amyase core homology
 C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysacc
 F:1-33/Domain: signal sequence #status predicted <SIG>
 F:35-548/Product: alpha-amyase #status experimental <MAT>
 F:335-366/Domain: alpha-amyase core homology <AMY>
 F:139,237,212/Binding site: calcium (asp, asp, his) #status predicted
 F:268,298,365/Active site: asp, glu, asp #status predicted

Query Match 95.6%; Score 2720.5; DB 1; Length 548;
 Best Local Similarity 96.7%; Pred. No. 7.6e-189;
 Matches 497; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

QY 1 AAPNGTMMQYFENYLPDDGTLMTKVANEANNLSLGLTALMLPPAYKTSRSDVGVGY 60
 DB 35 AAPNGTMMQYFENYLPDDGTLMTKVANEANNLSLGLTALMLPPAYKTSRSDVGVGY 94
 QY 61 DLYDGEFNQKGTATKTKGTAQYLOAIOAAHAAQMVYADVDFDKGADGTEWDAVE 120
 DB 95 DLYDGEFNQKGTATKTKGTAQYLOAIOAAHAAQMVYADVDFDKGADGTEWDAVE 154
 QY 121 VNPSDRNOEISGTQIOAWTKFDFPGRGNTYSSFKRWYHFDGVDMDSRKLRIYKRG 180
 DB 155 VNPSDRNOEISGTQIOAWTKFDFPGRGNTYSSFKRWYHFDGVDMDSRKLRIYKRG 214
 QY 181 IGRAMDMEVDTENGNYDYLMYADLMDHPEVYTELKNMGKYYVNTNIDGFRDLDAVGHK 240
 DB 215 IGRAMDMEVDTENGNYDYLMYADLMDHPEVYTELKNMGKYYVNTNIDGFRDLDAVGHK 274
 QY 241 FSFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITTKDGTSLFDAPLHKKFYTAK 300
 DB 275 FSFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITTKDGTSLFDAPLHKKFYTAK 334
 QY 301 SGAFPMRMTLMTNTLMKQOPTLAVTFVNDHTEPGALQSWVDPFMRPLAVAFILTRQEG 360
 DB 335 SGAFPMRMTLMTNTLMKQOPTLAVTFVNDHTEPGALQSWVDPFMRPLAVAFILTRQEG 393
 QY 361 YPCVFYGDYGIPOYNIPSLKSKIDPLIARDAVYGTQHDYLDHSDIIGWREGTEK 420
 DB 394 YPCVFYGDYGIPOYNIPSLKSKIDPLIARDAVYGTQHDYLDHSDIIGWREGTEK 453
 QY 421 GSGIALITDGPQSGKMYVQKHAKVYDITGNRSDVTITNSDGWGFKNQGSVSVW 480
 DB 454 GSGIALITDGPQSGKMYVQKHAKVYDITGNRSDVTITNSDGWGFKNQGSVSVW 513
 QY 481 VPKTIVSTIARPIITRPWTGEFVWTEPRLVAM 514
 DB 514 VPKTIVSTIARPIITRPWTGEFVWTEPRLVAM 547

RESULT 5

A27705 alpha-amyase (EC 3.2.1.1) precursor - Bacillus sp.
 N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amyase
 C/Species: Bacillus sp.
 C/Date: 31-Mar-1989 #sequence revision 18-Aug-1995 #text_change 18-Jun-1999
 C/Accession: A27705
 R/Author: A. Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.
 Biochem. Biophys. Res. Commun. 151, 25-31, 1988
 A/Title: Nucleotide sequence of the maltohexase-producing amyase gene from an alkaloph
 A/Reference number: A27705; MUID:88162814; PMID:3258152
 A/Accession: A27705
 A/Molecule type: DNA
 A/Residues: 1-518 <TSU>
 A/Cross-references: GB:M18862; NID:g142496; PIDN:AAA22231.1; PID:g142497
 A/Experimental source: chromosomal DNA of strain 707
 A/Note: amino end of mature protein also determined
 C/Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.
 C/Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation
 C:Superfamily: alpha-amylase, amyloliquefaciens type, alpha-amylase core homology
 C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
 F:1-33/Domains: signal sequence #status predicted <SIG>
 F:34-518/Product: alpha-amylase #status experimental <MAM>
 F:236-369/Domains: alpha-amylase core homology <AMY>
 F:139,238,273/Binding site: calcium (Asn, Asp, His) #status predicted
 F:289,299,366/Active site: Asp, Glu, Asp #status predicted

Query Match 65.8%; Score 1874.5; DB 1; Length 518;
 Best Local Similarity 67.2%; Pred. No. 9,4e-128;
 Matches 321; Conservative 76; Mismatches 80; Indels 1; Gaps 1;
 5 NGTMMQYFENVLPDGLTMTKRVANEANNLSLGLTALMLPPAYKGRSRDPVGYDLYD 64
 39 NGTMMQYFENVLPDGLTMTKRVANEANNLSLGLTALMLPPAYKGRSRDPVGYDLYD 98
 65 LGFENQKGTATKTKYKTKAQTALQAAHAAQGVYADVDFHKGADGTEWDAVEVNS 124
 99 LGFENQKGTATKTKYKTKAQTALQAAHAAQGVYADVDFHKGADGTEWDAVEVNS 158
 125 DRNGEISGTQIQMTKTPDPFGKNTYSSFKRWYHEDGVDMESRPL-SRIKFKGICK 183
 159 NRNGEISGTQIQMTKTPDPFGKNTYSSFKRWYHEDGVDMESRPL-SRIKFKGICK 218
 184 AMDREVTENGNVDYLYADLDMDHPEVTELEKMGKMYNTNIDGFRLLDAVKHIFSF 243
 219 AMDREVTENGNVDYLYADLDMDHPEVTELEKMGKMYNTNIDGFRLLDAVKHIFSF 278
 244 FPDWLSVRSCTGKPLTGVGYMSYDINKLHNYITKTDGMSLFDAPLHNFKFTASKSG 303
 279 TRDWINHRSATYGMKPAVAFPMWNDIGALENYLOKNNHMSYFVDFLHNLNASKSG 338
 304 AFDRTMTNTLMQDQPLATVFNHDETFGQALQGVDPWFPEPLAAYAILTROEGYPC 363
 339 NYDRKRNIFNGVGRHPSHATFVDNDSQCEELBSFVEMWEPALATLTLREGYPS 398
 364 VFQDYGYIGFQYNTPLSKLTDPLILAPRDVAYGTQDYDSDITGWTREGTEKPSG 423
 399 VFQDYGYIGFQYNTPLSKLTDPLILAPRDVAYGTQDYDSDITGWTREGTEKPSG 458
 424 LAALITGPGGSKMYVYKQKAGKFFVDTLGNREGDTYINSDDGEFKVNGSGSVYV 481
 459 LATMSDAGGSKMFMFGKRNKAGQVMDITGNKIGYITINADGNGSVNGSGSVYV 516

RESULT 6

ALBBL
 alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis
 N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C:Species: Bacillus licheniformis
 C:Date: 30-Jun-1997 #sequence revision 24-Apr-1998 #text change 15-Sep-2000
 C:Accession: A91997, B24549, A51796, A21663, I39772, A26151, S53788, A00844
 R:Yukki, T.; Nomura, T.; Tetsuka, H.; Tsuboi, A.; Yamaguchi, N.; Uchida, S.
 J. Biochem. 98, 1147-1156, 1985
 A:Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amylase deduced from the DNA sequences.
 A:Reference number: A91997, MUID:86111694, PMID:2418011
 A:Accession: A91997
 A:Molecule type: DNA
 A:Residues: 1-162, 'R', 164-512 <YU>
 A:Cross-references: GB:X03236, NID:G39551, PIDN:CAA26981.1; PID:G39552
 A:Experimental source: ATCC 27811
 R:Gray, G.L.; Mainzer, S.E.; Rey, M.M.; Lamesa, M.H.; Kandle, K.L.; Carmona, C.; Reguadt,
 J. Bacteriol. 166, 635-643, 1985
 A:Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus
 A:Reference number: A91817, MUID:86195857, PMID:3009417
 A:Accession: B24549
 A:Molecule type: DNA
 A:Residues: 1-338, 'G', 340-348, 'S', 350-512 <GRA>
 A:Cross-references: GB:M13256, NID:G142510, PIDN:AAA22240.1; PID:G142511
 A:Experimental source: NCIB 8061
 R:Stephens, M.A.; Ortlepp, S.A.; Ollington, J.F.; McConnell, D.C.

J. Bacteriol. 158, 369-372, 1994
 A:Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase
 A:Reference number: A91796, MUID:84185455, PMID:6609154
 A:Accession: A91796
 A:Molecule type: DNA
 A:Residues: 1-104 <STB>
 A:Cross-references: GB:X01984, NID:G142432, PIDN:AAA22193.1; PID:G142433
 R:Stakoy, M.; Palva, I.
 J. Biochem. 145, 567-572, 1984
 A:Title: Isolation and the 5' end nucleotide sequence of Bacillus licheniformis alpha-amylase
 A:Reference number: A21663, MUID:85076654, PMID:6334606
 A:Accession: A21663
 A:Molecule type: DNA
 A:Residues: 1-3, 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', 82
 A:Experimental source: chromosomal DNA of ATCC 14580
 A:Note: the authors translated the codon CGT for residue 48 as Gly and GAC for residue 64
 R:Stakoy, M.; Palva, I.
 J. Bacteriol. 171, 2435-2442, 1989
 A:Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-independent
 A:Reference number: 139773, MUID:89213924, PMID:2540150
 A:Accession: 139774
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-28 <LMO>
 A:Cross-references: GB:M26412, NID:G341477, PIDN:AAA22237.1; PID:G516590
 R:Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
 Gene 96, 37-41, 1990
 A:Title: In vivo genetic engineering: homologous recombination as a tool for plasmid cont
 A:Reference number: 139772, MUID:91092499, PMID:2265757
 A:Accession: 139772
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-32, 'I', <JCR>
 A:Cross-references: GB:M26337, NID:G142498, PIDN:AAA22232.1; PID:G142499
 R:Kuhn, H.; Fietzek, P.P.; Lampen, J.O.
 J. Bacteriol. 149, 372-373, 1982
 A:Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: comparis
 A:Reference number: A26151, MUID:82098050, PMID:6172418
 A:Accession: A26151
 A:Molecule type: protein
 A:Residues: 30-37, 'E', 39-41, 'X', 43-47 <KDH>
 R:Macinus, M.; Wiegand, G.; Huber, R.
 J. Mol. Biol. 246, 545-558, 1995
 A:Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase at 2.
 A:Reference number: S53788, MUID:95182462, PMID:7877175
 A:Accession: S53788
 A:Molecule type: protein
 A:Residues: 1-220-227 <MAC>
 A:Note: sequence represents amino end of an internal fragment created by a single enzymat
 R:Macinus, M.; Wiegand, G.; Huber, R.
 submitted to the Brookhaven Protein Data Bank, July 1995
 A:Reference number: A65206; PDB:1BPL
 A:Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 32-210,222-511
 A:Note: these structural studies suggest 163 is a Leu rather than Arg
 R:Song, H.K.; Huang, K.Y.; Chang, C.; Sun, S.W.
 submitted to the Brookhaven Protein Data Bank, October 1996
 A:Reference number: A68860; PDB:1IVS
 A:Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-210,222-511
 C:Genetics:
 A:Gene: amyL
 A:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
 C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysacch
 F:1-29/Domains: signal sequence #status predicted <SIG>
 F:30-512/Product: alpha-amylase #status experimental <MAM>
 F:227-260/Domains: alpha-amylase core homology <AMY>
 F:103,229,264/Binding site: calcium (Asn, Asp, His) #status experimental
 F:260,290,357/Active site: Asp, Glu, Asp #status experimental

Query Match 63.0%; Score 1794.5; DB 1; Length 512;
 Best Local Similarity 65.0%; Pred. No. 5.6e-122;

Matches 316; Conservative 68; Mismatches 97; Indels 5; Gaps 2;

```
QY 1 AAPFGTMMQYFEWYLPDDGTLMTKYNANNNLSLIGTALMLPPAYKGTSSDVGYYV 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 29 AANLNGTLMQYFEWYMPNDGQMKRLQNDSSAYLAHGLTAWMI PPAYKGTSSQADVGAY 88
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 DLYDGEFNQKGTVTYKTYGTAQYLAQIAAAGQVADVPFKHGADSTEWADAVE 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 89 DLYDGEFNQKGTVTYKTYGTAQYLAQIAAAGQVADVPFKHGADSTEWADAVE 148
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 VNPSPDNQISGTYYQIQANTKEDPFGKNTYSSFKRWYHPGVDMDESRKLSRIYKTRG 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 149 VNPADENRVISGEHLIKAWTHFFPGRGSGTSDFKWYWHFPGTDMDESRKLSRIYKTRG 207
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 IGKAMPMEVDTERNGVDYLMYADLMDHPEVVTTELKWKWKVYNTNIDGFLDAVKIK 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 208 -GRAMMEVSNENGVNDYLMYADLMDHPEVVTTELKWKWKVYNTNIDGFLDAVKIK 266
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 FSPFPDMLSYVRSQTKPLFTVGEWYSDINKLHNTYTKDGTSLPDAPLHNFYDASK 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 267 FSPFLRDMVNVHVEKTKEMETVAEYQNDLGALENTKTNHNSVFDVPLHYCFHAAS 326
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 SGCAFPMRLTMTNLTMKDQPTLAVFVDNDHTEPGQALQSWDPMFKPLAVALITRREG 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 327 QGGGYDMRKLNSVTSKPELKAATVVDNDHTOPGQSLSTYQTMFKPLAVALITRREG 386
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 YPCVFYGYDYG---PQYNIPSLKSKIDPLIARRDYAGTQHDYLDHSDIIGWTRREG 417
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 387 YPCVFYGYDYG---PQYNIPSLKSKIDPLIARRDYAGTQHDYLDHSDIIGWTRREG 446
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 418 EKSGSLAALITDGPGRSKMYVKGQKAGKVFYDLTGNSDVTYVINSQMGKFNKGSV 477
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 447 SVANSGLAALITDGPGRSKMYVKGQKAGKVFYDLTGNSDVTYVINSQMGKFNKGSV 506
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 478 SVWVPR 483
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 507 SIYVOR 512
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 7

ALBISN
alpha-amylase (EC 3.2.1.1) precursor - *Bacillus amyloliquefaciens*

N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: *Bacillus amyloliquefaciens*
C/Date: 30-Nov-1980 #sequence revision 30-Jun-1987 #text_change 18-Jun-1999

C/Accession: A92389; A90307; I39756; I39763; A00843
R/Takkinen, K.; Petersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L
J. Biol. Chem. 258, 1007-1013, 1983
A/Title: Amino acid sequence of alpha-amylase from *Bacillus amyloliquefaciens* deduced fr
A/Reference number: A92389; MUID:83108808; PMID:6185474
A/Contents: PUB110
A/Accession: A92389

A/Molecule type: DNA
A/Residues: 1514 <TAK>
A/Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:G142428; PIDN:AAA221
Biochem. J. 185, 387-395, 1980
A/Title: Sequence of the N-terminal half of *Bacillus amyloliquefaciens* alpha-amylase.

A/Reference number: A90307; MUID:80241725; PMID:6156671
A/Accession: A90307
A/Molecule type: protein
A/Residues: 32-53, 'L', '55-63', 'L', '65-78', 'V', '80-83', 'S', '85-222 <CHU>
R/Palva, I.; Petersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Savyas, M.; Soderlund, H.;
Gene 15, 43-51, 1981
A/Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of t
A/Reference number: I39756; MUID:82051296; PMID:6170539
A/Accession: I39756

A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-96 <RBS>
A/Cross-references: EMBL:V00092; NID:G39297; PIDN:CAA23430.1; PID:G39298
R/Rohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karenen, S.
Gene 59, 161-170, 1987

A/Title: Efficient secretion of *Bacillus amyloliquefaciens* alpha-amylase cells by its ow

A/Reference number: I39763; MUID:8817952; PMID:2830166
A/Accession: I39763
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-39 <R2>
A/Cross-references: GB:M18424; NID:G142430; PIDN:AAA22192.1; PID:G142431
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F/1-31/Domain: signal sequence #status predicted <Sig>
F/32-514/Product: alpha-amylase #status predicted <MP>
F/122-362/Domain: alpha-amylase core homology <AM>
F/133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted
F/262,292,359/Active site: Asp, Glu, Asp #status predicted

Query Match 62.3%; Score 1773.5; DB 1; Length 514;
Best Local Similarity 65.4%; Pred. No. 1,8e-120;
Matches 316; Conservative 57; Mismatches 105; Indels 5; Gaps 2;

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QY 5 NGTMMQYFEWYLPDDGTLMTKYNANNNLSLIGTALMLPPAYKGTSSDVGYYV 64
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 33 NGTMMQYFEWYLPDDGTLMTKYNANNNLSLIGTALMLPPAYKGTSSDVGYYV 92
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 65 LGSEFNQKGTVTYKTYGTAQYLAQIAAAGQVADVPFKHGADSTEWADAVEVNS 124
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 93 LGSEFNQKGTVTYKTYGTAQYLAQIAAAGQVADVPFKHGADSTEWADAVEVNS 152
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 125 DRNDEISGTYYQIQANTKEDPFGKNTYSSFKRWYHPGVDMDESRKLSRIYKTRG 184
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 153 DRNDEISGTYYQIQANTKEDPFGKNTYSSFKRWYHPGVDMDESRKLSRIYKTRG 212
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 185 DMWEVDTERNGVDYLMYADLMDHPEVVTTELKWKWKVYNTNIDGFLDAVKIK 244
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 213 DMWEVDTERNGVDYLMYADLMDHPEVVTTELKWKWKVYNTNIDGFLDAVKIK 272
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 245 PDMLSYRSQTKPLFTVGEWYSDINKLHNTYTKDGTSLPDAPLHNFYDASK 304
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 273 PDMLSYRSQTKPLFTVGEWYSDINKLHNTYTKDGTSLPDAPLHNFYDASK 332
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 305 FDKMTLNTNLTMKDQPTLAVFVDNDHTEPGQALQSWDPMFKPLAVALITRREG 364
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 333 FDKMTLNTNLTMKDQPTLAVFVDNDHTEPGQALQSWDPMFKPLAVALITRREG 392
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 365 FYGYGYG---PQYNIPSLKSKIDPLIARRDYAGTQHDYLDHSDIIGWTRREG 420
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 393 FYGYGYG---PQYNIPSLKSKIDPLIARRDYAGTQHDYLDHSDIIGWTRREG 451
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 GSGALAALITDGPGRSKMYVKGQKAGKVFYDLTGNSDVTYVINSQMGKFNKGSV 480
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 452 GSGALAALITDGPGRSKMYVKGQKAGKVFYDLTGNSDVTYVINSQMGKFNKGSV 511
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 481 VPR 483
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 512 VOK 514
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 8

AH2079
alpha-amylase (imported) - *Nostoc* sp. (strain PCC 7120)

C/Species: *Nostoc* sp. PCC 7120
A/Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence revision 14-Dec-2001 #text_change 09-Dec-2002

C/Accession: AH2079
R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A/Reference number: AB1807; MUID:21595285; PMID:11759840
A/Accession: AH2079
A/Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-492 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA073889.1; PID:g17131281; GSPDB:GN00179
 A:Experimental source: strain FCC 7120
 A:Genetics:
 A:Gene: alr2190
 C:Superfamily: alpha-amylase, amy1oliquefaciens type; alpha-amylase core homology

Query Match 47.3%; Score 1345.5; DB 2; Length 492;
 Best Local Similarity 52.8%; Pred. No. 1.5e-89;
 Matches 261; Conservative 67; Mismatches 147; Indels 19; Gaps 7;

```

QY 2 APPNGTMOYFEWYLPDDGTLMTKVAANEANNTSLGITLMLPPAYKGTSSRSDVGVYDLYD 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 AONKGTMOYFHWYIENDGNLMSKVEASAPELADAGFTAMMLPPAYKGPAGSFDVGVY 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 DLYDLGEPNOKGTFRKTKYGAQYLOAIQAAHAGQVYADVFPKHGGADGTEWDAVE 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 DLFDLGEPNOKGSVTRKTKGTROQYLDVAVSLQTHGLQYADAVLNHKGADAVETPKATP 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 VNPSPDNQISGTQYQIANTKDFPGRGNTYSSFKRWYHEDGVWDG--SRKLSRIYKF 178
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 122 FPDDDLNPKRGIGDITKTHYFPGROKYSNFEMHMHFDVAVYENNSGDRSTVLL 181
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 179 RG:GRKAMDVEVDENGNVYDLYADLDMDHPEVTELKRWGKMYNTNIDGFRDVAH 238
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 182 E--GKRFDDYVALEKRNFAVLMGCDLDPNENWVRGEVTVWGKCCDITTKVDFRIDAIKH 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 239 IKFSFPPMLSVYRSQTKRPLFTVGEYMSYDINKLHNITTKDGTMSLFPADLINKFYTA 298
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 240 ISTWPFPEWIDALERHAGDLPFVGEYVYNDINTLIMYADAVARGKMSYFVDVLIHNFHOA 299
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 299 SSSGGAFFDRITLMTNLMKDOPFLAVTFVDNHDTEPGALQSWDPMFKPLAVAFILTRQ 358
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 300 SSSGGNYDRRIIDGTMMQGRPHAVTFVENHDSQPLQLSVVEBWFPELXAIILLRQ 359
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 359 EGYPCVFGYDYGIR-----QYNI--PSLSKIDPELLARRDAYGTGHDYLDHSD 407
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 360 EGYPCVFHADYGAEEYEDWGKDNRYNIFMPSHRWIIDKLILYARKHYAGPQYNLDHWN 419
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 408 IIGMTEEGTEKRGSLAALLIDGPGSKMYVYKQHAQKAYVDLTGNRSQDVTYINSQW 467
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 420 TIGMTILGDAHDH-QGMVAIVMSDSEGIKMEVEKNT--KIDILTEIKKAVYTNEGWM 476
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 468 GEFKVNAGSVSVWV 481
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 477 GEFRCIGGSYSVWV 490
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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RESULT 9

G95160
 alpha-amylase [imported] - Streptococcus pneumoniae (strain TIGR4)
 C:Species: Streptococcus pneumoniae
 C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #ext_change 24-Aug-2001
 C:Accession: G95160
 R:Retelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 nson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A.; Title: Complete Sequence of a Virulent Isolate of Streptococcus pneumoniae.
 A:Reference number: A95000; MUID:21357209; PMID:11463916
 A:Accession: G95160
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-484 <KUR>
 A:Cross-references: GB:AE005672; PIDN:AAK75480.1; PID:g14972868; GSPDB:GN00164; TIGR:SP4
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SP1382
 C:Superfamily: alpha-amylase, amy1oliquefaciens type; alpha-amylase core homology

Query Match 46.2%; Score 1315; DB 2; Length 484;

Best Local Similarity 50.7%; Pred. No. 2.3e-87;
 Matches 248; Conservative 73; Mismatches 158; Indels 10; Gaps 4;

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QY 5 NGTMOYFEWYLPDDGTLMTKVAANEANNTSLGITLMLPPAYKGTSSRSDVGVYDLYD 64
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 NOTLMQYFEWYLPDQGHMTRLAENAPHLAHLGISHWMPAPFAKATNEKDVGYYDLPD 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 65 LGEPNOKGTFRKTKYGAQYLOAIQAAHAGQVYADVFPKHGGADGTEWDAVEVAPS 124
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 LGEPNOKGTFRKTKYGAQYLOAIQAAHAGQVYADVFPKHGGADGTEWDAVEVAPS 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 125 DRNQSISGTQYQIANTKDFPGRGNTYSSFKRWYHEDGVWDGSRKLSRIYKFRGIGKA 184
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 123 DRIVEAGEPPTINGWSTFEDGRQDTYNGFHHMHFTGTDYDARKSKGITYLIGDNKG 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 185 WDNE--VDTENGNYDILMTADLDMDHPEVTELKRWGKMYNTNIDGFRDVAHGIKFS 242
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 183 WANBEIYDNGNNGYDLYADLDLDFKEPEVIONIYDADWFMTTGVAGFRDLAVKHIDSF 242
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 243 FFPDMLSVYRSQTKRPLFTVGEYMSYDINKLHNITTKDGTMSLFPADLINKFYTASKG 302
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 243 FMRNPFIDMKKYGDDFYVFGSEFNPDKKANLDYLEKTEHFDLVDRLHOMLFESQAG 302
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 303 GAFFMRLMTNLMKDOPFLAVTFVDNHDTEPGALQSWDPMFKPLAVAFILTRQEGVP 362
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 303 ANYDLRGIFDLSVLELKPDRAVTFVNDHTORGQALSTVEEMFKPAAVALILLRQDGLP 362
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 363 CVFYGYDYIR-QYNI-PSLSKIDPELLARRDAYGTGHDYLDHSDIIGMTEEGTEKRG 421
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 363 CVFYGYDYIR-QYNI-PSLSKIDPELLARRDAYGTGHDYLDHSDIIGMTEEGTEKRG 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 422 SGLAALITDGPSSKMYVYKQHAQKAYVDLTGNRSQDVTYINSQWGEFKNAGSVSVWV 481
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 421 SPLAIVLSNQGSKMSFVQGEWNTQTFVDLGNHGQYTLIDEGYGGPVSARSYSVW- 479
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 482 PRKTVSTI 490
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 480 ----AVNTI 484
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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RESULT 10

P98026
 alpha-amylase (EC 3.2.1.1) precursor [imported] - Streptococcus pneumoniae (strain R6)
 C:Species: Streptococcus pneumoniae
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #ext_change 02-Nov-2001
 C:Accession: P98026
 R:Hockins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Balitz, R.H.; Jastrunas, S.R.;
 A.; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A:Reference number: A97872; MUID:21429245; PMID:11544234
 A:Accession: P98026
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-484 <KUR>
 A:Cross-references: GB:AE007317; PIDN:AAJ00043.1; PID:g15458876; GSPDB:GN00174
 C:Genetics:
 A:Gene: amy
 C:Superfamily: alpha-amylase, amy1oliquefaciens type; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase

Query Match 46.0%; Score 1311; DB 2; Length 484;
 Best Local Similarity 50.5%; Pred. No. 4.5e-87;
 Matches 247; Conservative 74; Mismatches 158; Indels 10; Gaps 4;

```

QY 5 NGTMOYFEWYLPDDGTLMTKVAANEANNTSLGITLMLPPAYKGTSSRSDVGVYDLYD 64
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 NOTLMQYFEWYLPDQGHMTRLAENAPHLAHLGISHWMPAPFAKATNEKDVGYYDLPD 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 65 LGEPNOKGTFRKTKYGAQYLOAIQAAHAGQVYADVFPKHGGADGTEWDAVEVAPS 124
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```


Db 63 LGFENQKGTVRTKYGKREDYLOALQALKAGIOIPMAVDVNLNKAADHREAPQVIEVDE 122
QY 125 DRNOEISGTYOIQAMTKFDPGKNTYSSFKRWYHFDGVMDSEKSLRIYKFRIGKA 184
Db 123 DRTVELOEPFTINGMTSFTFDGRQDTYNGFHHMYHFTGTDYDAKSKSGIYLIDQDNKG 182
QY 185 MDWE--VDTENGVNDYLMYADLMDHDEVEVTELKNNKXVYVNTNIDGPRDLVHKIKRS 242
Db 183 MANDELVDNENGNVDYMDLDPKHEVLCQNIYDMADWMEFTIGVAGFELDAVKHIDSEF 242
QY 243 FFPDMLSYVSQTKPLFTVGEWYSYDINKLHNYITKTGDSMLPAPLHNKRYTASKSG 302
Db 243 FMRFFIDMEKEKGDDEYVFEFNSDKKANLDYLEKTEEHFDLVRLHQLNFEASQSG 302
QY 303 GAFPMRLMTNLTLMKQDPTLAVTFVNDHTEPGQALQSWDPMFKPLAYAFILTRQEGVP 362
Db 303 ANYDLRGITFDSLVLELPPDAVTFVNDHDTQGOALSTVEEMFKPAAYALILLRQDGLP 362
QY 363 CVFYGDYVYGP-QYNIPSLKSIDPLLIARDYAYGTQHDYLDHSDIIGWTRGTEKKG 421
Db 363 CVFYGDYVYGISGQYAOQDFKEILDRLAIRKDLAYGQNDYFPHANCIGWVRSGAENQ-- 420
QY 422 SGLAALLTDPGSKMYVYKQAHAKVFDLTGNRSPTVTINSDDGGEFKNKGSVSVW 481
Db 421 SPLAVLISNDQENSKSMFVGQEWNTQTFVDLQSHQGVITIDEGYGGQFVSARSVSW- 479
QY 482 PRKTTVSTI 490
Db 480 ----AVNTI 484

RESULT 11
S15713
alpha-amyase (EC 3.2.1.1) - *Bacillus circulans*
C:Species: *Bacillus circulans*
C:Date: 18-Feb-1994 #sequence_rev:10-Nov-1995 #text_change 22-Jun-1999
C:Accession: S15713
R:Marcel, T.
submitted to the EMBL Data Library, May 1991
A:Reference number: S15713
A:Accession: S15713
A:Molecule type: DNA
A:Residues: 1-493 <MAR>
A:Cross-references: EMBL:X60779; NID:G39411; PIDD:CAA43194.1; PIDD:G39412
C:Gene: amyE
C:Genetics:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amyase, amyloliquefaciens type; alpha-amyase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:200-333/Domain: alpha-amyase core homology <Amr>

Query Match 44.8%; Score 1278.5; DB 2; Length 493;
Best Local Similarity 48.5%; Pred. No. 1e-84;
Matches 232; Conservative 84; Mismatches 159; Indels 3; Gaps 2;

QY 5 NGTMOYFEMYLPPDDGLMTKVNENNTLSLIGTILMLPRAVKGRSDVGYGVYDYL 64
Db 4 NHTMGOFFEMHLLAADGHHMKELAMAPELKAKGIDTVAVPPTKAVSAETGIVGVYDYL 63
QY 65 LGFENQKGTVRTKYGKTAQYLOALQAAHAGMAYADVDPHKGAGDGTGEMVDAVENPS 124
Db 64 LGFEPDQGTVRTKYGKQELIEALAEQKNGIAYVDLVNHNKAGADETEVFVIEVDN 123
QY 125 DRNGEISGTYOIQAMTKFDPGKNTYSSFKRWYHFDGVMDSEKSLRIYKFRIGKA 184
Db 124 DRTVEISPELISBMTYFTFGREDQYSSFKNSSEHNGTDFPARERTVFPRIAGENKK 183
QY 185 MDWEVDTENGVNDYLMYADLMDHDEVEVTELKNNKXVYVNTNIDGPRDLVHKIKRS 244
Db 184 MNEKVDTEFNGVNDYLMYADLMDHDEVEVTELKNNKXVYVNTNIDGPRDLVHKIKRS 243

QY 245 PDMLSYVSQTKPLFTVGEWYSYDINKLHNYITKTGDSMLPAPLHNKRYTASKSGA 304
Db 244 KEFAEMTKRKGQDFYVGEFNSNDLACREFLTVDYQIDLFPVSLATKLHESLKGKD 303
QY 305 FDMRLMTNLTLMKQDPTLAVTFVNDHTEPGQALQSWDPMFKPLAYAFILTRQEGVP 364
Db 304 FDLKSIDPDLTVQTHPFAVTFVNDHDSQPHALESWIGDMFKSAVALTLIRADGYPV 363
QY 365 FYGDYVYGP-QYNIPSLKSIDPLLIARDYAYGTQHDYLDHSDIIGWTRGTEKKG 422
Db 364 FYGDYVYGPGE-PVDGKEKELDILLARCKKAKAGEDEDFDHANTIGWVRGVEELGGS 422
QY 423 GLAALLTDPGSKMYVYKQAHAKVFDLTGNRSPTVTINSDDGGEFKNKGSVSVW 480
Db 423 GCAYVISGDDGEXRMFGEHRAGEVWVDLTKSCDDQITIEEDGMAFFHCGGGSVSW 480

RESULT 12
C66781
alpha-amyase (imported) - *Lactococcus lactis* subsp. *lactis* (strain IL1403)
C:Species: *Lactococcus lactis* subsp. *lactis*
C:Date: 23-Mar-2001 #sequence_rev:23-Mar-2001 #text_change 03-Aug-2001
C:Accession: C66781
R:Boillot, A.; Winkler, P.; Manger, S.; Jallion, O.; Malame, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ss
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: C66781
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-491 <STO>
A:Cross-references: GS:AE005176; PIDD:G12724224; PIDD:AAK05349.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: amyL
C:Superfamily: alpha-amyase, amyloliquefaciens type; alpha-amyase core homology

Query Match 43.2%; Score 1229; DB 2; Length 491;
Best Local Similarity 47.5%; Pred. No. 3.8e-81;
Matches 231; Conservative 73; Mismatches 176; Indels 6; Gaps 5;

QY 7 TMOYFEMYLPPDDGLMTKVNENNTLSLIGTILMLPRAVKGRSDVGYGVYDYL 65
Db 3 TILQAFEMYLPSDSQHMNNIKENIPDLQKLGFSGLMPPASKASGVEDYGYTDLFDL 62
QY 66 GEFNOKGTVRTKYGKTAQYLOALQAAHAGMAYADVDPHKGAGDGTGEMVDAVENPSD 125
Db 63 GEFNOKGTVRTKYGKQELIEALAEQKNGIAYVDLVNHNKAGADETEVTEA-DIAED 121
QY 126 RN-QEISGTYOIQAMTKFDPGKNTYSSFKRWYHFDGVMDSEKSLRIYKFRIGKA 184
Db 122 NHTMNIENKXVYVNTKTFPPRGQKDNVITMHNANTGIDYDRKQBELTEB--GHE 179
QY 185 MDWEVDTENGVNDYLMYADLMDHDEVEVTELKNNKXVYVNTNIDGPRDLVHKIKRS 244
Db 180 WDENSDENNNPDYLMGADLPFSVSEVLEKKGHMFSEMTKIDGPRDLVHKIKRS 239
QY 245 PDMLSYVSQTKPLFTVGEWYSYDINKLHNYITKTGDSMLPAPLHNKRYTASKSGA 304
Db 240 DKMLQKRAKQDLKFLYGEWYSDDKLELYLQSSSRILFVPLHFNKKESSNNGE 299
QY 305 FDMRLMTNLTLMKQDPTLAVTFVNDHTEPGQALQSWDPMFKPLAYAFILTRQEGVP 364
Db 300 FDMRLTLPHTLTLASQPELSTVFNHDTQEQALQSWIPAFKHAVALTLIRKKEPTV 359
QY 365 FYGDYVYGP-QYNIPSLKSIDPLLIARDYAYGTQHDYLDHSDIIGWTRGTEKKG 422
Db 360 FWDGTYGIPSHNVNDVGNLNTMLARKOSFLENDPDPDILIGWNTILKINKEGL 419
QY 425 AALLTDPGSKMYVYKQAHAKVFDLTGNRSPTVTINSDDGGEFKNKGSVSVWPRK 484
Db 420 SCILTNKNGSKMYVIDKAYAGKYIDLFGSHFIPITLDQGAGAFYVNDGSSVSWVD-K 478

Oy 485 TTVSSTI 490
Db 479 EIVSKI 484

RESULT 13

B45738
alpha-amylase (EC 3.2.1.1), cytosolic - *Salmonella typhimurium*
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: *Salmonella typhimurium*
C/Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C/Accession: B45738
R/Rana, M.; Kawagishi, I.; Mueller, V.; Khara, M.; Macnab, R.M.
J/Bacteriol. 174, 6644-6652, 1992
A/Title: *Escherichia coli* produces a cytoplasmic alpha-amylase, amyA.
A/Reference number: A45738; MUID:93015717; PMID:1400215
A/Accession: B45738
A/Molecule type: DNA
A/Residues: 1-494 <PAR>
A/Cross-references: GB:L01643; NID:G154043; PIDN:AAA27110.1; PID:G154045
C/Genetics:
A/Gene: amyA
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C/Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation
P/202-335/Domain: alpha-amylase core homology <AMY>
F/235,265,332/Active site: His, Glu, Asp #status predicted

Query Match 39.1%; Score 1112.5; DB 1; Length 494;
Best Local Similarity 44.0%; Pred. No. 1e-72;
Matches 216; Conservative 83; Mismatches 175; Indels 17; Gaps 5;

Oy 5 NGTMMQYFEMYPDDGTLMTKVAENNNLSLIGTALMLPPAYKTSRS-DVGYGVYDLY 63
Db 3 NPTLLQYFHWYYPDGGKLMSELAEADGLNDIGIMVWLPPACKGASGYSVGSDYDLF 62
Oy 64 DLGEFNQKTVTKYGTAKYQYLOAIQAHAAGMAYADVVDHKGADGTEWDAVENP 123
Db 63 DLGEFDQKTLTKYGDRLTALDALKONNIALVLDVVVNHKXGADKERRIRVQVNO 122
Oy 124 SDRNCEISGTQIOAWTKFDPFGKNTYSSFKRMWYHFDGVWDSRKLRIYFRG-I 181
Db 123 DDRTOIDNNIIECEGRTYTPPARAGQYSNFTWDHCSGDHLENPDDEGIFKIVNDYT 182
Oy 182 GKAMDEVDTEGNANDYLMYADLMDHPEVTELEKMGKMYVNTNIDGFLDAVKIKF 241
Db 183 GDGMNDQVDDDEGNNDYLMGENIDPRNNAVTELEIKYMARWMEQHCGRFLDAVKHPA 242
Oy 242 SFEPDWLSYRSQTKPLFTYGEYWSYDINKLHNTYTTDGTMSLFDAPLHNKFTASKS 301
Db 243 WYKEMIEHVQAVAPKPLFIYAEVWSHEVDKQITIDVDKTMFLDAPLQMKHEASRQ 302
Oy 302 GGAFMRITMTNTLTKDQPTLAVTFVNDHDEPGALQSWDPWPKPLAVAFILTRQGY 361
Db 303 GAEYDMRHTFTGLVEADFFAVTLVANHDTQLALBAPVBPMPKPLAYLILRENGV 362
Oy 362 PCVFGDYGYIP-----QYNIPSLSKIDPELLIARDVAVGTQHDYLDHSDITG 410
Db 363 PSVFYFDLIGASYEDNGENETCRVDMPIV-NQDLRLILARORFPHAGIOTLFFPHNPIA 421
Oy 411 WTRGGTEKPGSLALITDGPGRKMYVVGKQAHGXVYFDLTGRSDTVTINSQWGEF 470
Db 422 FRSRGTENP--GCYVVLNSNDGDEKTLILGDNVANKTWDRPFGSKRDEYVVTNDGEXATF 479
Oy 471 KVNAGSVSVVW 481
Db 480 FCNAGSVSVVW 490

RESULT 14
AD0751

Cytoplasmic alpha-amylase [imported] - *Salmonella enterica* subsp. *enterica* serovar Typh
C/Species: *Salmonella enterica* subsp. *enterica* serovar Typh
A/Note: this species has also been called *Salmonella typh*
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AD0751
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AD0751
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-494 <PAR>
A/Cross-references: GB:AL51382; PIDN:CAD05711.1; PID:G16503204; GSPDB:GN00176
C/Genetics:
A/Gene: STY2171
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 38.7%; Score 1101.5; DB 2; Length 494;
Best Local Similarity 44.0%; Pred. No. 6.3e-72;
Matches 216; Conservative 82; Mismatches 176; Indels 17; Gaps 5;

Oy 5 NGTMMQYFEMYPDDGTLMTKVAENNNLSLIGTALMLPPAYKTSRS-DVGYGVYDLY 63
Db 3 NPTLLQYFHWYYPDGGKLMSELAEADGLNDIGIMVWLPPACKGASGYSVGSDYDLF 62
Oy 64 DLGEFNQKTVTKYGTAKYQYLOAIQAHAAGMAYADVVDHKGADGTEWDAVENP 123
Db 63 DLGEFDQKTLTKYGDRLTALDALKONNIALVLDVVVNHKXGADKERRIRVQVNO 122
Oy 124 SDRNCEISGTQIOAWTKFDPFGKNTYSSFKRMWYHFDGVWDSRKLRIYFRG-I 181
Db 123 DDRTOIDNNIIECEGRTYTPPARAGQYSNFTWDHCSGDHLENPDDEGIFKIVNDYT 182
Oy 182 GKAMDEVDTEGNANDYLMYADLMDHPEVTELEKMGKMYVNTNIDGFLDAVKIKF 241
Db 183 GDGMNDQVDDDEGNNDYLMGENIDPRNNAVTELEIKYMARWMEQHCGRFLDAVKHPA 242
Oy 242 SFEPDWLSYRSQTKPLFTYGEYWSYDINKLHNTYTTDGTMSLFDAPLHNKFTASKS 301
Db 243 WYKEMIEHVQAVAPKPLFIYAEVWSHEVDKQITIDVDKTMFLDAPLQMKHEASRQ 302
Oy 302 GGAFMRITMTNTLTKDQPTLAVTFVNDHDEPGALQSWDPWPKPLAVAFILTRQGY 361
Db 303 GAEYDMRHTFTGLVEADFFAVTLVANHDTQLALBAPVBPMPKPLAYLILRENGV 362
Oy 362 PCVFGDYGYIP-----QYNIPSLSKIDPELLIARDVAVGTQHDYLDHSDITG 410
Db 363 PSVFYFDLIGASYEDNGENETCRVDMPIV-NQDLRLILARORFPHAGIOTLFFPHNPIA 421
Oy 411 WTRGGTEKPGSLALITDGPGRKMYVVGKQAHGXVYFDLTGRSDTVTINSQWGEF 470
Db 422 FRSRGTENP--GCYVVLNSNDGDEKTLILGDNVANKTWDRPFGSKRDEYVVTNDGEXATF 479
Oy 471 KVNAGSVSVVW 481
Db 480 FCNAGSVSVVW 490

RESULT 15

AD3038
alpha-amylase amyA [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
C/Species: *Agrobacterium tumefaciens*
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C/Accession: AD3038
R/Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayian, T.; Levy, R.; Li, M.; McClellan,
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Parry, M.; Gordon-Kamm, I.

ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AD3038
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1495 <KID>
A:Cross-references: GB:AB006889; PIDN:AAL4722.1; PID:917742354; GSPDB:GN00187
A:Experimental source: strain C58 (Duponc)
C:Genetics:
A:Gene: amya
A:Map position: linear chromosome
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 37.9%; Score 1078.5; DB 2; Length 495;
Best Local Similarity 44.4%; Pred. No. 2.9e-70;
Matches 218; Conservative 75; Mismatches 179; Indels 19; Gaps 6;

QY 7 TMMQYFEWYLPDDGTLMTKVAEANNLSLIGTALMLPAAKGTGRS-DVGYGYDYLDL 65
DB 5 TLQGFHMYPPDGKLMSEVAEKAESLAKMGITDVLPPAYKGAAGSVGYDFYDLFDL 64
QY 66 GEFNKGKTYRTYGTGAQYLAIAQAHAAGQYADYVFDHKGADGEMTDVAEAVNPSD 125
DB 65 GEFNKGKTYRTYGTGAQYLAIAQAHAAGQYADYVFDHKGADGEMTDVAEAVNPSD 124
QY 126 RMOEISGTYQIQAMTKFDPGKRGNTYSSPFKRWYHFDGVDMDSEKLSRIYKF--RGIG 182
DB 125 RTDIDDEDEPALAYTRFTTPGNGKSKFTINDLKCFSGVDHTEPTEDGIFRLVNEYGDG 184
QY 183 KAMDEVDTEGNGNYLYADLDMDHPEYVTELEKMGKMYVNTNIDGFRIDAVKHIFS 242
DB 185 E-WNEEVDQENGNFYLMGADVEFRRAVYEELKYMGRMLSEQYQVDGFRIDAAKHIPAW 243
QY 243 FFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNFYASKSG 302
DB 244 FFRDVGKMRRTVDPDLFVVAEYHBDLEALSKSYLELDKQMLDFVALHSHFDASKOG 303
QY 303 GAFDRTLMNTIMKDQPTLAFTVFNHDETEPGQALQSWDPEFKPLAFAFLTRQEGYP 362
DB 304 GDFDKRSIFDGLSIVSAVFPDHAFTLVNHDTPLOSLFAVEBPFKPLAFAFLTRQEGYP 363
QY 363 CWFYGDYVGI-----QYNIPSLKSIDPILLARDAYGTOHDYLDHSDILGW 411
DB 364 CVFYPLDFTSYTDTGNDGNEKYKIDIPALEC-LPKLIEKSRFPANGPOTDIFDASCTAF 422
QY 412 TREGTEKPSGLAALITDGPQSKMYVKQHAQKVPYDLTGNRSDVTYINSQMGGEFK 471
DB 423 IHHGTADAP--GCVVYMSNGEPGEKQADLGPFRAGSVWRDPLGHREHITLDESCKTFP 480
QY 472 VNGGSYSVWVP 482
DB 481 TNGGSYSVWVP 491

Search completed: May 3, 2004, 20:54:07
Job time : 15.6161 secs


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Db 95 DLYDLGFNQKGVTRTKYGTAKQYLQAIQAHAAGQVYADVDFDHKGADGTEWDAVE 154
Qy 121 VNPSPDRNOEISGTQYQIQAMTKFDPPGRGNTYSSFKRMWYHFDGVDMDSEKLSRIYKFRG 180
Db 155 VNPSPDRNOEISGTQYQIQAMTKFDPPGRGNTYSSFKRMWYHFDGVDMDSEKLSRIYKFRG 214
Qy 181 ICKAMDWEVDTENGNYDYLYATADLMDHPEVYTELKWGKKYVNTTINDGRDLAVGHIK 240
Db 215 ICKAMDWEVDTENGNYDYLYATADLMDHPEVYTELKWGKKYVNTTINDGRDLAVGHIK 274
Qy 241 FSPFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHNFYTASK 300
Db 275 FSPFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHNFYTASK 334
Qy 301 SGAFDMRTMTNTLMKQOPTLAVTFVNDHTEPQALQSWVDWPFKFLAYAFILTRQEG 360
Db 335 SGAFDMRTMTNTLMKQOPTLAVTFVNDHTEPQALQSWVDWPFKFLAYAFILTRQEG 394
Qy 361 YPCVYGYDYGGIPQYNIPLSKSIDPLLIARDYAVGTQHDYLDHSDIIGWTRGCTEKP 420
Db 395 YPCVYGYDYGGIPQYNIPLSKSIDPLLIARDYAVGTQHDYLDHSDIIGWTRGCTEKP 454
Qy 421 GSGLAALITDGPQSKMNVGKQHAGKVFYDLTGNSDTVTINSQWGEFKNQGSVSV 480
Db 455 GSGLAALITDGPQSKMNVGKQHAGKVFYDLTGNSDTVTINSQWGEFKNQGSVSV 514
Qy 481 VPKRTVSTIARPIITRPWTGFEVATBRLVAM 514
Db 515 VPKRTVSTIARPIITRPWTGFEVATBRLVAM 548
```

RESULT 2

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Q9KMY6 PRELIMINARY: PRT; 549 AA.
ID 09KMY6
AC 09KMY6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amyase (EC 3.2.1.1).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US100;
RA Beijer S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y17557; CAB351.7.1; -.
DR PIR; A54541; A54541.
DR HSSP; P06278; IVUS.
DR GO; GO:0004556; F:alpha-amyase activity; IEA.
DR GO; GO:0016798; F:hydrolyase activity; acting on glycosyl bonds; IEA.
DR InterPro; IPR006589; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006589; A:alpha-amy1_cat.
DR InterPro; IPR006589; A:alpha-amy1_cat_sub.
DR Pfam; PF00128; G:Glyco_hydro_13.
DR PRINTS; PR00110; alpha-amyase; 1.
DR SMART; SM00642; Amyy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 549 AA; 62582 NM; 8DA3B66DF9120BCE CRC64;
```

Query Match 98.7%; Score 2811; DB 2; Length 549;
Best Local Similarity 99.0%; Pred. No. 2, 5e-184;
Matches 509; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
Qy 1 AAPNGTMQYFEWYLPDDGTLMTKYANANNLSIGITATLWLPAYKGTSSDVGYGY 60
Db 35 AAPNGTMQYFEWYLPDDGTLMTKYANANNLSIGITATLWLPAYKGTSSDVGYGY 94
Qy 61 DLYDLGFNQKGVTRTKYGTAKQYLQAIQAHAAGQVYADVDFDHKGADGTEWDAVE 120
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Db 95 DLYDLGFNQKGVTRTKYGTAKQYLQAIQAHAAGQVYADVDFDHKGADGTEWDAVE 154
Qy 121 VNPSPDRNOEISGTQYQIQAMTKFDPPGRGNTYSSFKRMWYHFDGVDMDSEKLSRIYKFRG 180
Db 155 VNPSPDRNOEISGTQYQIQAMTKFDPPGRGNTYSSFKRMWYHFDGVDMDSEKLSRIYKFRG 214
Qy 181 ICKAMDWEVDTENGNYDYLYATADLMDHPEVYTELKWGKKYVNTTINDGRDLAVGHIK 240
Db 215 ICKAMDWEVDTENGNYDYLYATADLMDHPEVYTELKWGKKYVNTTINDGRDLAVGHIK 274
Qy 241 FSPFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHNFYTASK 300
Db 275 FSPFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHNFYTASK 334
Qy 301 SGAFDMRTMTNTLMKQOPTLAVTFVNDHTEPQALQSWVDWPFKFLAYAFILTRQEG 360
Db 335 SGAFDMRTMTNTLMKQOPTLAVTFVNDHTEPQALQSWVDWPFKFLAYAFILTRQEG 394
Qy 361 YPCVYGYDYGGIPQYNIPLSKSIDPLLIARDYAVGTQHDYLDHSDIIGWTRGCTEKP 420
Db 395 YPCVYGYDYGGIPQYNIPLSKSIDPLLIARDYAVGTQHDYLDHSDIIGWTRGCTEKP 454
Qy 421 GSGLAALITDGPQSKMNVGKQHAGKVFYDLTGNSDTVTINSQWGEFKNQGSVSV 480
Db 455 GSGLAALITDGPQSKMNVGKQHAGKVFYDLTGNSDTVTINSQWGEFKNQGSVSV 514
Qy 481 VPKRTVSTIARPIITRPWTGFEVATBRLVAM 514
Db 515 VPKRTVSTIARPIITRPWTGFEVATBRLVAM 548
```

RESULT 3

```
P71034 PRELIMINARY: PRT; 521 AA.
ID P71034
AC P71034;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amyase precursor.
OS Bacillus sp. MK 716.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=54116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MK 716;
RA Sidhu G.S., Chakrabarti T.;
RL Molecular cloning and expression of the gene encoding for
RT thermolabile alpha-amyase of a thermophilic bacterial isolate.
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75445; AAB18785.1; -.
DR HSSP; P06278; IVUS.
DR GO; GO:0004556; F:alpha-amyase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; A:alpha-amy1_cat.
DR InterPro; IPR006589; A:alpha-amy1_cat_sub.
DR InterPro; IPR006046; G:Glyco_hydro_13.
DR Pfam; PF00128; G:Glyco_hydro_13.
DR PRINTS; PR00110; alpha-amyase; 1.
DR SMART; SM00642; Amyy; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 521 AA; 59311 NM; 5612A88596D922E1 CRC64;
```

Query Match 93.4%; Score 2658; DB 2; Length 521;
Best Local Similarity 99.2%; Pred. No. 7, 1e-174;
Matches 480; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy 1 AAPNGTMQYFEWYLPDDGTLMTKYANANNLSIGITATLWLPAYKGTSSDVGYGY 60
Db 35 AAPNGTMQYFEWYLPDDGTLMTKYANANNLSIGITATLWLPAYKGTSSDVGYGY 94
Qy 61 DLYDLGFNQKGVTRTKYGTAKQYLQAIQAHAAGQVYADVDFDHKGADGTEWDAVE 120
```

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Db 95 DLYDGEFNQGAIVTKYGTQAQYLOALIOAAHAAQMVYADVDFDHKGADGTEWDAVE 154
Qy 121 VNPSPRNOEISGTQYQIOAMTKFDPFGRGNTYSSFFKRWYHFDGVDMDSRLSLIYKRG 180
Db 155 VNPSPRNOEISGTQYQIOAMTKFDPFGRGNTYSSFFKRWYHFDGVDMDSRLSLIYKRG 214
Qy 181 ICKAMDWEVDTENGYVYLYMADLMDHPEVTELEKMGKMYVNTTINIDGFRIDAVGHIK 240
Db 215 ICKAMDWEVDTENGYVYLYMADLMDHPEVTELEKMGKMYVNTTINIDGFRIDAVGHIK 274
Qy 241 SFPPDMWLSYRSQGTGKPLFTVGEWYSDINKLHNYITKTGDMSLFDAPLHNNFYTASG 300
Db 275 SFPPDMWLSYRSQGTGKPLFTVGEWYSDINKLHNYITKTGDMSLFDAPLHNNFYTASG 334
Qy 301 SGAFDMRTLMTNTLMKQDPTLAVTFVNDHDEPQALQSWDPMFKPLAVAFILTRQEG 360
Db 335 SGAFDMRTLMTNTLMKQDPTLAVTFVNDHDEPQALQSWDPMFKPLAVAFILTRQEG 394
Qy 361 YPCVFGDYGIPOYNIPLSKSIDPILARDDYAGTQHDYLDHSDIIGWTRGCTEK 420
Db 395 YPCVFGDYGIPOYNIPLSKSIDPILARDDYAGTQHDYLDHSDIIGWTRGCTEK 454
Qy 421 GGLAALITDPGGSKMYVKGKHAQVYFDLTGNRSDPTVINSQMGSEFKVNGSVW 480
Db 455 GGLAALITDPGGSKMYVKGKHAQVYFDLTGNRSDPTVINSQMGSEFKVNGSVW 514
Qy 481 VPRK 484
Db 515 VPRR 518

RESULT 4
059222 PRELIMINARY; PRT; 613 AA.
ID 059222;
AC 059222;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE Alpha-amyase (EC 3.2.2.1).
GN AMY.
OS Bacillus sp. TS-23.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=38441;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TS-23;
RA Lin U.-L., Chu W.S., Hsu W.H.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
EMBL: U22045; AAA63900.1; -.
HSSP: P06278; IVOS.
DR GO:GO:0004556; F:alpha-amyase activity; IEA.
DR GO:GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO:GO:000877; F:purine nucleosidase activity; IEA.
DR GO:GO:000575; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_ami_1_cat.
DR InterPro: IPR006046; Glyco_hydro_13.
DR InterPro: IPR006045; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amyase; 1.
DR PRINTS: PRO0110; ALPHAMYLASE.
DR PRODOM: PD001568; CBD_4; 1.
DR SMART: SM00642; Amy; 1.
DR GlycoSite: Hydrolase.
SQ SEQUENCE 613 AA; 69537 MW; 14684A30FC2895E8 CRC64;

Query Match 84.4%; Score 2404; DB 2; Length 613;
Best Local Similarity 84.2%; Pred. No. 2.2e-156;
Matches 43; Conservative 31; Mismatches 50; Indels 0; Gaps 0;
```

```
Db 33 APINETMOYFEMDLNDGTLMTKVNANLSSLGITLMLPAPYKGTSGSDVGYVD 92
Qy 62 LYDGEFNQGAIVTKYGTQAQYLOALIOAAHAAQMVYADVDFDHKGADGTEWDAVE 121
Db 93 LYDGEFNQGAIVTKYGTQAQYLOALIOAAHAAQMVYADVDFDHKGADGTEWDAVE 152
Qy 122 NPSDRNOEISGTQYQIOAMTKFDPFGRGNTYSSFFKRWYHFDGVDMDSRLSLIYKRG 181
Db 153 NPSDRNOEISGTQYQIOAMTKFDPFGRGNTYSSFFKRWYHFDGVDMDSRLSLIYKRG 212
Qy 182 GKAMDWEVDTENGYVYLYMADLMDHPEVTELEKMGKMYVNTTINIDGFRIDAVGHIK 241
Db 213 GKAMDWEVDTENGYVYLYMADLMDHPEVTELEKMGKMYVNTTINIDGFRIDAVGHIK 272
Qy 242 SFPPDMWLSYRSQGTGKPLFTVGEWYSDINKLHNYITKTGDMSLFDAPLHNNFYTASG 301
Db 273 SFPPDMWLSYRSQGTGKPLFTVGEWYSDINKLHNYITKTGDMSLFDAPLHNNFYTASG 332
Qy 302 SGAFDMRTLMTNTLMKQDPTLAVTFVNDHDEPQALQSWDPMFKPLAVAFILTRQEG 361
Db 333 SGAFDMRTLMTNTLMKQDPTLAVTFVNDHDEPQALQSWDPMFKPLAVAFILTRQEG 392
Qy 362 PCVFGDYGIPOYNIPLSKSIDPILARDDYAGTQHDYLDHSDIIGWTRGCTEK 421
Db 393 PCVFGDYGIPOYNIPLSKSIDPILARDDYAGTQHDYLDHSDIIGWTRGCTEK 452
Qy 422 SGLAALITDPGGSKMYVKGKHAQVYFDLTGNRSDPTVINSQMGSEFKVNGSVW 481
Db 453 SGLAALITDPGGSKMYVKGKHAQVYFDLTGNRSDPTVINSQMGSEFKVNGSVW 512
Qy 482 PKRTVSTIARPIITRPTGSEFVWTEPRIVAN 514
Db 513 AKTSNVTFTVNNATTSQGVVYVANIPELGNW 545

RESULT 5
082839 PRELIMINARY; PRT; 516 AA.
ID 082839;
AC 082839;
DT 01-NOV-1998 (TREMREL. 08, Created)
DT 01-NOV-1998 (TREMREL. 08, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE "Improved thermostability of a Bacillus alpha-amyase by deletion of an arginine-glycine residue is caused by enhanced calcium binding."
GN Ozaki K., Ito S.;
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-1378;
RA MEDLINE=98342036; PubMed=9675143;
RA Igataishi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T.,
RA Ozaki K., Ito S.;
RT "Improved thermostability of a Bacillus alpha-amyase by deletion of an arginine-glycine residue is caused by enhanced calcium binding."
RL Biochem. Biophys. Res. Commun. 248:372-377(1998).
DR EMBL: AB008763; BA032451.1; -.
DR HSSP: P06278; IVOS.
DR GO:GO:0004556; F:alpha-amyase activity; IEA.
DR GO:GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_ami_1_cat.
DR InterPro: IPR006046; Glyco_hydro_13.
DR InterPro: IPR006045; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amyase; 1.
DR PRINTS: PRO0110; ALPHAMYLASE.
DR SMART: SM00642; Amy; 1.
SQ SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;

Query Match 67.1%; Score 1910.5; DB 2; Length 516;
Best Local Similarity 66.8%; Pred. No. 1.1e-122;
Matches 329; Conservative 69; Mismatches 79; Indels 1; Gaps 1;
```

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2 APNETMOYFEMDLNDGTLMTKVNANLSSLGITLMLPAPYKGTSGSDVGYVD 61
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5 NGTMOYFEMDLNDGTLMTKVNANLSSLGITLMLPAPYKGTSGSDVGYVD 64
```

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Db      37 NGTMQVPEHMLPNDGHNMRRLDDAANKSKGTTAVWIPAMGTSQNDVGCAVLYD 96
Qy      65 LGFENQKGTVRTKTKYGAQYLOAIQAAMAGMAYADVDPDKGADGTEWDAVEVNS 124
Db      97 LGFENQKGTVRTKTKYGAQYLOAIQAAMAGMAYADVDPDKGADGTEWDAVEVNS 156
Qy      125 DRNGEISGTQIOATKTFDPGRGNTYSSFKRWYHPDGVNDSSRL-SRIYFRGIGK 183
Db      157 NRNGEISGTQIOATKTFDPGRGNTYSSFKRWYHPDGVNDSSRL-SRIYFRGIGK 216
Qy      184 AMDVEVDIENGNDYLYMADLDMDHPEVTELEKMGKVVNTTIDGFRDAVGHKFSF 243
Db      217 AMDVEVDIENGNDYLYMADLDMDHPEVTELEKMGKVVNTTIDGFRDAVGHKFSF 276
Qy      244 FPDMLSYRSQGTGRLFTVGEVMSYDINKLNYITKDGIMSLEDAPLHNKFTYASKSG 303
Db      277 TRDWLTHVRNTTGGKMEFAVAFKNDLAIENYLNKTSWNHVSFVPLHYNLYNASSSG 336
Qy      304 AFDMKTLTNTLMKDOPTLAVTVFVNDHDEPGALQSWVDPMFKPLAVAFILTRQSGYPC 363
Db      337 YFDMRNINGSVVOGHPHATVFDVNDHDSQGEALLESFVSQFPLALITREOGYPS 396
Qy      364 VFYGDYIGIPQYINPSLSKSIDPELLIARDYAVGTQHDYLDHSDIIGWTRGSGTEKFGSG 423
Db      397 VFYGDYIGIPTHGVPSMSKSIDPELLIARDYAVGTQHDYLDHSDIIGWTRGSGSHPSNG 456
Qy      424 LAALITDPPGSKMNYVKGQHAKGVFDLTGNSDVTITNSDGEFKVNGSVVW 481
Db      457 LATIMSDDPGSKMNYVKGQHAKGVFDLTGNSDVTITNSDGEFKVNGSVVW 514

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RESULT 6

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Q9A054 ID 09A054 PRELIMINARY; PRT; 533 AA.
AC Q9A054;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Alpha-amyase.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,
RA Park K.-H.;
RT "Cloning of maltopentase-producing amyase from Bacillus megaterium
RT KSM B-404."
RT Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF220440; AA00598.1; -
DR HSSP; P06278; IYUS.
DR GO; GO:0004556; F:alpha-amyase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_ami_cat.
DR InterPro; IPR006589; Alp_ami_cat_sub.
DR Pfam; PF00128; alpha-amyase; 1.
DR SMART; SM00642; Aamy; 1.
SQ SEQUENCE 533 AA, 60557 MW, 7899CECD6A19C7DDE CRC64;

```

Query Match 64.7%; Score 1841.5; DB 2; Length 533;
 Best Local Similarity 65.8%; Pred. No. 6.2e-118;
 Matches 317; Conservative 70; Mismatches 92; Indels 3; Gaps 1;

```

Qy      5 NGTMQVPEHMLPNDGHLMTKVAANEANNLSLIGITAMLPAYKGTSSDVGYGYDLYD 64
Db      52 NGTMQVPEHMLPNDGHLMTKVAANEANNLSLIGITAMLPAYKGTSSDVGYGYDLYD 111
Qy      65 LGFENQKGTVRTKTKYGAQYLOAIQAAMAGMAYADVDPDKGADGTEWDAVEVNS 124
Db      112 LGFENQKGTVRTKTKYGAQYLOAIQAAMAGMAYADVDPDKGADGTEWDAVEVNS 171
Qy      125 DRNGEISGTQIOATKTFDPGRGNTYSSFKRWYHPDGVNDSSRL-SRIYFRGIGK 184

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Db      172 NRNGEISGTQIOATKTFDPGRGNTYSSFKRWYHPDGVNDSSRL-SRIYFRGIGK 231
Qy      185 KMEVVDIENGNDYLYMADLDMDHPEVTELEKMGKVVNTTIDGFRDAVGHKFSF 244
Db      232 KMEVVDIENGNDYLYMADLDMDHPEVTELEKMGKVVNTTIDGFRDAVGHKFSF 291
Qy      245 FPDMLSYRSQGTGRLFTVGEVMSYDINKLNYITKDGIMSLEDAPLHNKFTYASKSG 304
Db      292 KDMVNVNRQGTGRLFTVGEVMSYDINKLNYITKDGIMSLEDAPLHNKFTYASKSG 351
Qy      305 FDMKTLTNTLMKDOPTLAVTVFVNDHDEPGALQSWVDPMFKPLAVAFILTRQSGYPC 364
Db      352 YDMRNILKGTVAANPHTLAVTVFVNDHDEPGALQSWVDPMFKPLAVAFILTRQSGYPC 411
Qy      365 FYGDYIGIPQYINPSLSKSIDPELLIARDYAVGTQHDYLDHSDIIGWTRGSGTEKFG 421
Db      412 FYGDYIGIPQYINPSLSKSIDPELLIARDYAVGTQHDYLDHSDIIGWTRGSGTEKFG 471
Qy      422 SGIALITDPPGSKMNYVKGQHAKGVFDLTGNSDVTITNSDGEFKVNGSVVW 481
Db      472 SGIALITDPPGSKMNYVKGQHAKGVFDLTGNSDVTITNSDGEFKVNGSVVW 531
Qy      482 PR 483
Db      532 QR 533

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RESULT 7

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Q9A054 ID 09A054 PRELIMINARY; PRT; 519 AA.
AC Q9A054;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Raw starch digesting amyase precursor.
OS Cytophaga sp.
OC Bacteria; Bacteroidetes; Sphingobacteriales;
OC Flexibacteriaceae; Cytophaga.
OX NCBI_TaxID=29535;
RN [1]
RP SEQUENCE FROM N.A.
RA Jeang C.L., Chen L.S., Chen M.Y.;
RA Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF067653; AAP00567.1; -
DR HSSP; P06278; IYUS.
DR GO; GO:0004556; F:alpha-amyase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_ami_cat.
DR InterPro; IPR006589; Alp_ami_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Aamy; 1.
DR SIGNAL.
FT CHAIN 1 57
FT SIGNAL 58 519
SQ SEQUENCE 519 AA, 58337 MW, 3E6B88A4D998B163 CRC64;

```

Query Match 64.5%; Score 1837.5; DB 2; Length 519;
 Best Local Similarity 67.4%; Pred. No. 1.1e-117;
 Matches 326; Conservative 57; Mismatches 98; Indels 3; Gaps 1;

```

Qy      1 AAPNGTMQVPEHMLPNDGHLMTKVAANEANNLSLIGITAMLPAYKGTSSDVGYGYD 60
Db      34 AAPNGTMQVPEHMLPNDGHLMTKVAANEANNLSLIGITAMLPAYKGTSSDVGYGYD 93
Qy      61 DLYDLGFEHQKGTVRTKTKYGAQYLOAIQAAMAGMAYADVDPDKGADGTEWDAVEVNS 120
Db      94 DLYDLGFEHQKGTVRTKTKYGAQYLOAIQAAMAGMAYADVDPDKGADGTEWDAVEVNS 153
Qy      121 VNSDRNGEISGTQIOATKTFDPGRGNTYSSFKRWYHPDGVNDSSRL-SRIYFRGIGK 180
Db      154 VNSDRNGEISGTQIOATKTFDPGRGNTYSSFKRWYHPDGVNDSSRL-SRIYFRGIGK 213

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QY 181 IGRANDWEVDENGNYDYLMDADLMDHPEVTELEKMGKMYVTNTNIDGFLDAVKIK 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 214 TGRKADWEVSSENGNYDYLMDADIDYDHDVNVEMKMGKMYANVGLDGRRLDAVKIK 273
QY 241 FSGFPDMSIYRSQGTGKPLFTVGEYSYDINKLHNYITKTGTMGLFPAFLHNFYTASK 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 274 FSLKMDVNDARAANGKEMFTVGEYQNDLGALNNYLAKVNNQSLFPAFLHNFYAAST 333
QY 301 SGGAPEMTLMTNTLMKQDPTLAVTFVDNDHTEPGQALQSWDPMFKPLAYAFILTRQEG 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 334 GGGYDMRILNNTLVASNPYKAVTLVENHDTQPGQSLSTVQPMFKPLAYAFILTRQEG 393
QY 361 YPCVPEYGDY---GIPQYNPISLKSRIEPLILARRDAYGTQHDYLDHSITIGWTRGCT 417
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 394 YSVPFYGDYGTGKGTTRREIPLAKSKIEPLILARRDAYGTQHDYLDHSITIGWTRGDS 453
QY 418 EKRGSGLALITDGPQSGKMYVYKQKAGKVFYDLTGNSRDTVTINSQMGSEFKYNGGSV 477
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 454 TTKASGLATVITDGPQSGKMYVYKQKAGKVFYDLTGNSRDTVTINSQMGSEFKYNGGSV 513
QY 478 SVWV 481
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 514 SVWV 517
```

RESULT 8

```
Q81AS4 PRELIMINARY; PRT; 513 AA.
ID Q81AS4;
AC Q81AS4;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, last annotation update)
DE Glucan 1,4-alpha-maltohexaosidase (EC 3.2.1.98).
GN BC3482.
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kaparova N., Battacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goldsman E., Larsen N., D'Souza M., Walunas T.,
RA Greckin Y., Pusch G., Haselkorn R., Fongstein M., Ehrlich S.D.,
RA Overbeek R., Kyriides N.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL; AE017009; AAP10417.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; P:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_Amyl_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KM Glucosidase; Hydrolase; Complete proteome.
SQ SEQUENCE 513 AA; 58306 MW; 05C4611C4BF9FF6 CRC64;
```

Query Match 64.3%; Score 1829.5; DB 16; Length 513;
Best Local Similarity 65.6%; Pred. No. 3.9e-117;
Matches 315; Conservative 70; Mismatches 92; Indels 3; Gaps 1;

```
QY 5 NGTMQYFEMWLPDDGTLMTKVAEANNLSLGITLALMPAYKGTSRSDVGYGVYDLD 64
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 32 NGTLMQYFEMWLPDDGTLMTKVAEANNLSLGITLALMPAYKGTSRSDVGYGVYDLD 91
QY 65 LGEPNQGKTVRTKYGTAQYIQAIAAAGMOYVADYVDHKGADGTEWDAVEVNS 124
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 92 LGEPNQGKTVRTKYGTAQYIQAIAAAGMOYVADYVDHKGADGTEWDAVEVNS 151
QY 125 DRNQSISGTVQIAQMTKFPDPRGGRNTYSSFKMEWYHFDVDMDESKRLSHYKFRGIGKA 184
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Db 152 NRNVEVSGDYELISAMTGFPNPGRDSYSNFKMKMYHFDGTDWDEGKLRIRIKFRIGKA 211
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 185 WMEVDPDENGNYDYLMDADLMDHPEVTELEKMGKMYVTNTNIDGFLDAVKIKFSPF 244
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 212 WMEVSSENGNYDYLMDADLMDHPEVTELEKMGKMYANVGLDGRRLDAVKIKHIDHEYL 271
QY 245 PDLISYRSQGTGKPLFTVGEYSYDINKLHNYITKTGTMGLFPAFLHNFYTASK 304
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 272 RDMWNHVRQQTGKEMFTVGEYQNDLGALNNYLAKVNNQSLFPAFLHNFYAAST 331
QY 305 FDMRTLMTNTLMKQDPTLAVTFVDNDHTEPGQALQSWDPMFKPLAYAFILTRQEG 364
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 332 YDMRNLKGTIVANHPFLAVTLVENHDTQPGQSLSTVQPMFKPLAYAFILTRQEG 391
QY 365 FYGDYGTGKNSYELIPALDKIDPILITARKNAYGTQHDYLDHSITIGWTRGCTEKG 421
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 392 FYGDYGTGKNSYELIPALDKIDPILITARKNAYGTQHDYLDHSITIGWTRGCTEKG 451
QY 422 SGALATLISDGPQSGKMYVYKQKAGKVFYDLTGNSRDTVTINSQMGSEFKYNGGSV 481
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 452 SGALATLISDGPQSGKMYVYKQKAGKVFYDLTGNSRDTVTINSQMGSEFKYNGGSV 511
```

RESULT 9

```
Q81YJ4 PRELIMINARY; PRT; 513 AA.
ID Q81YJ4;
AC Q81YJ4;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, last annotation update)
DE Alpha-amylase.
GN AMYS OR BA3551.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Oksstad O.A., Helgeson E., Ristone J., Wu M.,
RA Kolonay J.F., Beaman N.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA Deboy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Hammond Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plant R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaiter J.B., White O., Salzberg S.L.,
RA Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
DR EMBL; AE017035; AAP27311.1; -.
DR TIGR; BA3551; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_Amyl_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KM Complete proteome.
SQ SEQUENCE 513 AA; 58445 MW; 558DEFF282FD159B CRC64;
```

Query Match 64.2%; Score 1827.5; DB 16; Length 513;
Best Local Similarity 65.8%; Pred. No. 5.3e-117;
Matches 316; Conservative 69; Mismatches 92; Indels 3; Gaps 1;

```
QY 5 NGTMQYFEMWLPDDGTLMTKVAEANNLSLGITLALMPAYKGTSRSDVGYGVYDLD 64
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 32 NGTLMQYFEMWLPDDGTLMTKVAEANNLSLGITLALMPAYKGTSRSDVGYGVYDLD 91
QY 65 LGEPNQGKTVRTKYGTAQYIQAIAAAGMOYVADYVDHKGADGTEWDAVEVNS 124
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D	b	92	LGEPNQKGVTRTKYTKKAOLKSAIEHLNQNDIVGDVYVNHKKGADYTEIVTAAVEDRN	151
Q	y	125	DRNOELSGTYQIQAMTKFDFPGRGNTYSSFKRMVYHPDGVMDSEKLSRIYKFRGIGKA	184
D	b	152	NRNVEVSGDYELISAMTGFNFPGRGDNYSFKMKVYHPDGTMDSEKLSRIYKFRGIGKA	211
Q	y	185	MDMEVCTGNGNRYLYMAYADLMDHPVYVELNMGKRYVNTNIDGFIADVKIKTSFE	244
D	b	212	MDMEVSENGNRYLYMAYADLMDHPVYVELNMGKRYVNTNIDGFIADVKIKTIDETYL	271
Q	y	245	PDMLSYVRSQTKGPLEFTVGEWYSYDINKLHNYITTDGTMSLFDAPLHNKEVYTSKSGGA	304
D	b	272	RDWVNEHROQTGKEMETVAEWMQNDIQLTNNYLAKVYNQSFADPLEYVNHVYASKNGN	331
Q	y	305	PDWRLLMTNTLMDQGTFLAVFDVNDHDEPGALQSWDPMKPLAAYAFILTRREGVPCV	364
D	b	332	YDRKNITNGTVMQHHPLAVTLVENDSDPQGSLSVVSPMFKPLAYAFILTRREGVPSV	391
Q	y	365	FYGDYDI---PQYNIPSLSKSIDPILLIARDVAYATGHDYLDHSDIIGMTREGTEPG	421
D	b	392	FYGDYGTGSGNSSYIEIPALCKDKIDPILTKAKNFAYGTQGDYLDHPDYIGMTREGDSYHAN	451
Q	y	422	SGLAALITLDPGSKMYVCKQKAGKAFDILNGNSDPTVINSQDQWGFKNQSGSVSVV	481
D	b	452	SGLATTILSDPFGSKMYWDGKKNAGVWMDMTGNGQNTVYLTKQGWGGFVHSVGSVSILY	511

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RESULT 10
ID      087HG6      PRELIMINARY;      PRT;      507 AA.
AC      Q87HG6;
DT      01-JUN-2003 (TREMBLrel. 24, Created)
DT      01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT      01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE      Alpha-amyLase.
GN      VPA0999.
OS      Vibrio parahaemolyticus.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC      Vibrionaceae; Vibrrio.
OX      NCBI_TaxID=670;
RN
RP      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=RIKD 2210633 / Serotype O3;K6;
RX      MEDLINE=22508454; PubMed=12620739;
RA      Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA      Iijima Y., Naito M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA      Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT      "Genome sequence of Vibrio parahaemolyticus: a pathogenesis mechanism
RT      distinct from that of V. cholerae.";
RL      Lancet 361:743-749(2003).
RL      EMBL; AP005087; BAC62342.1; -.
DR      GO; GO:0004556; F:alpha-amyLase activity; IEA.
DR      GO; GO:0005975; P:carboxylate metabolism; IEA.
DR      InterPro; IPR006047; Alpha_aml1_cat.
DR      Pfam; PF00128; alpha-amyLase; 1.
KW      complete proteome.
SQ      SEQUENCE 507 AA; 58428 MW; 91B549E2BE0700BD CRC64;

```

Query Match	59.7%	Score 1700	DB 168	Length 507
Best Local Similarity	63.1%	Pred. No. 2	8e-108	
Matches 305	Conservative 66	Mismatches 102	Indels 10	Gaps 6
QY	5	NCITMAYFEMVYIPDDGTLMTKYANEEANISLIGITALMTPYAKGTSRS-DVIGYGYDLY	63	
DB	26	NCITMAYFEMVYIPDDGTLMTKYANEEANISLIGITALMTPYAKGTSRS-DVIGYGYDLY	85	
QY	64	DIGEFNOKATVETKTKGTAKQYLCALQALAAAGQYVADVFPFHKGASDTEWDAVEVNP	123	
DB	86	DIGEFDDQKGSVATKTKGTAKQYLSAIAAHNNNIQIGDVYFPHRGGADSKRSWMDTRVDW	145	
QY	124	SDRNOEISTGYOIQAMTKFDFPGRGNTYTSFKRWYTHFPGVMDSEKSLRIYKFEGLGK	183	

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Dh 146 DUNNEL-GDKXIMEAVNEENFPGRRDKKSNEMHTWYHFDGDVMDGAKERKIFKXEGEK 204
Qy 184 AMWMEVDTENGNYDVLYMTAD.LDMDBEVEVTE.KOMGKMYVNTNIDGFR.LDAVYKILKFSF 243
Dh 205 AMWMEVSSKGNVYDLYMTAD.LDMDBEVEVTE.KOMGEMVYINMTCYVDSFRRDAXIKHILKYQ 264
Qy 244 FPDMLSYVASOTGKPLFTVGEYSYDINKLHNYYTKTDGMSLFDAPLENKFTYASKSG 303
Dh 265 LOEMIHILFMWTKGKELFTVGEYMNVDVQOHNFTIKTSGMSLSLDA.LHNNFNPAKSGG 324
Qy 304 AFEMRLTLMNTLTKMOOPLAFTFVONHDTBEGALOSWVDMEFKPLAYAEILTROEBGPC 363
Dh 325 NYDMROQINMGLTKONPVAYATLVENHOTOGLQALLESYVDWMEFKPLAYAFILREBGPFS 384
Qy 364 VFPGDYIYGPQ-----YNPBLK-SKIDULLAARDYAYGTODYDLBDSILIGMTRREGTE 418
Dh 385 VFAADYDYGQYSDKGNINMAKVPYIEELVTLREYAYGKONS.LYDMWDVIGMTRBDAE 444
Qy 419 KPSSGLAALITDGPSSKMYVGKXHAARVEYD.LGNASDPTVILNSDMGEFKYNGGSVS 478
Dh 445 HPRS-MAVIMSOPGGTKMYTIGKSTR--YVDKLGIRTEVMTDANGMAEFPVNGGSVS 501
Qy 479 VVV 481
Dh 502 VVV 504

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SEQUENCE	501 AA;	57485 MW;	1240E46739A5CC11 CRC64;
SO	SEQUENCE	501 AA;	57485 MW; 1240E46739A5CC11 CRC64;
DR	PIAN; PF00128;	alpha-amylase; 1.	
DR	INTERPC; IPR006447;	Alpha_amy1_cat.	
DR	GO; GO:0005975;	P:carbohydrate metabolism; IEA.	
DR	GO; GO:0004556;	F:alpha-amylase activity; IEA.	
DR	EMBL; AB051102;	BAB71820.1; "	
RL	Submitted (NOV-2000)	to the EMBL/Genbank/DBJ databases.	
RT	"Isolation of a new <i>Bacillus</i> alpha-amylase."		
RA	Hayashi Y.;		
RC	STRAIN=KSM-K36;		
RP	SEQUENCE FROM N.A.		
RN	[1]		
OX	NCBI_TaxID=129736;		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; <i>Bacillus</i> .		
OS	<i>Bacillus</i> sp. KSM-K36.		
DE	Amylase.		
CN	AMYK38.		
DT	01-DEC-2001 (TREMBlrel. 19, last sequence update)		
DT	01-JUN-2003 (TREMBlrel. 24, last annotation update)		
AC	093148;	PRELIMINARY;	FRT; 501 AA.
TD	093148;		
RESULT 11			

Query Match	56.8%	Score 1618	DB 2	Length 501
Best Local Similarity	59.3%	Pred. No. 1,2e-102		
Matches	283	Conservative 80	Mismatches 112	Indels 2
			Gaps	1
Qy	5	NGTMMQYFEWYL.PDDGTLMTKYANEANNLSGLITLMLPRAYKGTSSDYGYYDLYD	64	
Db	25	NGTMMQYEWMLBNDGCHMRLHDDAALLSAGCITAIWIPIAYKGNSGADYGYGYDLYD	84	
Qy	65	LGEFQKGTAVTKKGTAKAYLOALQAAAGQYVADVPFHKGADTEWDAVEVNP	124	
Db	85	LGEFQKGTAVTKKGTAKALBRALGSLKSNQINYYGADVYNNHKGADTEVAQAVNP	144	
Qy	125	DNQEIISGTYQIQAMTKFDPQGRNTYSSFKRWYHFPQGVMDBSRKSLRYKFFGIGKA	184	
Db	145	NKMODISAGYITDAWTGDFSGGRNNAVSDFKRWYHFNFGVMDQCYQNNHIFRENNTN--	202	
Qy	185	MDWEVDTENGVYDYLMTYADLLMDHEVYTELKMGKWTYVNTINIDGFEPLDAVKAIFGFF	244	
Db	203	MMWRDEBENGNYDYLGSNIDPFSHEVQDEKDMQSWFTDELDDYGLDAIKHIFWYT	262	
Qy	245	PDMLSYVASQYCKPFLTVGQYWSYDINKLHNYITKTDSGMSLFDAPLNKKYTAASKSGA	304	

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DB 263 SWVHRQRNEADODLEFVGEYWKDVGALIEFLDENMNMESLFDPFLNFTYRASQGGG 322
QY 305 FDMRLTMTLTKMDQPTLATVFDVNDHTEPGALQSWDPWFKEPLAYAFILTROEGPCV 364
DB 323 YDMENLRSLAEVBAHMHAVTFVDNHDTPGESLSWADNFKPLAYATILTRGGYENV 382
QY 365 FPGDYIGIPQVNIPLSKSIDPELLARPYAGTGHDIIDHSDIIGMTREGTEKPGSG 424
DB 383 FPGDYIGIPNDNISAKKMDIDELARQVAYGTGHDYFDHWDVGVWTRGSSSRPNSGL 442
QY 425 AALITPGGSKMVMYVKOHAGVFYDLTGNRSPTVITNSDGMGEFKVNGSVSYVW 481
DB 443 ATIMSGPGSKMVMYGRNAGQGTWDTLIGNNGASTITNGDMGEFTNGGSVSIVYV 499
```

RESULT 12

```
Q8YU21 PRELIMINARY; PRT; 492 AA.
ID 08YU21
AC 08YU21;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amy1ase.
GN ALR2190.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneo T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Matanabe A., Iiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsuno M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003588; BAB73889.1; -.
DR PIR; AH2079; AH2079.
DR GO; GO:0004556; F:alpha-amy1ase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
KM Complete proteome.
SQ SEQUENCE 492 AA; 57063 MW; 11B5D6EGF2P18288 CRC64;
```

Query Match 47.3%; Score 1345.5; DB 16; Length 492;
Best Local Similarity 52.8%; Pred. No. 5, 2e-84;
Matches 261; Conservative 67; Mismatches 147; Indels 19; Gaps 7;

```
QY 2 APNGTMMQYFEWYLPDDGFLMTKVNANNNLSLITLMLPRAKGTSSRS-DVGYGY 60
DB 2 AQANGTMMQYFHTYIIPDGNLMSKVEASAPELADAGFTLMLPRAKGFAGSFDGYGY 61
QY 61 DLYDLGFNQKGTVRTKTYGTAQYLOAIQAHAAGQVYADVFDHKGADGTEWDAVE 120
DB 62 DLEDFLGFQKGSVTRTYGTRQOYLDAVKSILQTHGQVYADAVLNHMKMGDAVERPKATP 121
QY 121 VNSSDRQELSGYVOIQAMTKFDPGKGNYSFFKRWYHFGVDVDE--SRKLSRYKF 178
DB 122 PPDDRLNPKGGLQDILITTYHNFPGKQKYSNFEHMHAFDAVDYNEVNSGSRSTVILL 181
QY 179 RGIGKADWEVDTENGNYDYLYADLDMDHPEVYTELKQWGXVYNTINIDGRLDAVKG 238
DB 182 E--GKNFDYVALLEKGFAYLMGCDLDFQNEWVRGAVTYWKGKCLDTTKVDGFRIDAKH 239
QY 239 IKSFPEDMLSYRSQSGKELFTVGEYWSYDINKLNYITKIDGTMSLDAPLHNKFTYA 298
DB 240 ISTWFEPEWIDALEHRAHGKDLFMVGEYWNIDITLLMYDVAVGRKMSVDFPLHNFQHA 299
```

```
QY 299 SKSGAFDMRLTMTLTKMDQPTLATVFDVNDHTEPGALQSWDPWFKEPLAYAFILTRO 358
DB 300 SKSGGNDMRLILDTGTMQQRPTHAVTFVENHDSQPLQALSVVEPFKEPLAYATILTRO 359
QY 359 EGYPCVFGDYGIP-----QYNI--PSLSKSIDPELLARPYAGTGHDIIDHSD 407
DB 360 EGYPCVPHADYGAEBVDMKQGNRNINIPSHRMIIIDKLRYARKGYAYGPQVNYLDHNM 419
QY 408 IIGWTRGGTEKXGSGALITLTPGSGSKMVMYVKOHAGVFYDLTGNRSPTVITNSDGM 467
DB 420 TIGWTRLGDGDHPL--QGMVAVIMSDBGISGIKWMEVGKNT--KFLDITLHIEAVYTNEMGW 476
QY 468 GEFKNGSVSYVW 481
DB 477 GEFKNGSVSYVW 490
```

RESULT 13

```
Q89YPI PRELIMINARY; PRT; 481 AA.
ID 089YPI
AC 089YPI;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amy1ase precursor.
GN BT4690.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=2250858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
RL Science 299:2074-2076(2003).
DR EMBL; AB016946; AAC79795.1; -.
DR GO; GO:0004556; F:alpha-amy1ase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR SMART; SM00642; Amy; 1.
KM Complete proteome.
SQ SEQUENCE 481 AA; 55343 MW; B6BF237011F5EB1A CRC64;
```

Query Match 46.5%; Score 1322.5; DB 16; Length 481;
Best Local Similarity 49.3%; Pred. No. 1, 9e-87;
Matches 236; Conservative 89; Mismatches 153; Indels 1; Gaps 1;

```
QY 5 NGTMMQYFEWYLPDDGFLMTKVNANNNLSLITLMLPRAKGTSSRS-DVGYGY 64
DB 3 NGVMQYFEMHLPDGLMTKQIKEDALHLDIGTAVWIPRAYKADQDEGATYDLYD 62
QY 65 LGFNQKGTVRTKTYGTAQYLOAIQAHAAGQVYADVFDHKGADGTEWDAVEVNS 124
DB 63 LGFDDQKGTVRTKTYGTAQYLOAIQAHAAGQVYADVFDHKGADGTEWDAVEVNS 122
QY 125 DRNDELSTGYOIQAMTKFDPGKGNYSFFKRWYHFGVDVDESRKLSRYKRGIGKA 184
DB 123 ERTKALBEPFELQWGTYSFHKRDKSDPKFMHYNHSGTGFDDAKRSGVFOIQEGSKA 182
QY 185 WDMVVDTENGNYDYLYADLDMDHPEVYTELKQWGXVYNTINIDGRLDAVKGKRSF 244
DB 183 WSEGVDSNGYDDELNCNDIDLDHPEVASELNRRGKVSNEELNDGRLDAIKRMKQFV 242
QY 245 PDMLSYRSQSGKELFTVGEYWSYDINKLNYITKIDGTMSLPDAPLHNKFTYA 304
DB 243 AQFLDAYRSEKGNDFVAVGEYWNIDLEALDAYIEAVGHKNLPDVPRLHYMMFQASQSGKD 302
```

```

QY      303  FDRRLTMTNTLMKDCQLTAVTFVFNHNDPESGALSNWDPMWKFPLAYAFILTRQEGYPCV 364
      303  YDIDRLDKLDTLVHHHPLAVTLVDNHNDRGSSLESNEVDMEKPLAYGLILMKRGGPCL 364
Db
QY      365  FYGPGYGIPOYNIIPSLKSKIDPFLIARRDAYGTOMYLDHSDIIGMWRREGATEKPGSL 422
      363  FYGDDYIYIKKEKSPHRI-IDILLDRKKRYAGDQIEYDHSHTGFIIRTODESHNSGL 422
Db
QY      425  AAILTDPGGSKMWYVYGVKOHAGKYFYDLTGNSDVTYIINSDGGEFKYNGGSSVWVPR 483
      422  VFLMSNDPASKISSLGCKRKGVEVHEITGSISEBITLDESGNGEVSFVSRNLAVWYXK 480
Db

```

[illegible]

```

Dh 183 MAMEELVDMENSNRYLYMAD.LDFGHSPVIONIDMADWEMETIGVAGFELDAVKIDSR 242
Qy 243 FFDPMZSYRSGTGRPLFTVGEYMSYDINLKHYNTITTDGMSLFDAPLHNKFYTSKSG 302
Dh 243 FPMNFPRDMKEXGDDFYVGEFNNPDEALVDLEKTEBEHFDLVDRILQNLFEASQAG 302
Qy 303 GAFDMRLMTNTLMKODPTLAVTVYNDHDEFGAOLGSWDPMFKPLAVALFTRQEGYR 362
Dh 303 ANYDLGIFTSDIVELKPDKATVPDNDHDTORGALSTVEBWKPAAYALLILRODGLP 362
Qy 363 CVYGGYGYGPR-OYNIPLSKSIDILLARRDYVYGTOHDYLDHSDITLGMTREGGTEKPG 421
Dh 363 CVYGGYGYISQYAOEDPKELIDDLILKRDILAYGBNDVFDLANCLIGWRSANEG-- 420
Qy 422 SGLAALITDGPQGSKMYGVGKOHAKRVYDILGNRSPTVITINSQWGEFKYNGGSYVWV 481
Dh 421 SPLAVLISNDQENSKSMFVGEWNTQOTFVDDLGNHOGVITIDEGYGQOFVRSARSVW- 479
Qy 482 PRAKTIVSTI 450
Dh 480 ----AVNTI 484

```

RESULT 15	ID	OSDPc8	PRELIMINARY;	PRT,	484 AA.
AC	08DPc8;				
DT	01-MAR-2003 (T-EMBLrel_23, Created)				
DT	01-MAR-2003 (T-EMBLrel_23, Last sequence update)				
DT	01-JUN-2003 (T-EMBLrel_24, Last annotation update)				
DE	Alpha-amylose (EC 3.2.1.1).				
GN	AMY OR SPRI239.				
OS	Streptococcus pneumoniae (strain ATCC BAA-255 / R6).				
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OC	Streptococcus.				
EN	NCBI_TaxID=171101;				
EN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21429245; PubMed=11544234;				
RA	Hoskins J., Albom W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,				
RA	Hoskins B.S., Battem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,				
RA	Gilmore R., Glass J.S., Khoja H., Kraft A.R., Lacase R.E.,				
RA	Leslang D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushina P.,				
RA	McHenry S.M., McHenry M., McInnes K., Mundy C.W., Nicot T.I.,				
RA	Norris F.H., O'Gara W., Peery R.B., Robertson G.T., Rockey P.,				
RA	Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,				
RA	Zook C.A., Balz R.H., Jaskunas S.R., Kostek P.R. Jr., Skatrud P.L.,				
RA	Glass J.I.;				
RT	"Genome of the bacterium Streptococcus pneumoniae strain R6."				
RL	J. Bacteriol. 183:5709-5717(2001).				
DR	EMBL; AEO08495; AAL00043.1; -				
DR	PIR; P98026; P98026				
DR	GO; GO:0004556; F:alpha-amylose activity; IEA.				
DR	GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.				
DR	GO; GO:00035975; P:carbohydrate metabolism; IEA.				
DR	InterPro; IPR006047; Alpha_amy_cat.				
DR	InterPro; IPR006589; Alp_amy1_cat_sub.				
DR	InterPro; IPR006046; Glyco_hydro_13.				
DR	Pfam; PF00128; alpha-amylose; 1.				
DR	PRINTS; PR00110; ALPHAAMYLASE.				
DR	SMART; SM00642; Amyy; 1.				
DR	GlycoLase; Hydrolase; Complete; Proteome.				
DR	SEQUENCE 484 AA; 35880 MW; DA5118681870AFC CXC64;				
DR	SEQUENCE				
QY	Query Match	46.0%;	Score 1311;	DB 16;	Length 484;
QY	Best Local Similarity	50.5%;	Pred. No. 1.2e-81;		
QY	Matches 247;	Conservative 74;	Mismatches 158;	Indels 10;	Gaps 4
QY	5 NGTMMQVEFMY;EDDDGTLTWTKYANENNNSIGSIALTLPAYVGTGSRDVGXYVDLYD	64			
QY	3 NGTMMQVEFMY;EDDDGTLTWTKYANENNNSIGSIALTLPAYVGTGSRDVGXYVDLYD	62			
QY	65 LGEEFNQGVIRVITYGTRKAYQLQALQAAHAGNQVADYVDFHKGADQGTETVDAEVENPS	1244			

Tue May 4 14:34:50 2004

us-10-644-187-6.rspt

Page 9

Db 63 LGFBNKGTVRTKYGKEDYLQALQALKAQGIQPMADVVLANKHKAADHREAFQVIEVDPV 122
QY 125 DRNQETISGTYQIQAMTKFDFPGRGNTYSSFKRWHTFDDGVWDDESXLSRIYKFRGIGKA 184
Db 123 DRTVEIGEPFTINGMTSFTFGRODYNGFHHMHFTGTIDYDAKRSKSGIYLIQDNKG 182
QY 185 WDMF--VDTENGNYDYLMYADLMDHPEVYTELXNGKXVYVNTNIDGFRLDVAVKHIFS 242
Db 183 WANEELVDNENGNIDYLMYADLMDHPEVYTELXNGKXVYVNTNIDGFRLDVAVKHIDSF 242
QY 243 FPDWLSYRSQTGKPLFTVGEYWSYDINKLANYITKDTWSLFDAPLHKKFYTASKSG 302
Db 243 FMEHFIRDMKEKYGDDFYVGEFWMNSDKCANLDYLEKTEHFDLVDRHLHONLFEASQAG 302
QY 303 GAFDMRTLMNTIMKQOPLTAVTEVDNHDPEPGALQSWVDPWFKPLAYAFILITRQEGYP 362
Db 303 ANYDLRGITFDSLVELKPKAVTFVDNHDITQROGQLESTVEEMFKPAAYALILRQDGLP 362
QY 363 CVFYGDYYP-GYNTFSLSKIDPPLIARADYAGTQHDYLDHSDIIGMTRGGTEKPG 421
Db 363 CVFYGDYYPISGOYAQDFKEILDRLAIRKDLAYGEONDYFDHANCIGWVRSQAMN-- 420
QY 422 SGLAALITDGPGRSKMYVKGKQAKVFDLTGNRSDTYTINSDGWGEFKNGSGYSYVAV 481
Db 421 SPIAVLISNDQENSKSMFVGQEWNTQTFVDLGSHQGVITIDEGYGFVVSARSYSVM- 479
QY 482 PRKTVSTI 490
Db 480 ----AVNTI 484

Search completed: May 3, 2004, 20:53:14
Job time : 37.5403 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:45:43 ; Search time 13.6493 Seconds
(without alignments)
3382.735 Million cell updates/sec

Title: US-10-644-187-4

Perfect score: 2624

Sequence: 1 VNGTLMQYFEWYTPNDGQHW.....KIGSDGWCDFHNDGSIV 480

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2624	100.0	514	1	ALBSN
2	2173	82.8	512	1	ALBSL
3	1826	69.6	518	1	A27705
4	1768.5	67.4	549	1	A54541
5	1758.5	67.0	549	1	A24436
6	1754.5	66.9	548	1	A24549
7	1695	64.6	549	1	ALBSF
8	1253	47.8	493	2	S15713
9	1217	46.4	484	2	G95160
10	1212	46.2	484	2	F98026
11	1197	45.6	492	2	AH2079
12	1137	42.9	491	2	C86781
13	1050	40.0	495	2	AD3038
14	1050	40.0	506	2	G98477
15	1035	38.7	494	1	B45738
16	1006	38.3	494	2	AD0751
17	999	38.1	495	2	B90962
18	998	38.0	495	1	A45738
19	980	37.3	495	2	B85810
20	620	23.6	217	2	A19506
21	351.5	13.4	826	2	E96720
22	3346	13.2	440	2	S14858
23	3324	12.7	421	2	S10514
24	3324	12.3	437	2	S14956
25	323	12.3	1196	2	A29130
26	319	12.2	438	2	S14957
27	318	12.1	435	2	S12625
28	317	12.1	435	2	JC7137
29	315.5	12.0	437	2	CT0946

30	315.5	12.0	437	2	JC7138	alpha-amyase (EC
31	315	12.0	413	1	ALMT3	alpha-amyase (EC
32	310	11.8	504	2	A55861	alpha-amyase (EC
33	307.5	11.7	423	2	T09942	alpha-amyase (EC
34	307.5	11.7	438	1	ALBS	alpha-amyase (EC
35	305	11.6	439	2	T02956	alpha-amyase (EC
36	289	11.0	429	1	JR0406	alpha-amyase (EC
37	287	10.9	428	2	T05521	alpha-amyase (EC
38	285.5	10.9	713	2	S09196	cyclomaltohextrin
39	284.5	10.8	443	2	J01527	alpha-amyase (EC
40	284.5	10.8	445	2	S19990	alpha-amyase (EC
41	283	10.8	427	1	ALBSB	alpha-amyase (EC
42	282.5	10.8	437	2	S07040	alpha-amyase (EC
43	279.5	10.7	482	2	S31478	alpha-amyase (EC
44	277.5	10.6	713	2	A58800	cyclomaltohextrin
45	272	10.4	713	1	ALBSG7	cyclomaltohextrin

ALIGNMENTS

RESULT 1
ALBSN
alpha-amyase (EC 3.2.1.1) precursor - Bacillus amyloliquefaciens
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Bacillus amyloliquefaciens
C:Date: 30-Nov-1980 #sequence_revision 30-Jun-1987 #ext_change 18-Jun-1999
C:Accession: A92389; A90307; I39756; I39763; A00843
R:Takkinen, K.; Petersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L
J. Biol. Chem. 258, 1007-1013, 1983
A:Title: Amino acid sequence of alpha-amyase from Bacillus amyloliquefaciens deduced fr
A:Reference number: A92389; PMID:83108806; PMID:6185474
A:Content: pub110
A:Accession: A92389
A:Molecule type: DNA
A:Residues: 1-514 <TRX>
A:Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:G142428; PIDN:AAA221
R:Chung, H.S.; Friedberg, F.
Biochem. J. 185, 387-395, 1980
A:Title: Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-amyase.
A:Reference number: A90307; PMID:80241725; PMID:6156671
A:Accession: A90307
A:Molecule type: protein
A:Residues: 32-53; I, 55-63, 'L', 65-78, 'D', 80-83, 'S', 85-222 <CH>
R:Palva, I.; Petersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.;
Gene 15, 43-51, 1981
A:Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of t
A:Reference number: I39756; PMID:82051296; PMID:6170339
A:Accession: I39756
A:Status: translated from GB/EWBL/DBJ
A:Molecule type: DNA
A:Residues: 1-96 <RES>
A:Cross-references: EMBL:V00092; NID:G39297; PIDN:CAA23430.1; PID:G39298
R:Ruchonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karenen, S.
Gene 59, 161-170, 1987
A:Title: Efficient secretion of Bacillus amyloliquefaciens alpha-amyase cells by its ow
A:Reference number: I39763; PMID:88137952; PMID:2830166
A:Accession: I39763
A:Status: preliminary; translated from GB/EWBL/DBJ
A:Molecule type: DNA
A:Residues: 1-59 <RE2>
A:Cross-references: GB:M18424; NID:G142430; PIDN:AAA22192.1; PID:G142431
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amyase, amyloliquefaciens type; alpha-amyase core homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-11/Domain: signal sequence #status predicted <SIG>
F:32-514/Product: alpha-amyase #status predicted <MP>
F:1229-362/Domain: alpha-amyase core homology <AMY>
F:133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted
F:262,292,359/Active site: Asp, Glu, Asp #status predicted

Query Match 100.0%; Score 2624; DB 1; Length 514;
Best Local Similarity 100.0%; Pred. No. 1.5e-178;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 VNGTLMQYFEMWYFNDGQHWKRLQNDAEHLSDIGITAWIPPAKYGLSGSDNGYGPYDLY 60
DB 32 VNGTLMQYFEMWYFNDGQHWKRLQNDAEHLSDIGITAWIPPAKYGLSGSDNGYGPYDLY 91
QY 61 DLGFGQOKGIVRTKTKGKSELODAIGLSHRNVOYGVADVLANHKAADATEDVTAEVNP 120
DB 92 DLGFGQOKGIVRTKTKGKSELODAIGLSHRNVOYGVADVLANHKAADATEDVTAEVNP 151
QY 121 ANRNOETSEEOYKAMTDPRFPFGGNTYSDPKMHWYFDGADNDESKISRIKFGEGK 180
DB 152 ANRNOETSEEOYKAMTDPRFPFGGNTYSDPKMHWYFDGADNDESKISRIKFGEGK 211
QY 181 AMDMEVSENGNYLYKADYDHPDVVAETKMGVYANWELSDGFRIDAANKHIFSF 240
DB 212 AMDMEVSENGNYLYKADYDHPDVVAETKMGVYANWELSDGFRIDAANKHIFSF 271
QY 241 LRDWQAVRQATGKEMFTVAEYWMONNAKLENYLNTKTSFNQSVFDPVLFHNLQAAASQGG 300
DB 272 LRDWQAVRQATGKEMFTVAEYWMONNAKLENYLNTKTSFNQSVFDPVLFHNLQAAASQGG 331
QY 301 GYDKRRLIDGTWVSRHPKAVTFPEMNDHTOPGQSLSTVQTFWEPFLAYAFILTEESGYFQ 360
DB 332 GYDKRRLIDGTWVSRHPKAVTFPEMNDHTOPGQSLSTVQTFWEPFLAYAFILTEESGYFQ 391
QY 361 VFYGMVYTKGTSPEKPEISLKNONIEPIKAKEXYAYGQPHQYIDHPVIGTRGDSAA 420
DB 392 VFYGMVYTKGTSPEKPEISLKNONIEPIKAKEXYAYGQPHQYIDHPVIGTRGDSAA 451
QY 421 KSGLAALITDGGSGKRYAGLKNAGETWYDITGNRSPTVYIGSDGGEFHNWNGSYIY 480
DB 452 KSGLAALITDGGSGKRYAGLKNAGETWYDITGNRSPTVYIGSDGGEFHNWNGSYIY 511
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RESULT 2

AlbSL
alpha-amyLase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis

Nlternate names: 1,4-alpha-D-glucan glucanohydrolase

CSpecies: Bacillus licheniformis

CDate: 30-Jun-1987 #sequence revision 24-Apr-1998 #text change 15-Sep-2000

CAccession: A21997; B24549; A91796; A21663; I39774; I39772; A26151; S53788; A00844

R.Yuuki, T.; Nomura, T.; Tezuka, H.; Tsuboi, A.; Yamagata, H.; Tsukaguchi, N.; Uda, S.

J. Biochem. 98, 1147-1156, 1985

A>Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amy

ases deduced from the DNA sequences

A:Reference number: A91997; MUID:86111694; PMID:2418011

A:Accession: A91997

A:Molecule type: DNA

A:Residues: 1-162, 'R', 164-512 <YU>

A:Cross-references: GB:M3236; NID:G39551; PIDN:CAA26981.1; PID:G39552

A:Experimental source: ATCC 27811

R.Gray, G.L.; Weiner, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Reguadr,

J. Bacteriol. 166, 635-643, 1986

A>Title: Structural genes encoding the thermophilic alpha-amyLases of Bacillus stearother

A:Reference number: A91817; MUID:86195857; PMID:3009417

A:Accession: B24549

A:Molecule type: DNA

A:Residues: 1-338, 'G', 340-348, 'S', 350-512 <GA>

A:Cross-references: GB:M3236; NID:G142510; PIDN:AAA22240.1; PID:G142511

A>Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-am

A:Reference number: A21663; MUID:85076654; PMID:6334606

A:Accession: A21663

A:Molecule type: DNA

A:Residues: 1-3, 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', 8;

A:Experimental source: Chromosomal DNA of ATCC 14580

A>Note: the authors translated the codon CGT for residue 48 as Gly and GAC for residue 6;

R.iaotide, B.W.; Chambliss, G.H.; McConnell, D.J.

J. Bacteriol. 171, 2435-2442, 1989

A>Title: Bacillus licheniformis alpha-amyLase gene, amyL, is subject to promoter-independent

A:Reference number: I39773; MUID:89213924; PMID:2540150

A:Accession: I39774

A:Molecule type: DNA

A:Residues: 1-28 <LMO>

A:Cross-references: GB:M26412; NID:G341477; PIDN:AAA22237.1; PID:G516550

R.Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.

Gene 96, 37-41, 1990

A>Title: In vivo genetic engineering: homologous recombination as a tool for plasmid com

A:Reference number: I39772; MUID:91092499; PMID:2265757

A:Accession: I39772

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-32, 'I' <JOR>

A:Cross-references: GB:M2637; NID:G142498; PIDN:AAA22232.1; PID:G142499

R.Kuhn, H.; Fietzek, P.P.; Lampen, J.O.

J. Bacteriol. 149, 372-373, 1982

A>Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amyLase: compari

A:Reference number: A26151; MUID:82098050; PMID:6172418

A:Accession: A26151

A:Molecule type: protein

A:Residues: 30-37, 'E', 39-41, 'X', 43-47 <KUH>

R.Machius, M.; Wiegand, G.; Huber, R.

J. Mol. Biol. 246, 545-559, 1995

A>Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amyLase at 2.

A:Reference number: S53788; MUID:95182462; PMID:7877175

A:Accession: S53788

A:Molecule type: protein

A:Residues: 'D', 220-227 <MAC>

A>Note: sequence represents amino end of an internal fragment created by a single enzymat

R.Machius, M.; Wiegand, G.; Huber, R.

submitted to the Brookhaven Protein Data Bank, July 1995

A:Reference number: A65206; PDB:1BPL

A:Contents: annotation: X-ray crystallography, 2.2 angstroms, residues 32-210/222-511

A>Note: these structural studies suggest 163 is less rather than Arg

R.Song, H.K.; Huang, K.Y.; Chang, C.; Suh, S.W.

submitted to the Brookhaven Protein Data Bank, October 1996

A:Reference number: A66860; PDB:1VUS

A:Contents: annotation: X-ray crystallography, 1.7 angstroms, residues 32-210/222-511

C:Genetics:

A:Gene: amyL

A:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

[illegible]

RESULT 3

alpha-amylase EC 3.2.1.1) precursor - *Bacillus* sp.
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase
C/Species: *Bacillus* sp.
C/Date: 31-Mar-1989 #sequence_revision 18-Aug-1995 #text_Change 18-Jun-1995
C/Accession: A27705
R:Tsukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.
Biochem. Biophys. Res. Commun. 151, 25-31, 1988
A:Title: Nucleotide sequence of the maltotriose-producing amylase gene from an alkalophilic
A:Reference number: A27705; MUID:88162814; PMID:3258152
A:Accession: A27705
A:Molecule type: DNA
A:Residues: 1-518 <TSU>
A:Cross-references: GB:M1862; NID:G142496; PIDN:AA22231.1; PID:G142497
A:Experimental source: Chromosomal DNA of strain 707
A:Note: amino end of mature protein also determined
C/Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.
C/Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-518/Product: alpha-amylase #status experimental <MNT>
F:236-359/Domain: alpha-amylase core homology <AMY>
F:193,228,273/Binding site: calcium (asn, asp, his) #status predicted
F:269,299,356/Active site: asp, glu, asp #status predicted

Query Match	69.6%;	Score 1826;	DB 1;	Length 518;
Best Local Similarity	66.6%;	Pred. No. 6.8e-122;		
Matches 321;	Conservative 63;	Mismatches 90;	Indels 8;	Gaps 3

QY	2	NGTLMOYEWTTPNDGQHWKRLQNDADHEHSDIGITAWTTPPYXKLSQSDNGYGYDYLTD	61
Db	39	NGTMMQYEWYLPNDGNMNRRLNSDASNLKSGITAWTTPAMKGSQNDVGYGAYDILD	98
QY	62	LGEFOOKTVPRTKYGTKESELODAISLSHRNOYGYDVVLNKGADATEDYTAVEVNP	121
Db	99	LGEFPOKGTVPRTKYGTRSQLQAAVTSLKNNGIQVGDVVMNKHGGADAEWYTAVEVNP	158
QY	122	NRNOETSEBYQIKAWTDFRFPGRGNTYSDPFKNWHYFHDADWDESKRI-SRIEFGEGCK	180
Db	159	NRNGEVTGYTTEAWTRPDPFGRGMTHSFKRMWHFDDVDWDQSRLLNRLTYKFRGHGX	218
QY	181	AMDWEVSSENGNVDTYMTADVTDYDHPDVVAETKKGCIWTANELISLDFRIDAKIKKEF	240

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Db      213  AAMDWEVDTEGNARYDYLTMADIDMDHEPVEVNLRRNGWYWTITGLIDSEFRIDAVGHIKXSF 278
Qy      241  LRPWVAATQAQAKGEMFTVAEYEQMNGAKLKENYLNKTSFENOSVFEVDFLHNLDAASOGG 300
Db      279  TRWIMNHVSAAQKKMFAVEAEKNDLALENTYQKTIKMHSHVADVDFLHNLNLAASGSG 338
Qy      301  GYDMRRLDGTVAVSRRPEKAVTFVENHDTPQGSLESTVQTFWPKLVAFLITRESGIPQ 360
Db      339  NYDMRMI FNGIYVQRHPSHAVTFFVNHDSQEEALLESFVEEWFKPLVAALITLREGYPS 398
Qy      361  VFEGMDYNG--TKGTSPKELPSLKONIEDILAKRKYAAGPCHYIDHPDVIGMTRGDSG 418
Db      399  VFEGDYYGFLPTG----VFMRKSLIDILLRQKYAAGKNDVLDDHNIIGMTRBNTA 455
Qy      419  AAKSGIALITDPGGSKMYAGLNAGEIYWDITGNKSDTVKIGSDQGEFFHYNDSSYS 478
Db      454  HPSNGIATIMSDGAGGSKMFFVGRKAKQAVMSDITGNRTGTVITINADGQMGFVSNGGSVS 513
Qy      479  IY 480
Db      514  IW 515

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RESULT 4

alpha-amylase (EC 3.2.1.1) precursor - *Bacillus stearothermophilus* (strain DN1792)
 MAlternate names: 1,4-alpha-D-glucan-D-glucanohydrolase
 CSpecies: *Bacillus stearothermophilus*
 CDate: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
 CAccession: A54541
 R:Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
 FEBS Microbiol. Lett. 77, 271-276 1991
 ATitle: Cloning of a chromosomal alpha-amylase gene from *Bacillus stearothermophilus*.
 AReference number: A54541
 AAccession: A54541
 A:Molecule type: DNA
 A:Residues: 1-549 <JOR>
 A:Cross-references: GB:X59476
 A:Experimental source: chromosomal DNA of strain DN1792
 CComment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
 C:Genetics:
 A:Start codon: GTG
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: alpha-amylase, amyloliquefactors type; alpha-amylase core homology
 C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysacc
 P:1-34/Domains: signal sequence #status predicted <SIG>
 P:35-549/Product: alpha-amylase #status predicted <AMY>
 P:235-366/Domains: alpha-amylase core homology <AMY>
 P:139/23/,272/Binding site: calcium (Asp, Asp, His) #status predicted
 P:266/296,365/Active site: Asp, Glu, Asp #status predicted

Query Match	67.4%;	Score 1768.5;	DB 1;	Length 549;
Best Local Similarity	65.6%;	Pred. No. 8.9e-118;		
Matches 315;	Conservative 56;	Mismatches 104;	Indels 5;	Gaps 2;

QY	2	NGTLMQYEWMTPLNDGQHKRLQNDADHLSIDIGTAWIIPRAYKLSGSDNGYGYDLYD	61
Db	39	NGIMMYYEWMYLPBDGILMTKVAHEANNTLSISLIGTALMLPRAYKJTSISDYGIVYDLYD	98
QY	62	LGEFOQKGVTRTKYSGKSELDAIGSLHSRWVQYGVDLVNHKAGADATEDVTAVERNPA	121
Db	99	LGEFQKGVTRTKYSGKSELDAIGSLHSLRWVQYGVDLVNHKAGADATEDVTAVERNPA	158
QY	122	NNQGTSEBYQIKANTDFRPGRGNTYSDFFKHHYTHFPGADWDSERKLSRIFFKFGEGKA	181
Db	159	DNNQGTSEBYQIKANTDFRPGRGNTYSDFFKHHYTHFPGADWDSERKLSRIFFKFGEGKA	218
QY	182	WMWYSSSENGNDYLMYADVDPDDEHDVAETKMGIVANEHLSLDEGRFIDAKAHKFSFEL	241
Db	219	WMWYSSSENGNDYLMYADVDPDDEHDVAETKMGIVANEHLSLDEGRFIDAKAHKFSFEL	278


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QY      242  RDWVGAARAKATGKEMFVAVEWQNNAGKLENTLNTSFPNGSFVDVPLHFNLAASSGGG 301
Db      279  PDMISVYRSGTGPFLFTVGEWYSYDINKHNHYITTDGMSLFDPALHNKRYTASKGGGA 338

QY      302  YDMERLLDGTVAVRHEPEKATVEVFNHDTPQGSLESTVQWEPKPLAAYFILTRESGPV 361
Db      339  FDRRLTNTNTLMDQPLATVFDNHDDEPGALGSWDPMWKPLAAYFILTREGIPCV 398

QY      362  FYGDMYGTGKGTSPK-EIPSLKDNIEPILAKREYAVGPHDYIDHPVYIGWTRBGDSAA 420
Db      399  FYGDIYGI----PQYNIPSLKSKIDPELLARDDYAVGQHDYLDHSDIIGWTRBGTEKP 454

QY      421  KSGAALITDGPGRSKRMAYGLKNAEETWYDITGNRSTVYKSGTGAKSEFVNDGSYIY 480
Db      455  GSGAALITDGPGRSKRMVYGLQAKAVYDITGNRSDIVTINSQGWSEFVNDGSYVW 514

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RESULT 5

alpha-amylase[EC 3.2.1.1] precursor - *Bacillus stearothermophilus* plasmid pAT5
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: *Bacillus stearothermophilus*
C:Date: 05-Jun-1987 #sequence_revistion 18-Aug-1995 #text_change 18-Jun-1999
J:Accession: A24436, J19777
R:Nakajima, R.; Imanaka, T.; Alba, S.
J. Bacteriol. 163, 401-406, 1985
A:Reference number: A24436; PMID:85234394; PMID:3924897
A:Accession: A24436
A:Molecule type: DNA
A:Residues: 1-549 <NA>
A:Cross-references: GB:M11450
A:Experimental source: plasmid pAT5
A>Note: amino end of the mature protein also determined
R:Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Dietrichsen, B.
Gene 96, 37-41, 1990
A>Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con
A:Reference number: J19772; PMID:91092499; PMID:1265757
A:Accession: J19777
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-45 <RES>
A:Cross-references: GB:M62638; NID:g142514; PIDN:AAA22242.1; PID:g142515
C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C:Genetics:
A:Gene: amys
A:Genome: plasmid
A:Start codon: GTG
C:Function:
A:Description: catalyses the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloglucosidase type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide
F:1-14/Domain: signal sequence #status predicted <SIG>
F:35-549/Product: alpha-amylase #status experimental <ANT>
F:235-366/Domain: alpha-amylase core homology <ANT>
F:133,231,272/Binding site: calcium (asp, asp, his) #status predicted
F:266,298,365/Active site: asp, glu, asp #status predicted

Query Match	67.0%;	Score 1758.5;	DB 1;	Length 549;
Best Local Similarity	65.4%;	Pred. No. 4.6e-117;		
Matches 3:4; Conservative	57;	Mismatches 104;	Indels 5;	Gaps 2;

QY	2	IGITLMQYEWMTPTNPGNGCMXRLONDAAEHLSDIGITAWIPRAXYCTSGSDNGXPRPYLD	61
Db	39	NGTMMQYEWLPLPDGTLMTKVAHEANNLSSGLITALLMTPRAXYCTSRSDYGYGYTYLD	98
QY	62	LGEPOQKTYVTKTKYKTSKSELDAIGLSHRVQYGYVYLNHKKAGADATEVYTAVERNPA	121
Db	99	LGEEFQKAAVTKYGTGKAQYLOALIOAAHAAGQYADVFPYHKKAGADTEVWDAVEYNPS	156
QY	122	NRNDETSEYIOIKAMTDFRFFGRGNTYSDFKMHWHTFEGADWDESRKLSRIFKERECEKA	181
Db	159	DRNEISETYOIOAWTKEDFPGRGNTYSSFKMRWHTFEGVWDESRKLSRYKFERGIGKA	216

QY 18 MDWEVSEKNGNDYALMYADVDYEDHDDVAAETKQMIWYANSLSDGRIIDAKIKRFSFL 241

Db 219 MDWEVDTEKNGNDYALMYADLDMDHDEYVTELSKMGKRVVNTTNIDGRLLDVAKIKGFSF 278

QY 242 RDMVQVAVRQATKEKMEFTAAEVYQNNAGGLEUYLNTKSNOSVFPQVPHFNQAASQGGG 301

Db 279 EDLSTSVRSQGTKEPLFTYGEVETWSYDINKLHMYIKMTNQTSLFPAFLHNKRYTAKSGGT 338

QY 302 YDMRLDLDYVSRHPEKAYFVFNHDDQPOGOSLESTYQTFKFLAAAFILTPSSGQVQY 361

Db 339 FDMKRLMTNTLMKDDQPLAVTVYDNDHDEPQGLQSWYDPEFKFLAAAFILTRQSGTFCV 398

QY 362 FYDMDYGTGAGTSPK-EIISLKONIEPILAKAEVAYGQEHYLDHPVLTGHTREGBSAA 422

Db 399 FYDMDYGTGAGTSPK-EIISLKONIEPILAKAEVAYGQEHYLDHPVLTGHTREGBSAA 458

QY 421 KSGSLAALITDGPGRKEMAYGLKKNAGETWYDITGNRSPTVYKISDQNGEFPVHNDGSYIY 480

Db 455 GSGSLAALITDGPGRKEMAYGLKKNAGETWYDITGNRSPTVYKISDQNGEFPVHNDGSYIY 514

RESULT 6

alpha-amylase (loc.3.2.1.1) precursor - *Bacillus stearothermophilus* (strain NZ-3)
N|Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C|Species: *Bacillus stearothermophilus*
C|Date: 30-Jun-1988 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C|Accession: A24549; 139501; 139770
J|Gray, G.L.; Manzner, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Reguadt, R.
J. *Bacteriol.* 166, 635-643, 1986
A|Title: Structural genes encoding the thermophilic alpha-amylases of *Bacillus stearothermophilus*
A|Reference number: A91817; NCID:86195857; PMID:3009417
A|Accession: A24549
A|Molecule type: DNA
A|Rebids: 1-549 <GBA>
A|Cross-references: GB:MI1355; NID:G142512; PIDN:AAA22241.1; PID:G142513
A|Experimental source: genomic DNA of strain NZ-3
J|Sato, H.; Nishida, H.; Isono, K.
J. *Bacteriol.* 170, 1034-1040, 1988
A|Title: Evidence for movement of the alpha-amylase gene into two phylogenetically distant
A|Reference number: I39501; NCID:86139156; PMID:3257753
A|Accession: 139501
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Rebids: 536-549 <RES>
A|Cross-references: GB:MI29577; NID:G142476; PIDN:AAA22225.1; PID:G142478
A|Experimental source: strain DY-5
A|Accession: 139770
A|Status: translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Rebids: 536-549 <RES>
A|Cross-references: GB:MI29578; NID:G142484; PIDN:AAA22228.1; PID:G142486
A|Experimental source: strain 799
A|Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
A|Genetics:
A|Start codon: GTG
A|Function:
A|Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A|Pathway: glycogen/starch degradation
C|Superfamily: alpha-amylase, amyloliquefactors type: alpha-amylase core homology
C|Keywords: extracellular protein, glycosidase, heat-stable protein, hydrolase, polysaccharide
F|1-34/Domain: signal sequence #status predicted <Sig>
F|35-549/Product: alpha-amylase #status predicted <Stc>
F|235-368/Domain: alpha-amylase core homology <AMT>
F|139,227,272/Binding site: calcium (Asp, Asp, His) #status predicted
F|268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 66.9%; Score 1754.5; DB 1; Length 549;
Best Local Similarity 65.2%; Pred. No. 8,7e-117;
Matches 313; Conservative 58; Mismatches 104; Indels 5; Gaps 2;
2 NGTLMGFENYITENDQHWKRLONDAEHLSDIGITAWIPAPYKGISGSDNGGPPDYLD 61

[illegible]

RESULT

alpha-amy-lase[EC 3.2.1.1] precursor - *Bacillus stearothermophilus* (strain DY-5) plasmid
M1:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: *Bacillus stearothermophilus*
C:Date: 30-Jun-1987 #sequence revision 30-Jun-1997 #text_change 16-Feb-1997
J:Accession: J01999, J01804, A00845
R:Rihara, H., Sasaki, T., Tsuboi, A., Yamasaka, H., Tsukagoshi, N., Ueda, S.
J:Biochem. 98, 95-103, 1985
A:Article: Complete nucleotide sequence of a thermophilic alpha-amy-lase gene:
R:Reference number: J01999, M0186008166, PMID:3876333

A:Molecule type: DNA
A:Residues: 1-548 <IH1>
A:Cross-references: GB:X02769
A:Experimental source: plasmid PH1300 from strain DY-5
A:Accession: B91999
A:Molecule type: protein
A:Residues: 35-48 <IH2>
A:Experimental source: strain DY-5
A:Rikudoagoshi, N.; Iritani, S.; Sasaki, T.; Takemura, T.; Ihara, H.; Idota, Y.; Yamagata, U. *Bacteriol.* 164, 1182-1187, 1985
A>Title: Efficient synthesis and secretion of a thermophilic alpha-amylase by protein-pr
A:Reference number: A91804; MUID:86059211; PMID:2999073
A:Contents: PBAM101
A:Accession: A91804
A:Molecule type: DNA
A:Residues: 1-29, 'Q', 31-75, 'W', 77-122 <TSU>
A:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C:Genetics:
A:Genome: plasmid
A:Start codon: GTG

A.description catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A.pathway: glycoген/starch degradation
C.superfamily: alpha-amylase, amylolipofaciens type, alpha-amylase core homology
C.keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
P.1-4/Domains: signal sequence #status predicted <SIG>
P.35-548/Product: alpha-amylase #status experimental <MAT>
P.235-368/Domains: alpha-amylase core homology <HY>
P.139,237,272/Binding site: calcium (ASP, ASP, ASP) #status predicted

F:268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match	64.6%;	Score 1695;	DB 1;	length 548;
Best Local Similarity	64.0%;	Pred. No. 1.5e-112;		
Matches 307;	Conservative 56;	Mismatches 111;	Indels 6;	Gaps 3;

Oy	2	NGTLMOYFEMTYEPNNGCHMEKLONDADASHLSIGITLWMIPEYAKGISOSDNGIGPDL	61
Db	39	NGTMOYFEMTYEPDGTILMTKVAANEANNTLSIGITLALSEPAPKGRSBDVGAYDLYD	98
Oy	62	LGEPOOKGTVRKYXTKSELQDAIGSLHSRNOYVGEDVLTNKAQADATEDVTAHVNA	121
Db	99	LGEFNOKGTVRKYXTKAQYLOAIQAHAAGMOYVADVAFDHGAGDGTENWDVAEVRNS	158
Oy	122	NRNGEISEIYOKANTDREPRGRNTYSDPEKMHYHEDGADMESEKRIKIFPRGEGRA	181
Db	159	DRNGEISGTYOQAATKDFPRGRNTYSSPEKMYHHDGVDMESEKLRITKFRIGRA	218
Oy	182	MDNEVSEKNGTDYLTMAADVJDHPDVAETKKWGIYANELSLDEFRIDAKHIKESFL	241
Db	219	MDNEVDTEKNGTDYLTMAADMDNDEPVYTELKMGKRYVNTNIDGFRIDGLKHIKESF	278
Oy	242	RDWVQAVRQATGKEMFTVAEYMONNAGKLENYLNTKISFNOSVDFVLPHNLQAASSQGG	301
Db	279	PDWLSVRSQTKSPLFTYGEYWSYDINKLNHYIKTNGTMSLPEADLENNKFTYASKSGA	338
Oy	302	YDMKRLIDGTVSRHPEAAVTFVZHNHTOPQOSLESTVQTMFPCPLAFAFILHRESSTPOV	361
Db	339	FDKRLTMTLTKMDOPPLAATFVFNHHTNPAPKC-SHGRWEPKPLAFAFILHROBESPOV	397
Oy	362	FYGDWMTGTGTSBK-EIPSLKDNIEPLIKARKEAYAPODYIDHEDVIGMTREGSSPA	420
Db	398	FYGDYIGT----PQNNISLSKSIDPELLIARDAVATQGDYIDHSDIGMTREGYTEKP	453

2

RESULT 8
S15713
alpha-amylase (EC 3.2.1.1) - *Bacillus circulans*
C.Species: *Bacillus circulans*
C.Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C.Accession: S15713

submitted to the EMBL Data Library, May 1991

A:Accession: S15713
A:Molecule type: DNA
A:Residues: 1,493 <MAR>
A:Cross-references: EMBL:X60779 ; NID:G939411 ; PIDN:CAA43194.1 ; PID:G939412
C:Genetics:
A:Gene: amyE
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amyase, amyAoliuefaciens type, alpha-amyase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
E:200-333/domain: alpha-amyase core homology <AMT>

Query Match	47.8%;	Score 1253;	DB 2;	Length 493;
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Matches	226;	Conservative	74;	Mismatches	177;	Indels	2;	Gaps	1
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QY 2 NGTLTMYPMYTPNPGOHKRLONDAHEHLSIGTAVWIPPAKYGSLQSNKGPPDLVD 61
 Db 4 NHTMGGFEHMLAADGDHKKRLAEWAPRLKAKGIDITWVPPVPEKVAVSAGETGYGVLDLD 63
 QY 62 LGSFOOKGKATRETYGKSELDAIGSLSRNVQYGVNVAHKKAGADATEDVAVAEVNA 121
 Db 64 LGSFDDKGTVRTYGTGKQELTFAIECCQNGIAVYVLDVNNHKKAGADETEFVKVIEVDN 123

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QY 122 NRNOETSEYQIKAWTDFRFRGRNTYSDPKMHWYHEDGADMDSESRKISRIKFRGEGKA 181
D 124 DRTREISEPFEIEGWTFRFGTQYSSFRKNSSEHNHGDPDFARRERTGVFAGENKK 183
QY 182 WDWESSENGNYDYLYMADVDYDHPDYVAETKKMGWYANELSLDGRIDAAKHIFESL 241
D 184 WNEVNDDEFGNYDYLYMADVDYDHPDYVAETKKMGWYANELSLDGRIDAAKHIFESL 243
QY 242 RDWYQAVROATGKEMFTYAEYQWONNAGLENYLNTKTSFNOSVDFVPLHFNLOAASQGG 301
D 244 KEFAEMIRKRGQGFYIYGEFWSNSLDCREFLDTVDYQIDLPVSLHLYKHEHSLGRD 303
QY 302 YDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAVAFILITRESGYQV 361
D 304 FDLKIFPDITVQHTPHAVTFVNDHDSQFHEALSWIGDWFKSAVALTLIRDDGYPVV 363
QY 362 FYGDMYGTGTSPEIKNIEPILKARKEVYAGPOHDIYDHPDYIGWTRBEGSSAAK 421
D 364 FYGDYGGIGG--PEPYDGRKEILDLILSARCNKAYGEQEDYFDHANTIGWTRBEGIEG 421
QY 422 SGLAALITDGPQGSKRWYAGLKNAGETWYDITGNRSPTVK.GSDGMBEFHYNDGSVSI 480
D 422 SGCAVVISNGDDEKRWYAGLKNAGETWYDITGNRSPTVK.GSDGMBEFHYNDGSVSI 480
```

RESULT 9

```
G95160
alpha-amy1ase [imported] - Streptococcus pneumoniae (strain TIGR4)
C/Species: Streptococcus pneumoniae
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C/Accession: G95160
R/RefSeq: H. J. Nelson, K. E. Paulsen, I. T. Eisen, J. A. Read, T. D. Peterson, S. J. Heid
on, J. D. J. Unal, L. A. White, O. J. Salazar, S. L. Lewis, M. R. Radune, D. J. Holtzaple,
nson, T. J. Hickey, E. K. Holt, I. E.
Science 293, 498-506, 2001
A/Authors: Loftus, B. J.; Yang, F.; Smith, H. O.; Venter, J. C.; Dougherty, B. A.; Morrison,
A.; Reference number: A95000; MUID:21357209; PMID:11463916
A/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A/Accession: G95160
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-484 <KUR>
A/Cross-references: GB:AB005672; PIDN:AAK75480.1; PID:G14972868; GSPDB:GN00164; TIGR:SP4
A/Experimental source: strain TIGR4
C/Genetics:
A/Genes: SP1382
C/Superfamily: alpha-amy1ase, amy1oliquefaciens type; alpha-amy1ase core homology
```

Query Match 46.4%; Score 1217; DB 2; Length 484;

Best Local Similarity 47.0%; Pred. No. 1e-78;

Matches 226; Conservative 81; Mismatches 168; Indels 6; Gaps 3;

```
QY 2 NGLTMQYFEWYTPNDGQWKRLLQNDAEHLSDIGITAVIIPAYKGLSGSDNGYGYDLYD 61
D 3 NGLTMQYFEWYTPNDGQWKRLLQNDAEHLSDIGITAVIIPAYKGLSGSDNGYGYDLYD 62
QY 62 LGFPOQKGVTRKTYGKESLQDAIGSLHRSNRYGVAVLNHKAADATBDTAVENPA 121
D 63 LGFPOQKGVTRKTYGKESLQDAIGSLHRSNRYGVAVLNHKAADATBDTAVENPA 122
QY 122 NRNOETSEYQIKAWTDFRFRGRNTYSDPKMHWYHEDGADMDSESRKISRIKFRGEGKA 181
D 124 DRTREISEPFEIEGWTFRFGTQYSSFRKNSSEHNHGDPDFARRERTGVFAGENKK 183
QY 182 WDWESSENGNYDYLYMADVDYDHPDYVAETKKMGWYANELSLDGRIDAAKHIFESL 241
D 184 WNEVNDDEFGNYDYLYMADVDYDHPDYVAETKKMGWYANELSLDGRIDAAKHIFESL 243
QY 242 RDWYQAVROATGKEMFTYAEYQWONNAGLENYLNTKTSFNOSVDFVPLHFNLOAASQGG 301
D 244 KEFAEMIRKRGQGFYIYGEFWSNSLDCREFLDTVDYQIDLPVSLHLYKHEHSLGRD 303
QY 302 YDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAVAFILITRESGYQV 361
D 304 FDLKIFPDITVQHTPHAVTFVNDHDSQFHEALSWIGDWFKSAVALTLIRDDGYPVV 363
QY 362 FYGDMYGTGTSPEIKNIEPILKARKEVYAGPOHDIYDHPDYIGWTRBEGSSAAK 421
D 364 FYGDYGGIGG--PEPYDGRKEILDLILSARCNKAYGEQEDYFDHANTIGWTRBEGIEG 421
QY 422 SGLAALITDGPQGSKRWYAGLKNAGETWYDITGNRSPTVK.GSDGMBEFHYNDGSVSI 480
D 422 SGCAVVISNGDDEKRWYAGLKNAGETWYDITGNRSPTVK.GSDGMBEFHYNDGSVSI 480
```

RESULT 10

```
P98026
alpha-amy1ase (EC 3.2.1.1) precursor [imported] - Streptococcus pneumoniae (strain R6)
C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C/Accession: P98026
R/RefSeq: J. K. J. Arnold, J. W. Arnold, J. Blaszcak, L. J. Burgett, S. J. DeHoff, B. S. J. E
e, R. J. LeBlanc, D. J. Lee, L. N. J. Leckwitz, E. J. Lu, J. J. Matsushima, P. J. McAhren, S. J. M
e, R. J. Sun, P. M. J. Winkler, M. E.
Y. J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R. H.; Jaskunas, S. R.;
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; MUID:21429245; PMID:11544234
A/Accession: P98026
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-484 <KUR>
A/Cross-references: GB:AB007317; PIDN:AA00043.1; PID:G15458876; GSPDB:GN00174
C/Genetics:
A/Genes: amy1
C/Superfamily: alpha-amy1ase, amy1oliquefaciens type; alpha-amy1ase core homology
C/Keywords: glycosidase; hydrolase
```

Query Match 46.2%; Score 1212; DB 2; Length 484;

Best Local Similarity 46.6%; Pred. No. 2.4e-78;

Matches 224; Conservative 84; Mismatches 167; Indels 6; Gaps 3;

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QY 2 NGLTMQYFEWYTPNDGQWKRLLQNDAEHLSDIGITAVIIPAYKGLSGSDNGYGYDLYD 61
D 3 NGLTMQYFEWYTPNDGQWKRLLQNDAEHLSDIGITAVIIPAYKGLSGSDNGYGYDLYD 62
QY 62 LGFPOQKGVTRKTYGKESLQDAIGSLHRSNRYGVAVLNHKAADATBDTAVENPA 121
D 63 LGFPOQKGVTRKTYGKESLQDAIGSLHRSNRYGVAVLNHKAADATBDTAVENPA 122
QY 122 NRNOETSEYQIKAWTDFRFRGRNTYSDPKMHWYHEDGADMDSESRKISRIKFRGEGKA 181
D 124 DRTREISEPFEIEGWTFRFGTQYSSFRKNSSEHNHGDPDFARRERTGVFAGENKK 183
QY 182 WDWESSENGNYDYLYMADVDYDHPDYVAETKKMGWYANELSLDGRIDAAKHIFESL 241
D 184 WNEVNDDEFGNYDYLYMADVDYDHPDYVAETKKMGWYANELSLDGRIDAAKHIFESL 243
QY 242 RDWYQAVROATGKEMFTYAEYQWONNAGLENYLNTKTSFNOSVDFVPLHFNLOAASQGG 301
D 244 KEFAEMIRKRGQGFYIYGEFWSNSLDCREFLDTVDYQIDLPVSLHLYKHEHSLGRD 303
QY 302 YDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAVAFILITRESGYQV 361
D 304 FDLKIFPDITVQHTPHAVTFVNDHDSQFHEALSWIGDWFKSAVALTLIRDDGYPVV 363
QY 362 FYGDMYGTGTSPEIKNIEPILKARKEVYAGPOHDIYDHPDYIGWTRBEGSSAAK 421
D 364 FYGDYGGIGG--PEPYDGRKEILDLILSARCNKAYGEQEDYFDHANTIGWTRBEGIEG 421
QY 422 SGLAALITDGPQGSKRWYAGLKNAGETWYDITGNRSPTVK.GSDGMBEFHYNDGSVSI 480
D 422 SGCAVVISNGDDEKRWYAGLKNAGETWYDITGNRSPTVK.GSDGMBEFHYNDGSVSI 480
```

Db	Qy	Dd
420	480	479
-QS2PAAVLSINDQENSKMFWGQENTNQTFFVDLJGSHQGVTTIDEEGYGFPVARSVS	480 Y 480	479 W 479

RESULT 11

AH2079
 alpha-amyLase [imported] - Nostoc sp. (strain PCC 7120)
 C/Species: Nostoc sp. PCC 7120
 A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C/Accession: AH2079
 R/Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuch
 R.; Kaneko, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
 DNA Reel: 8, 205-213, 2001
 A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A/Reference number: AB1807; MUID:21595285; PMID:11759840
 A/Accession: AH2079
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-492 <XR>
 A/Cross-references: GB:BA000019; PIDN:BA073889.1; PID:G1731281; GSPDB:GN00179
 A/Experimental source: strain PCC 7120
 C/Genetic(s)
 A/Gene(s): alr2190
 A/Superfamily: alpha-amyLase, amyLlikefacians type; alpha-amyLase core homology

```

Query March 1997: 45.6%; Score 1197; DB 2; Length 492;
Best Local Similarity 47.3%; Pred. No. 2.8e-77;
Matches 234; Conservative 74; Mismatches 163; Indels 24; Gaps 7;

QY      1 VNGTLMOYFEYTYTNDGCHFKRLONDAEHLSDIGITAVIMPPAYKLSQS--DNGYCPDL 59
          :::::
Db      4 MNGTMMOYFHYIYINDGNLMSKVEASAPELADAFETAMLEPPAKGFSGSDVGVGYDL 63

QY      60 YDLPEFOOKGVRFTKYGTSKSELQDAIGSLHSRNVOYGVAVLNHKAADAFEDVTAV-- 116
          :::::
Db      64 FDLGEFPOKGSVRKIKYGRQGYLDAYKSLQTHGQYVADAVLNHMGSDAETTKATPFP 123

QY      117 ---EVNPANRNOETSEYQIKAMTDPRFPFGGNTYSDEPKMHWYHPDGDAMDESKISIF 173
          :::::
Db      124 QDRLNRPKGLOD-----IKTYHYNFPFGQGXSNEMHWMEHDAVDVYNSGDST 177

QY      174 KFRGEGKAMDEWSESSENGNYDYLMYADVDPVAVATKKMGIVANELSLDGRIDA 233
          :::::
Db      178 VYLLEGKNFDDYVALKEKNFAYLMGCDLDPQNEBWRGVSFTWGMKCLDTTKVDEGRIDA 237

QY      234 KHIFSFRLRWQVAVRQATGKEMFTVABYQNNNAKLENTYANKTSPNOSVDPVPLHFLO 293
          :::::
Db      238 KHITWFPFWIDALERHAGKDLFVNGEYWNIDITLLMYDVARGNKSVDPVPLHYNFH 297

QY      294 AASQSGGYDARRRLDGTIVGSRHPKAVTFEENHDTQGSLESTVQTFWPLAFAFLT 353
          :::::
Db      298 QASISGNGYDMRRIIDGTMMQGRPTHAVTFEENHDSQCLQLESVEBFWFPLAVALILL 357

QY      354 RESGYPOYFYGDMYGTK---GTSPEK---IPSLKNIIEPLKARKKAYAGFGQDYLDH 405
          :::::
Db      358 RQEGPQPCVFAHDYGALEYEDWKGQGNRYNIFPSPSRMIIIDKLLYARKKAYAGFPQNYLDH 417

QY      406 PDVIGMTREDSGSSAAKSGIALALITDGPQSGSKMYAGLNKAGETWDTIGNSDITYKIGSD 465
          :::::
Db      418 INTIGMTRLGDADHDQ--GMAVIMSDGSGIKMVEGXKPT--KFIDLFEHIKEAVYTNEW 474

QY      466 GWMGEFHWVDGSVSIV 480
          :::::
Db      475 GWMGEFRLCGGSVSIVW 489

```

```
RESULT 12
C86781
alpha-amylase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
```

C|Species: *Lactococcus lactis* subsp. *lactis*
C|Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #ext_change 03-Aug-2001
C|Accession: C86781
R|Bolotin, A.; Muncher, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A|Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ss
A|Reference number: A86625; MUID:21235166; PMID:11337471
A|Accession: C86781
A|Status: Preliminary
A|Molecule type: DNA
A|Residues: 1-491 <SNO>
A|CROSS-References: GB:AE005176; PID:G12724224; PIDN:AAK05349.1; GSPDB:GN00146
A|Experimental source: strain IL1403
C|Genetics:
A|Gene: amy^L
C|superfamily: alpha-amy^Lase, amy^Loliquetaciens type, alpha-amy^Lase core homology

[illegible]

RESULT 13
ADJ038
alpha-amy1aee amyA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C/Accession: ADJ038
R/Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo-
erger, G.; Gillet, P.; Grant, C.; Guenthermer, D.; Kuyavlin, T.; Levy, R.; Li, M.; McCl^e
rge, J.; Karp, D.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A/File: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21609550; PMID:11743193
A/Accession: ADJ038

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-495 <KUR>
 A:Cross-references: GB:AE008689; PIDN:AA44722.1; PID:G17742354; GSPDB:GN00187
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: amyA
 A:Map position: linear chromosome
 C:Superfamily: alpha-amyLase, amy101iquefaciens type; alpha-amyLase core homology

Query Match 40.0%; Score 1050; DB 2; Length 495;
 Best Local Similarity 43.6%; Pred. No. 7.66-67;
 Matches 213; Conservative 77; Mismatches 183; Indels 16; Gaps 6;

```

QY 4 TLMQYFEMWYTPNDGQHWKRLQNDAEHLSDIGITAVMTTPPAYKGLSGSDN-GYGPYDLYDL 62
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 TLLQFFHYWYDPDGKLMSEVAEKASLAKKQGITVWMLPPAYKGAAGYSGVGYDTYDL 64
QY 63 GEPQKGTATKTKYKSKSELQDAIGSLHSRNQYGVVYLNKAGADATEDVTAVEVNPAN 122
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
65 GEPDQKGTATKTKYKSKSELQDAIGSLHSRNQYGVVYLNKAGADATEDVTAVEVNPAN 124
QY 123 RNQETSEEVQIKAWTDFFPFGKNTYSDFKMWHYFDGADNDESKISRTFKF--RGE 179
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
125 RTDIDEDFPALAYTRFTFPGRNKHSKFIWDLKCFSGVDHIEPTEDGIFRLVNEYGDG 184
QY 180 KAMDVESENGNRYLYMAYDVYDHPVAVETKMGWYANELSLDGFRIIDAKHIFKS 239
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
185 E-WNEEVDQENGFYLMGADVEFRNRAVYELKYMGRMSEQYQVDFRLDAKHIPAW 243
QY 240 FLRDVQAVRQATGKEMFTVAEYQWNAKGLNTLNTKTSFNQSYFDVPLHFNLOAASSQ 299
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
244 FFRDVGHRRETVDPDLFVVAEYVHPDLEALKSYLELVKQMLFDVALHHSFHDASKQ 303
QY 300 GGYDMRRLDGTVSRHREKAVTFVENNDTOPGQSLSTVQTFKPLAYAFILTRBSGY 359
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
304 GDFMRSITFDGSLVSAVDAVTHVNDHTQPLQSLHAPVFPWPKPLAYAILTRBSGY 363
QY 360 QVFYDMYGTGKTSRK-----EIPSLKDNIEPILAKREYVYGPQHDYIDHPVIGW 411
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
364 CVFYFDLFTSTYTDGNGENYKIDIPAI-ECLPLIEARSRFANGPQTDIFDASCIAF 422
QY 412 TREBSSAAKSGLAALITDPPGSKRMVAGLKNAGETTYDITGNRSPTVKISGQMEFH 471
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
423 IRHGTA--PGCVVMSNGEPGEKQADLGERASVWRDLGHRHEHITLDESCKGTFP 480
QY 472 VNDGSYSY 480
DB 481 TNGGSYSVM 489

```

RESULT 14

G98247
 Cytoplasmic alpha-amyLase (1,4-alpha-D-glucan glucanohydrolase) [imported] - Agrobacteri
 C:Species: Agrobacterium tumefaciens
 C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
 C:Accession: G98247
 A:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirilo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: G98247
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-506 <KUR>
 A:Cross-references: GB:AE007870; PIDN:AAK89505.1; PID:G15159379; GSPDB:GN00170
 C:Genetics:
 A:Gene: AGR_L_1863
 A:Map position: linear chromosome
 C:Superfamily: alpha-amyLase, amy101iquefaciens type; alpha-amyLase core homology

Query Match 40.0%; Score 1050; DB 2; Length 506;

Best Local Similarity 43.6%; Pred. No. 7.96-67;
 Matches 213; Conservative 77; Mismatches 183; Indels 16; Gaps 6;

```

QY 4 TLMQYFEMWYTPNDGQHWKRLQNDAEHLSDIGITAVMTTPPAYKGLSGSDN-GYGPYDLYDL 62
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
16 TLLQFFHYWYDPDGKLMSEVAEKASLAKKQGITVWMLPPAYKGAAGYSGVGYDTYDL 75
QY 63 GEPQKGTATKTKYKSKSELQDAIGSLHSRNQYGVVYLNKAGADATEDVTAVEVNPAN 122
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
76 GEPDQKGTATKTKYKSKSELQDAIGSLHSRNQYGVVYLNKAGADATEDVTAVEVNPAN 135
QY 123 RNQETSEEVQIKAWTDFFPFGKNTYSDFKMWHYFDGADNDESKISRTFKF--RGE 179
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
136 RTDIDEDFPALAYTRFTFPGRNKHSKFIWDLKCFSGVDHIEPTEDGIFRLVNEYGDG 195
QY 180 KAMDVESENGNRYLYMAYDVYDHPVAVETKMGWYANELSLDGFRIIDAKHIFKS 239
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
196 E-WNEEVDQENGFYLMGADVEFRNRAVYELKYMGRMSEQYQVDFRLDAKHIPAW 254
QY 240 FLRDVQAVRQATGKEMFTVAEYQWNAKGLNTLNTKTSFNQSYFDVPLHFNLOAASSQ 299
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
255 FFRDVGHRRETVDPDLFVVAEYVHPDLEALKSYLELVKQMLFDVALHHSFHDASKQ 314
QY 300 GGYDMRRLDGTVSRHREKAVTFVENNDTOPGQSLSTVQTFKPLAYAFILTRBSGY 359
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
315 GDFMRSITFDGSLVSAVDAVTHVNDHTQPLQSLHAPVFPWPKPLAYAILTRBSGY 374
QY 360 QVFYDMYGTGKTSRK-----EIPSLKDNIEPILAKREYVYGPQHDYIDHPVIGW 411
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
375 CVFYFDLFTSTYTDGNGENYKIDIPAI-ECLPLIEARSRFANGPQTDIFDASCIAF 433
QY 412 TREBSSAAKSGLAALITDPPGSKRMVAGLKNAGETTYDITGNRSPTVKISGQMEFH 471
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
434 IRHGTA--PGCVVMSNGEPGEKQADLGERASVWRDLGHRHEHITLDESCKGTFP 491
QY 472 VNDGSYSY 480
DB 492 TNGGSYSVM 500

```

RESULT 15

B45738
 Alpha-amyLase (EC 3.2.1.1), cytosolic - Salmonella typhimurium
 N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C:Species: Salmonella typhimurium
 C>Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
 C:Accession: B45738
 R:Raha, M.; Kawagishi, I.; Mueller, V.; Khara, M.; Macnab, R.M.
 J. Bacteriol. 174, 6644-6652, 1992
 A>Title: Escherichia coli produces a cytoplasmic alpha-amyLase, amyA.
 A:Reference number: A45738; MUID:93015717; PMID:1400215
 A:Accession: B45738
 A:Molecule type: DNA
 A:Residues: 1-494 <KUR>
 A:Cross-references: GB:L01643; NID:G154043; PIDN:AAA27110.1; PID:G154045
 C:Genetics:
 A:Gene: amyA
 A:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: alpha-amyLase, amy101iquefaciens type; alpha-amyLase core homology
 C:Key words: cytosol; glycosidase; hydrolase; polysaccharide degradation
 F:202-335/Domain: alpha-amyLase core homology <AMY>
 F:239,265/332/Active site: His, Glu, Asp #status predicted

Query Match 38.7%; Score 1015; DB 1; Length 494;
 Best Local Similarity 41.2%; Pred. No. 2.3e-64;
 Matches 202; Conservative 77; Mismatches 197; Indels 14; Gaps 5;

```

QY 2 NGTLMQYFEMWYTPNDGQHWKRLQNDAEHLSDIGITAVMTTPPAYKGLSGSDN-GYGPYDLY 60
DB 3 NPTLMQYFEMWYTPNDGKLMSEVAEKASLAKKQGITVWMLPPAYKGAAGYSGVGYDTYDL 62

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Tue May 4 14:34:47 2004

us-10-644-187-4.rpr

QY 61 DLGEFOQKGTIVRTYKTKSELODAIGSIHSHNVQVYGVVJLNHKGADATEDVTAVEVNP 120
Db 63 DLGEFDQKGTATATYGDQRQLTALDALKKNINAVLLDVVYNHMGADBEKERIRVQRVNO 122
QY 121 ANRQOETSEEYQIATMDFRFPGRGNTYSDFKMTWYHFDGADNDESKRSRIKFRGE-- 178
Db 123 DDKTQIDNNIECGWTRTYTPPARAGQYSNFIWDYHCFSGIDHLENPDEDEGIFKIVNDYT 182
QY 179 GKAWDWEYSSENGVYDLYMADVDYDHPDVVAETKKGIMWYANELSLDGFRIDAKHIF 238
Db 183 GDGNNDQVDDMGNDYLMGENIDFRNNAVTBEIKWAPRWMEQTHCGFRIDAVKHIPA 242
QY 239 SFLRDWQAVQATGKEMFTVAETWQNNAGLENTLNKTSFNQSVFDPVPLHFNLOASSQ 298
Db 243 WPKYKEMIHHVQAVAPKPLFIVAETWWSHEDKLTQTYIDQVDGKTWLFDAPLQMKFHEASRQ 302
QY 299 GGGYDMRRLDGTIVSRHPEKAVTFVENHOTOPOGOSLES TVQTWFKPLAVAFILTRSGY 358
Db 303 GAETDMRHIFTGTLVEADPPHATVILVANHDTOPLOALEAPYEPWFKPLAYALLILRENGV 362
QY 359 PQVYGDWYGTK-----GTSPEKIPSLKONTIEPIKARKEYAYGBOHDYIDHPVIG 410
Db 363 PSVFYDPLYGASYEDSGENGECRCVDMPEVI-NQLDRLILARQRFAGHGIQTLFFDHPNCIA 421
QY 411 WTRBGDSAAKSGLAALITDGPBGSKRMVAGLKNAGETWYDITGNRSDTYKISDGWGEF 470
Db 422 FSRSG--TEENPGCVVVLNSGDDGKTIILLSDNTANKTWDPGSRDEYVVTNDQGEATF 479
QY 471 HUNDGSVSIY 480
Db 480 FCNAGSVSVW 489

Search completed: May 3, 2004, 20:54:06
Job time : 15.6493 secs

Tue May 4 14:34:47 2004

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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:36:03 ; Search time 10.3995 Seconds

(without alignments)
2403.363 Million cell updates/sec

Title: US-10-644-187-4

Perfect score: 2624

Sequence: 1 VNGITLMQYFEMWYTPNDQHM.....KIGSDGWFHVDGVSIV 480

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2624	100.0	514	1	AMY_BACAM
2	2176	82.9	512	1	AMY_BACLI
3	1826	69.6	518	1	AMT6_BACST
4	1758.5	67.0	549	1	AMY_BACST
5	1013	38.6	494	1	AMY2_SALTY
6	998	38.0	495	1	AMY2_ECOLI
7	346	13.2	440	1	AMY3_ORYSA
8	333.5	12.7	421	1	AMYA_VIGMU
9	324	12.3	437	1	AM3C_ORYSA
10	323	12.3	1196	1	AMVB_PABPO
11	319	12.2	438	1	AM3B_ORYSA
12	318	12.1	435	1	AM3D_ORYSA
13	315.5	12.0	437	1	AM3E_ORYSA
14	315	12.0	413	1	AMY3_WHEAT
15	307.5	11.7	438	1	AMY1_HORVU
16	289	11.0	429	1	AMY6_HORVU
17	285.5	10.9	713	1	CDGT_BACST
18	284.5	10.8	443	1	AM2A_ORYSA
19	284.5	10.8	445	1	AMC2_ORYSA
20	283	10.8	427	1	AMY2_HORVU
21	282	10.7	368	1	AMY3_HORVU
22	277.5	10.6	713	1	CDGT_BACLI
23	272	10.4	713	1	CDGT_BACSP
24	270	10.3	428	1	AMY1_STRLI
25	267.5	10.2	919	1	AMY_STRLI
26	255	9.7	712	1	CDGT_BACST
27	253	9.6	718	1	CDGT_BACST
28	253	9.6	718	1	CDGT_BACSS
29	251	9.6	713	1	CDGT_BACSO
30	246	9.4	581	1	AMY1_SCHPO
31	245	9.3	719	1	AMYM_BACST
32	244.5	9.3	478	1	Y029_SCHPO
33	244.5	9.3	528	1	AMY_BACCT

34	242.5	9.2	718	1	CDGT_BACLI	P14014 bacillus 14
35	241	9.2	564	1	AMY4_SCHPO	Q97789 schizosacch
36	240.5	9.2	710	1	CDGT_THETU	P26827 thermoaer
37	240	9.1	494	1	AMY1_SACFI	P21567 saccharomyc
38	234.5	8.9	711	1	CDGT_BACST	P11797 bacillus st
39	232	8.8	498	1	AMY3_DICIT	P14885 dictyoglomu
40	229	8.7	441	1	MGT4_THEMA	P80099 thermotoga
41	228.5	8.7	499	1	AMYA_ASFOR	P10529 aspergillus
42	228	8.7	676	1	AMY1_ECOLI	P25718 escherichia
43	225.5	8.6	442	1	MGT4_THENE	O86956 thermotoga
44	225.5	8.6	499	1	AMY ASPSH	P30292 aspergillus
45	222.5	8.5	498	1	AMYA_ASFAM	Q02905 aspergillus

ALIGNMENTS

RESULT 1	AMY_BACAM	STANDARD;	PRT;	514 AA.
AC	AMY_BACAM			
AC	P00692;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-JAN-1988 (Rel. 06, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan			
DE	glucanohydrolase).			
OS	Bacillus amyloliquefaciens			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_Taxid=1390;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=IH.			
RX	MEDLINE=8310808; PubMed=6185474.			
RA	Takkinen K., Petersson R.F., Kalkkinen N., Palva I., Seoderlund H.,			
RA	Kaeserlaeinen L.;			
RT	"Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens			
RT	deduced from the nucleotide sequence of the cloned gene.";			
RL	J. Biol. Chem. 258:1007-1013(1983).			
RL	[2]			
RP	SEQUENCE OF 32-222.			
RX	MEDLINE=80241725; PubMed=6156671;			
RA	Chung H.S., Friedberg F.;			
RT	"Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-			
RT	amylase.";			
RL	Biochem. J. 185:387-395(1980).			
RL	[3]			
RP	SEQUENCE OF 1-96 FROM N.A.			
RX	MEDLINE=82051296; PubMed=6170539;			
RA	Palva I., Petersson R.F., Kalkkinen N., Lehtoavaara P., Sarvas M.,			
RA	Soederlund H., Takkinen K., Kaeserlaeinen L.;			
RT	"Nucleotide sequence of the promoter and NH2-terminal signal peptide			
RT	region of the alpha-amylase gene from Bacillus amyloliquefaciens.";			
RL	Gene 15:43-51(1981).			
RL	[4]			
RP	SEQUENCE OF 1-39 FROM N.A.			
RX	MEDLINE=88137952; PubMed=2830166;			
RA	Ruohonen L., Hackman P., Lehtoavaara P., Knowles J.K.C., Karanen S.;			
RT	"Efficient secretion of Bacillus amyloliquefaciens alpha-amylase by			
RT	its own signal peptide from Saccharomyces cerevisiae host cells.";			
RL	Gene 59:161-170(1987).			
RL	[5]			
RP	X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-331.			
RX	MEDLINE=20384196; PubMed=10924103;			
RA	Brozowski A.M., Lawson D.M., Turkenburg J.P., Biegaard-Frantzen H.,			
RA	Sverdrup A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;			
RT	"Structural analysis of a chimeric bacterial alpha-amylase.			
RT	High-resolution analysis of native and ligand complexes.";			
RL	Biochemistry 39:909-9107(2000).			
CC	-1- CATALYTIC ACTIVITY: Endoamylolysis of 1,4-alpha-glucosidic			
CC	linkages in oligosaccharides and polysaccharides.			
CC	-1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.			
CC	-1- SUBUNIT: Monomer.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			

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-|- SIMILARITY: Belongs to family 13 of glycosyl hydrolases

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CC	-----
DR	EMBL; J01542; AAA22191.1; -
DR	EMBL; V00092; CAA23430.1; -
DR	EMBL; A20154; CAA01489.1; -
DR	EMBL; M18424; AAA22192.1; -
DR	PIR; A92389; ALBSN
DR	PDB; 1E3X; 21-JUN-01.
DR	PDB; 1E3Z; 24-JUN-03.
DR	PDB; 1E40; 24-JUN-03.
DR	PDB; 1E43; 21-JUN-01.
DR	InterPro; IPR006589; Alp_amy1_cat_sub.
DR	InterPro; IPR006047; Alpha_amy_cat.
DR	InterPro; IPR006046; Glyco_hydro_13.
DR	Pfam; PF00128; alpha-amy-lase; 1.
DR	PRINTS; PR00110; ALPHAAMYLAZE.
DR	SMART; SMO0642; Amyy; 1.
KW	Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding; Signal; 3D-structure.
FT	SIGNAL 1 31
FT	CHAIN 32 514
FT	ACT_SITE 262 262
FT	ACT_SITE 292 292
FT	ACT_SITE 359 359
FT	METAL 133 133
FT	METAL 190 190
FT	METAL 212 212
FT	METAL 214 214
FT	METAL 225 225
FT	METAL 231 231
FT	METAL 233 233
FT	METAL 235 235
FT	METAL 266 266
FT	METAL 331 331
FT	METAL 438 438
FT	METAL 461 461
FT	CONFLICT 54 54
FT	CONFLICT 64 64
FT	CONFLICT 79 79
FT	CONFLICT 84 84
FT	SEQUENCE 514 AA; 58403 MW; 3DSE6B3FBCDE7E CRC64;
BY SIMILARITY.	
CALCIUM 1.	
CALCIUM 2 AND SODIUM.	
CALCIUM 2 (VIA CARBOXYL OXYGEN).	
CALCIUM 1 AND SODIUM.	
CALCIUM 1 AND SODIUM.	
CALCIUM 1 AND SODIUM.	
CALCIUM 2.	
CALCIUM 2.	
CALCIUM 1 (VIA CARBOXYL OXYGEN).	
CALCIUM 3 (VIA CARBOXYL OXYGEN).	
CALCIUM 3 (BY SIMILARITY).	
CALCIUM 3 (BY SIMILARITY).	
L -> 1 (IN REF. 2).	
I -> 1 (IN REF. 2).	
S -> D (IN REF. 2).	
G -> S (IN REF. 2).	

Query Match	100.0%;	Score 2624;	DB 1;	Length 514;
Best Local Similarity	100.0%;	Pred. No. 1.7e-178;		
Matches 480;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	VNGTLMQYEWYTPNDGQHMKRLQNDAEHLSDIGITAVWI	PRAKYGLSOSDNGYGEYDLY	60
Db	32	VNGTLMQYEWYTPNDGQHMKRLQNDAEHLSDIGITAVWI	PRAKYGLSOSDNGYGEYDLY	91
Qy	61	DIGFQOKTVAATKXGTSELODAGSLHSRNVQYGDVYL	LHKAGADTEPDTAVANP	120
Db	92	DIGFQOKTVAATKXGTSELODAGSLHSRNVQYGDVYL	LHKAGADTEPDTAVANP	151
Qy	121	ANRNOETSEEYOIKAWTDFRPGKNTYSDFKKEMTH	FPQADMDESRKTSRIIFKFGEGK	180
Db	152	ANRNOETSEEYOIKAWTDFRPGKNTYSDFKKEMTH	FPQADMDESRKTSRIIFKFGEGK	211
Qy	181	ANDWEVSSENGVYDYLMTADVVDYDHDVVAETKMG	IWTANELSLGFRIDAATKIKFSF	240
Db	212	ANDWEVSSENGVYDYLMTADVVDYDHDVVAETKMG	IWTANELSLGFRIDAATKIKFSF	271
Qy	241	LADWQAVQACGKEMFTVAEYKQNNAGKLENTLNTS	FNQOSFVDVPIPHNLQAASSOGG	300
Db	272	LADWQAVQACGKEMFTVAEYKQNNAGKLENTLNTS	FNQOSFVDVPIPHNLQAASSOGG	331

QY	301	GYMRLLDGVTVSRHPEKATFVNHNHDTQCGQSLESTVQVWFPLVAFILITSESGY	360
Db	332	GYMRRLDGVTVSRHPEKATFVNHNHDTQCGQSLESTVQVWFPLVAFILITSESGY	391
QY	361	VFYGDVNGTGTGSPKIEPILKDNINIEPILKAREYAYGQHDYIDHPDVTGWTREDSAA	420
Db	392	VFYGDVNGTGTGSPKIEPILKDNINIEPILKAREYAYGQHDYIDHPDVTGWTREDSAA	451
QY	421	KSGIALIITDGPGRKMYAGLKNAGETWYDITGNRSDTVXIGSDGWEFFHNDGSYIY	480
Db	452	KSGIALIITDGPGRKMYAGLKNAGETWYDITGNRSDTVXIGSDGWEFFHNDGSYIY	511

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RESULT 2
ID AMY_BACLI STANDARD; PRT; 512 AA.
AC _AMY_BACLI
DT 065278; 08471;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase) (BLN).
GN AMYS OR AMYL.
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TextID=1402;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 27811;
RX MEDLINE=8611694; PubMed=2418011;
RA Yuuki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,
RA Tsukagoshi N., Udaoka S.;
RT "Complete nucleotide sequence of a gene coding for heat- and
RT pH-stable alpha-amylase of Bacillus licheniformis: comparison of the
RT amino acid sequences of three bacterial liquefying alpha-amylases
RT deduced from the DNA sequences.";
RL J. Biochem. 98:1147-1156(1985).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=86198857; PubMed=3009417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
RA Carmona C., Reguadt C.;
RT "Structural genes encoding the thermophilic alpha-amylases of
RT Bacillus stearotherophilus and Bacillus licheniformis.";
RL J. Bacteriol. 166:635-643(1986).
RN [3]
RN SEQUENCE FROM N.A.
RX Shahboshini M., Zisael A.A., Ghaemi N., Pourbabaei A.A.;
RT "An unusual DNA sequence encoded a hyperthermostable alpha-amylase.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE OF 1-104 FROM N.A.
RX MEDLINE=84185455; PubMed=6609154;
RA Stephens M.A., Ortlepp S.A., Ollington J.F., McConnell D.J.;
RT "Nucleotide sequence of the 5' region of the Bacillus licheniformis
RT alpha-amylase gene: comparison with the B. amyloliquefaciens gene.";
RL J. Bacteriol. 158:369-372(1984).
RN [5]
RN SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=89213924; PubMed=2540150;
RA Iacide B.M., Chambliss G.H., McConnell D.J.;
RT "Bacillus licheniformis alpha-amylase gene, amyA, is subject to
RT promoter-independent catabolite repression in Bacillus subtilis.";
RL J. Bacteriol. 171:2433-2442(1989).
RN [6]
RN SEQUENCE OF 30-47.
RX MEDLINE=82098050; PubMed=6172418;
RA Kuhn H., Fietzek P.P., Lampen J.O.;
RT "N-terminal amino acid sequence of Bacillus licheniformis
RT alpha-amylase: comparison with Bacillus amyloliquefaciens and
RT Bacillus subtilis enzymes.";
RL J. Bacteriol. 149:372-373(1992).

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[7]
RT MAPPING OF SUBSTRATE-BINDING SITE.
RX MEDLINE=21992788; PubMed=11997021.
RA Kandra J., Gyemant G., Remenyik J., Hovanszki G., Lipcak A.;
RT "Action pattern and substrate mapping of Bacillus licheniformis
RT alpha-amylase (BLA) with modified maltotriose oligosaccharide substrates.";
RL FEBS Lett. 518:79-82(2002).
[8]
RN MUTAGENESIS OF HIS-64; HIS-162; HIS-276; HIS-322; HIS-435 AND HIS-479.
RP STRAIN=ATCC 6598;
RX MEDLINE=90368748; PubMed=2394736;
RA Declerck N., Joyet P., Galliardin C., Masson J.M.;
RT "Use of amber suppressors to investigate the thermostability of
RT Bacillus licheniformis alpha-amylase. Amino acid replacements at 6
RT histidine residues reveal a critical position at His-133.";
RL J. Biol. Chem. 265:15481-15486(1990).
[9]
RN MUTAGENESIS OF ALA-238.
RP STRAIN=ATCC 6598;
RX MEDLINE=96367070; PubMed=8771184;
RA Declerck N., Joyet P., Trosser J.Y., Garnier J., Galliardin C.;
RT "Hyperthermostable mutants of Bacillus licheniformis alpha-amylase:
RT multiple amino acid replacements and molecular modelling.";
RL Protein Eng. 8:1029-1037(1995).
[10]
RN MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;
RP ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-298; GLU-300; GLN-359
RP AND GLU-365.
RX STRAIN=ATCC 6598;
RA MEDLINE=20425100; PubMed=10966804;
RT Declerck N., Machius M., Wiegand G., Huber R., Galliardin C.;
RT "Probing structural determinants specifying high thermostability in
RT Bacillus licheniformis alpha-amylase.";
RL J. Mol. Biol. 301:1041-1057(2000).
[11]
RN MUTAGENESIS OF GLN-293 AND ASN-294.
RP STRAIN=ATCC 6598;
RX MEDLINE=22622182; PubMed=12736372;
RA Declerck N., Machius M., Joyet P., Wiegand G., Huber R.,
RA Galliardin C.;
RT "Hyperthermostabilization of Bacillus licheniformis alpha-amylase and
RT modulation of its stability over a 50 degrees C temperature range.";
RL Protein Eng. 16:267-293(2003).
[12]
RN MUTAGENESIS OF TRP-292 AND VAL-315.
RP STRAIN=ATCC 27811;
RX MEDLINE=22797417; PubMed=12915728;
RA Rivera M.H., Lopez-Munguia A., Scheron X., Saab-Rincon G.;
RT "Alpha-amylase from Bacillus licheniformis mutants near to the
RT catalytic site: effects on hydrolytic and transglycosylation
RT activity.";
RL Protein Eng. 16:505-514(2003).
[13]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RP STRAIN=ATCC 27811;
RX MEDLINE=95182462; PubMed=7877175;
RA Machius M., Wiegand G., Huber R.;
RT "Crystal structure of calcium-depleted Bacillus licheniformis alpha-
RT amylase at 2.2-A resolution.";
RL J. Mol. Biol. 246:545-559(1995).
[14]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RP MEDLINE=98212915; PubMed=9551551;
RA Machius M., Declerck N., Huber R., Wiegand G.;
RT "Activation of Bacillus licheniformis alpha-amylase through a
RT disorder-to-order transition of the substrate-binding site mediated
RT by a calcium-sodium-calcium metal triad.";
RL Structure 6:281-292(1998).
[15]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 330-512.
RP MEDLINE=20384196; PubMed=10924103;
RA Brzozowski A.M., Lawson D.M., Turkemburg J.P., Bisgaard-Frantzen H.,
RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;

RT "Structural analysis of a chimeric bacterial alpha-amylase.
RT High-resolution analysis of native and ligand complexes.";
RL Biochemistry 39:9099-9107(2000).
[16]
RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT
RP STRAIN=ATCC 6598;
RX MEDLINE=22538505; PubMed=12540849;
RA Machius M., Declerck N., Huber R., Wiegand G.;
RT "Kinetic stabilization of Bacillus licheniformis alpha-amylase through
RT introduction of hydrophobic residues at the surface.";
RL J. Biol. Chem. 278:11546-11553(2003).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- BIOTECHNOLOGY: Used in the food industry for high temperature
CC liquefaction of starch-containing mashes and in the detergent
CC industry to remove starch. Sold under the name Remamy1 by
CC Novozymes.
CC -1- MISCELLANEOUS: Able to work at relatively high (alkaline) pH
CC values (up to pH 11) and at high temperatures (up to 100 degrees
CC Celsius).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X03236; CAA6981.1; -
DR EMBL; M38570; AAA2226.1; -
DR EMBL; M13256; AAA2240.1; -
DR EMBL; K01984; AAA22193.1; -
DR EMBL; AP438149; AAO26743.1; -
DR EMBL; W26412; AAA22237.1; -
DR EMBL; A19930; CAA01355.1; -
DR PIR; A91997; ALBSL.
DR PDB; 1BLI; 23-MAR-99.
DR PDB; 1BPL; 17-AUG-96.
DR PDB; 1E3X; 21-JUN-01.
DR PDB; 1E3Z; 24-JUN-03.
DR PDB; 1E40; 24-JUN-03.
DR PDB; 1E43; 21-JUN-01.
DR PDB; 1O80; 12-APR-03.
DR PDB; 1VUS; 03-MAR-97.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase_1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amyy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 512
FT ACT_SITE 260 260
FT ACT_SITE 264 264
FT ACT_SITE 357 357
FT METAL 133 133
FT METAL 190 190
FT METAL 210 210
FT METAL 212 212
FT METAL 223 223
FT METAL 229 229
FT METAL 231 231
FT METAL 233 233
FT METAL 233 233
Query March 82.9%; Score 2176; DB 1; Length 512;
Best Local Similarity 80.6%; Pred. No. 8.8e-147;

Matches	387;	Conservative	42;	Mismatches	49;	Indels	2;	Gaps	1
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Oy	1	VNGLTLNQFFYYTTRNDQGMKRLQNDALHSLDICTITAVMIPPAKGLQSQSDNCGYVDLY	60
Db	32	LNGLTLNQFFYYMYPNDQGMKRLQNDALHSLDICTITAVMIPPAKGLQSQSDNCGYVDLY	91
Oy	61	DLGEFOCKGTARTKXGTSELODAIGSLHSHNVGVYGDVLMNHKAGADATEDVTAENV	120
Db	92	DLGEFHQGTARTKGTGTGGELOSAIKSLHSDINWYGDVLMNHKAGADATEDVTAENV	151
Oy	121	ANRQNETSEEQIKAMDFPRPGGNTYSDPKMHMYHFDGADWPKESKISIFPERGEK	180
Db	152	ADNRNVISGEHRIKAMTFHFPPGKSTYSDPKMHMYHFDGADWPKESKUNRYKF--QK	209
Oy	181	AMDEVSSSENGNYDYLMADYDHPDVAETKMGKIWYANESLSDGRIDMAKHIFSF	240
Db	210	AMDEVSSSENGNYDYLMADYDHPDVAALIKKMGTYANESLSDGRIDVAKHIFSF	269
Oy	241	LRDWQAQAKQATGKEMFTVAEYQNMNGKLENTYNTKTSFNQSVDPVLPHEHTLOASSQG	300
Db	270	LRDWQAHREKTEGEMFTVAEYQNDQCALENTYNTKTNFNSVDVLPHEHTLOASSQG	329
Oy	301	GYDMRRLLDGTGVSSHPEKAVTFVENHDTQGGSLSTVQTWFKPLAVAFILTRSGYPO	360
Db	330	GYDMRKLINSTVSSHPLKAVTFVNDHTQGGSLSTVQTWFKPLAVAFILTRSGYPO	389
Oy	361	VFGYGMVGTCKMSPKEIPSLKDNTEPLIKARKEVAYGQGHYIHPDVGITREGSSAA	420
Db	390	VFGYGMVGTCKMSPKEIPALKNKTEPLIKARKQAYAGQGHYIHPDVGITREGSSAA	449
Oy	421	KSGIALALITDGPQGSKMYAGIKVAGETWYDITGNRSDTVKIGSDGCEHFVNDGSVY	480
Db	450	NSGLAALITDGPQGAKMYVGRONNGETWMDITGNRSEPVINSEMGCEHFVNDGSVY	509

RESULT 3	
AMT6_BACS7	
ID AMT6_BACS7	STANDARD: PRT; 518 AA.
AC P19571;	
DT 01-FEB-1991 (Rel. 17, Created)	
DT 01-FEB-1991 (Rel. 17, Last sequence update)	
DT 10-OCT-2003 (Rel. 42, Last annotation update)	
DE Glucan 1,4-alpha-maltohexosidase precursor (EC 3.2.1.98) (66-amylase)	
DE (Maltotetraose-producing amylase) (Exo-maltotetraohydrolase).	
DS Bacillus sp. (strain 707)	
DS Bacillus; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
NCBI_TaxID=1416;	
RN (1)	
RN SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.	
RX MEDLINE=88162814; PubMed=3258182;	
RA Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;	
RA "Nucleotide sequence of the maltotetraose-producing amylase gene from	
RT an alkaliphilic Bacillus sp. #707 and structural similarity to	
RT liquefying type alpha-amylases."	
RL Biochem. Biophys. Res. Commun. 151:25-31(1988).	
-1 CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages	
CC in amyloseous polysaccharides so as to remove successive	
CC maltotetraose residues from the non-reducing chain ends.	
CC -1 COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By	
CC similarity).	
CC -1 PATHWAY: Starch degradation.	
CC -1 SUBCELLULAR LOCATION: Secreted.	
CC -1 SIMILARITY: Belongs to family 13 of glycosyl hydrolases.	
CC -----	
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CC or send an email to license@isb-sib.ch).	
CC -----	
CC EMBL; M18662; AAA22231.1; -	

	DR	P1R; A2705; A27705.	
	DR	HSSP; P06278; IVUS.	
	DR	InterPro; IPR006589; Alp_ amyl_cat_sub.	
	DR	InterPro; IPR006047; Alpha_ amyl_cat.	
	DR	InterPro; IPR006046; Glyco_hydro_13.	
	DR	Fam; PF00128; alpha-amylose, 1.	
	DR	PRINTS; PR00110; ALPHAAMYLASE.	
	DR	SMART; SM00642; Amy; 1.	
	KW	Hydrolase; Glycosidase; Carbohydrate metabolism; signal.	
	FT	SIGNAL	1
	FT	CHAIN	33
	FT	ACT_SITE	34 518
	FT	ACT_SITE	269 269
	FT	ACT_SITE	273 273
	FT	ACT_SITE	366 366
	FT	METAL	139 139
	FT	METAL	166 166
	FT	METAL	219 219
	FT	METAL	221 221
	FT	METAL	232 232
	FT	METAL	238 238
	FT	METAL	240 240
	FT	METAL	242 242
	FT	METAL	273 273
	SEQ	SEQUENCE	518 AA; 59009 MW; 3A961E2261268204 CRC64;
	Query Match		69.6%; Score 1826; DB 1; Length 518;
	Best Local Similarity		66.6%; Pred. No. 5.5e-122;
	Matches 321; Conservative		63; Mismatches 90; Indels 8; Gaps 3
QY	2	NGTLNQYFEMWTENDQGHWKRLQNDADHLSIDGITLAWIPPAFKGLSGSDNCGPYDLD	61
DB	39	NGTMMQYFEMWTLENDGNHMNLNSDANLSKRGITAWIPPAFKGASQNDVGGAIDLTD	98
QY	62	LGEFOCKGVATPKYGTSELODAIGSLHSRVQCYGGVVLNHKGAGATEDVYADEVNPA	121
DB	99	LGEFNOKGVATPKYGTREQLQAATVTLKNNGIOYGGVVWNHHGGADATEMVAVEVNPN	158
QY	122	NRNQETSEEYQIKANTDFRFPGKNTYSDFPMHYHFHDGDWDNRSKL-SRIIFKRGDK	180
DB	159	NRKQSVTGTYTTEATFRDPFGKNGTHSSFPMRYTHFDGVDMQSRLNNRIYKFGHGK	218
QY	181	AMMEVYSENGNYDLAKTADVDYDHPDVVAETKKMGIVANELSLDGFRIDAACHTKFSF	240
DB	219	AMMEVDLTENGYDYDIAMTADIDMHPEVVELRWGWMTNTLLGLDGFRIADVGHITKFSF	278
QY	241	LGRVQAVQCATGKMFPYAEYWQNNAKLENLYANKTSFPOSFVDVPLEHNLOAAISOG	300
DB	279	TRDMINHVASATGKMMFAVAEFWRKDGLATENYIQKTNNHSHVFDEPLHLNLNAKSQGI	338
QY	301	GYNMRILDTGVASHBPEKAVTFVENHTDQPGQSLBSTVOCTWEKPILAAYAILTRBSGYQ	360
DB	339	NYDMRNIENGTVQHPSHAVTFEVDNHSOCEALLESFVEMEPFLAYALLTRBOGPS	398
QY	361	VFFGDDYG--TKGTSFKELPSLKDNIEFILAKREKYVGGCHYIDHPVDVIGTREBGDS	418
DB	399	VFFGDDYGGPTHG----VPARRSIDILTILARQKIVAHGKNDYLDHNIITGRGNIA	453
QY	419	AASGIALAITDGPQGSKMYAGLKNABETWYDITGNRSDTVKIGSGWGMEFFVNDGSYS	478
DB	454	HPMSGLAIIIMSGAGGSKMFFVRKAQGVMSDITGRRTGVITINADGMGNFVNGGSYS	513
QY	479	IY 480	
DB	514	IW 515	
	RESULT 4		
	AMY_BACST	STANDARD;	PRT; 549 AA.
	ID_AMY_BACST		
	P06279; Q45519;		
	01-JAN-1988 (Rel. 06, Created)		

DT 01-FEB-1996 (Rel. 33, last sequence update)
DT 15-MAR-2004 (Rel. 43, last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanomydrolase).
GN AMYS.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_Taxid:1422;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.
RX MEDLINE=85234394; PubMed=3924897;
RA Nakajima R., Imanaka T., Alba S.;
RT "Nucleotide sequence of the Bacillus stearothermophilus alpha-amylase
RT gene.";
RL J. Bacteriol. 163:401-406 (1985).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX STRAIN=D15/PH1300;
MEDLINE=86008166; PubMed=3876333;
RA Ihara H., Sasaki T., Tsuboi A., Yamagata H., Tsukagoshi N., Udaoka S.;
RT "Complete nucleotide sequence of a thermophilic alpha-amylase gene:
RT homology between prokaryotic and eukaryotic alpha-amylases at the
RT active sites.";
RL J. Biochem. 98:195-103 (1985).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=NZ-3;
MEDLINE=86195857; PubMed=3009417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
RA Carmona C., Reguadt C.;
RT "Structural genes encoding the thermophilic alpha-amylases of
RT Bacillus stearothermophilus and Bacillus licheniformis.";
RL J. Bacteriol. 166:635-643 (1986).
RN [4]
RP SEQUENCE FROM N.A.
RX Suominen I., Karp M., Lautamo J., Knowles J., Mantsaala P.;
RT "Thermotable alpha amylase of Bacillus stearothermophilus: cloning,
RT expression, and secretion by Escherichia coli.";
RL (In: Chaloupka J., Krumphanz V. (eds.);
RL Extracellular enzymes of microorganisms, pp.129-137, Plenum Press,
RL New York (1987).
RN [5]
RP SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48.
RX STRAIN=DY-5;
MEDLINE=86059211; PubMed=2999073;
RA Tsukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H.,
RA Idoka Y., Yamagata H., Udaoka S.;
RT "Efficient synthesis and secretion of a thermophilic alpha-amylase by
RT protein-producing Bacillus brevis 47 carrying the Bacillus
RT stearothermophilus amylase gene.";
RL J. Bacteriol. 164:1182-1187 (1985).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=21125602; PubMed=11226887;
RA Suvid D., Fujimoto Z., Takase K., Matsumura M., Mizuno H.;
RT "Crystal structure of Bacillus stearothermophilus alpha-amylase:
RT possible factors determining the thermostability.";
RL J. Biochem. 129:461-468 (2001).
RN [7]
RP CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
RN linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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DR FMRI M11450 AAA22235 2

DR EMBL; X02769; CAA26547.1; -;
DR EMBL; M57457; AAA22227.1; -;
DR EMBL; M13255; AAA22241.1; -;
DR PIR; A24436; A24436.
DR PIR; A91999; ALBSF.
DR PDB; 1HVX; OS-AUG-03.
DR InterPro; IPR006589; Alp amyl_cat sub.
DR InterPro; IPR006047; Alpha amyl_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.
FT SIGNAL 1 34
FT CHAIN 35 549
FT ACT_SITE 268 268
FT ACT_SITE 272 272
FT ACT_SITE 365 365
FT METAL 139 139
FT METAL 196 196
FT METAL 218 218
FT METAL 220 220
FT METAL 231 231
FT METAL 237 237
FT METAL 238 238
FT METAL 239 239
FT METAL 272 272
FT METAL 337 337
FT METAL 339 339
FT METAL 440 440
FT METAL 441 441
FT METAL 464 464
FT METAL 464 464
FT METAL 13 13
FT METAL 19 19
FT METAL 23 23
FT METAL 31 31
FT METAL 107 107
FT METAL 167 167
FT METAL 179 179
FT METAL 251 251
FT METAL 260 260
FT METAL 284 284
FT METAL 312 312
FT METAL 338 338
FT METAL 342 342
FT METAL 346 346
FT METAL 376 376
FT METAL 526 527
FT METAL 527 527
FT METAL 535 535
SQ SEQUENCE 549 AA; 62670 MM; 3A2DD93A955E79D3 CRC64;
Query Match 67.0%; Score 1758.5; DB 1; Length 549;
Best Local Similarity 65.4%; Pred. No. 3.6e-117;
Matches 314; Conservative 57; Mismatches 104; Indels 5; Gaps 2;
QY 2 NGTLMQVFEYTPNDQMKRLNDLDEHSDITVWTPPAKGSQSNDNGGPDIYD 61
DB 39 NGTLMQVFEYTPNDQMKRLNDLDEHSDITVWTPPAKGSQSNDNGGPDIYD 98
QY 62 LGSEFOQKGTVTKYKTSKSELDAIGSLASHSNVOVGVVTLNHRGADATEDVAVEVNP 121
DB 99 LGSEFOQKGTVTKYKTSKSELDAIGSLASHSNVOVGVVTLNHRGADATEDVAVEVNP 156
QY 122 NKNQETSEEVQIKAMDPRPRGNTYSDFKMTWHPDGDADMBESKISLIFFRGEGKA 161
DB 159 DRNQEISGTQIOAMTKFDPGKNTYSSFKMTWHPDGDADMBESKISLIFFRGEGKA 218
QY 182 WDMVESSNGNIVYLTADYDHPDVATKKKGIWYANLSDGFRIDPAKHIFESFL 241
DB 219 WDMVEVDYENGNIVYLTADYDHPDVATKKKGIWYANLSDGFRIDPAKHIFESFL 276

QY 242 RDWQVQVQATGKEMFTVAEYWMONNAGKLENYLNKTSFNQSVDPVPLHFNLOAASQGGG 301
DB 279 PDWISDVRSQTKSLFTVGEYWSYDINKLHNHYIKMTKWTMSLFPAPLHNFYTAASKSGGT 338
QY 302 YDMERLLDGTWVSSRPEKAVTFVENHDTPQGSLESTVQWTFKPLAVALITRESGYPCV 361
DB 339 FDMVTIMNTLMKQGPILAVTFVNHDPBQALQSWDPMFKPLAVALITLREQEGYPCV 398
QY 362 FYGDMYGTGKTSFK-ELPSLKDNIEPLIKAKERYAYPEQHDYIDHPVYIGMTRGDSAA 420
DB 399 FYGDTYGTGKTSFK-ELPSLKDNIEPLIKAKERYAYPEQHDYIDHPVYIGMTRGDSAA 454
QY 421 KSGLAALITDTPGSGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGMEFFHNDGSYSIV 480
DB 455 GSGLAALITDTPGSGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGMEFFHNDGSYSIV 514

RESULT 5

AMY2_SALTY

ID AMY2_SALTY STANDARD; PRT; 494 AA.

AC P26613;

DT 01-AUG-1992 (Rel. 23. Created)

DT 28-FEB-2003 (Rel. 41. Last sequence update)

DT 10-OCT-2003 (Rel. 42. Last annotation update)

DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan

DE glucanohydrolase).

GN AMYA OR STM1963.

OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OK NCBI_taxid=602;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JMW1103;

RX MEDLINE=93015717; PubMed=1400215;

RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;

RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.,"

RL J. Bacteriol. 174:6644-6652(1992).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=LT2 / SGSC1412 / ATCC 700720;

RX MEDLINE=21534948; PubMed=11677609;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

RA Courtney L., Porrolik S., Ali J., Dante M., Du F., Hou S., Layman D.,

RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

RA Ryan E., Sun H., Florea L., Miller W., Stoenking T., Nhan M.,

RA Waterston R., Wilson R.K.;

RA "Complete genome sequence of Salmonella enterica serovar Typhimurium

RT LT2.,"

RL Nature 413:852-856(2001).

RN [3]

RP SEQUENCE OF 1-6 FROM N.A.

RC STRAIN=JMW1103;

RX MEDLINE=92407478; PubMed=1527468;

RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;

RA "Subdivision of flagellar region III of the Escherichia coli and

RT Salmonella typhimurium chromosomes and identification of two

RT additional flagellar genes.,"

RL J. Gen. Microbiol. 138:1051-1065(1992).

RN [4]

RP SEQUENCE OF 476-494 FROM N.A.

RC MEDLINE=93381452; PubMed=8371104;

RX Raha M., Kihara M., Kawagishi I., Macnab R.M.;

RA "Organization of the Escherichia coli and Salmonella typhimurium

RT chromosomes between flagellar regions IIIa and IIIb, including a

RT large non-coding region.,"

RL J. Gen. Microbiol. 139:1401-1407(1993).

RN [5]

RP CALYPTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic

RN linkages in oligosaccharides and polysaccharides.

RN -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).

RN -1- SUBUNIT: Monomer (By similarity).

RN -1- SUBCELLULAR LOCATION: Cytoplasmic.

RN -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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DR EMBL: L01643; AAA27110.1; -
DR EMBL: AB087897; AAL20875.1; -
DR EMBL: M85241; AAA27079.1; -
DR EMBL: L13280; AAA11970.1; -
DR PIR: B45738; B45738.
DR HSSP: P06278; IVUS.
DR StyGene: SG10011; amyA.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR InterPro: IPR006047; AlpA_amy1_cat.
DR Pfam: PF00128; alpha-amylase; I.
DR SMART: SM00642; Amy; I.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KM Complete proteome.
FT ACT_SITE 235 235 BY SIMILARITY.
FT ACT_SITE 265 265 BY SIMILARITY.
FT ACT_SITE 332 332 BY SIMILARITY.
FT METAL 104 104 CALCIUM (BY SIMILARITY).
FT METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT FT
FT FT
SQ CONFIDENCE 462 462 L -> S (IN REF. 1).
SQ SEQUENCE 494 AA; 56522 MW; 5C1E862FEED5847C CRC64;

Query Match 38.6%; Score 1013; DB 1; Length 494;
Best Local Similarity 41.2%; Pred. No. 2e-64; Indels 14; Gaps 5;
Matches 202; Conservative 76; Mismatches 198

QY 2 NGTIMQFEFMYTPNDGQWKLQNDAEHLSDIGITAWVIPPAKGLSOSDN-GYGPYDLY 60
DB 3 NPTLQYFMYPPDGGKXLSLAERADGNDIGIMWMLPCKKASGYSGYDTYDLF 62
QY 61 DLGEFOGKTIVRTKYGTSSELDATIGLSHRVQYGVYVNLNKGADATEDVAVENP 120
DB 63 DLGEFOGKTIVRTKYGTSSELDATIGLSHRVQYGVYVNLNKGADATEDVAVENP 122
QY 121 ANRNOETSEYOKKAWTDRPFRGNTYSDFKMWHYFDGADWDSEKRSIRIFKRG-- 178
DB 123 DDTQTDNNITIECEGTRTFPRAAOQYSNFTWDYHCSGIDHINPDEGIFKLVNDY 182
QY 179 GKAMDEVSSENGNDYLVADVDYDHPDVVAETKKGIVANEISLGFRIIDAKNIFK 238
DB 183 GDGMNDQVDDEMGNEPDLMEGENIDPRNNAVTEIKYKRWMEQTHCGEFLDAVKH1PA 242
QY 239 SEFLDWVQVQATGKEMFTVAEYWMONNAGKLENYLNKTSFNQSVDPVPLHFNLOAASQ 298
DB 243 WPKWIEHVOAVRPLFIVAEYMSHEVDKQYIYDQDGTMTLFDAPLQKPFEDASQ 302
QY 299 GGGYDMERLLDGTWVSSRPEKAVTFVENHDTPQGSLESTVQWTFKPLAVALITRESGY 358
DB 303 GAEYDMERHIFGTGLVADPFHVAVTLVANHDTPQALAEVPEVFKPLAVALITLRENGV 362
QY 359 POYFGDMYGTGK-----GTSPEKIPSLKDNIEPLIKAKERYAYPEQHDYIDHPVIG 410
DB 363 PSVFPDLTGASIEDSGENGETCRVDMPIV-NQDLRLIARQRFAGIOTLFFDHPNCA 421
QY 411 WTRECDSSAKSGLAALITDTPGSGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGMEFF 470
DB 422 FSRSG--TEENPCCVAVLNSGDGEXTLLIGNVANKTRBPLGNRDEYVTVNDOGEATF 479
QY 471 HNVDGSYSIV 480
DB 480 FCNAGSVSVW 489

RESULT 6

AMY2_ECOLI STANDARD; PRT; 495 AA.
 ID AMY2_ECOLI
 AC P26612; P78072;
 DT 01-NOV-1992 (Rel. 23, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
 glucanohydrolase).
 GN AMYA OR B1927.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J11;
 RX MEDLINE=93015717; PubMed=1400215;
 RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
 RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
 RL J. Bacteriol. 174:6644-6652(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251358; PubMed=9097040;
 RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T.,
 RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Saito K., Sempel G., Seki Y., Sivasubraman S., Tagami H.,
 RA Takeda J., Takekoshi K., Wada C., Yamamoto Y., Horikuchi T.;
 RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 40.1-50.0 min region on the linkage map.";
 RL DNA Res. 3:379-392(1996).
 RN [4]
 RP SEQUENCE OF 1-5 FROM N.A.
 RC STRAIN=J11;
 RX MEDLINE=92407478; PubMed=1527488;
 RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
 RT "Subdivision of flagellar region III of the Escherichia coli and
 Salmonella typhimurium chromosomes and identification of two
 additional flagellar genes.";
 RL J. Gen. Microbiol. 138:1051-1065(1992).
 RN [5]
 RP SEQUENCE OF 475-495 FROM N.A.
 RC STRAIN=J11;
 RX MEDLINE=93381452; PubMed=8371104;
 RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
 RT "Organization of the Escherichia coli and Salmonella typhimurium
 chromosomes between flagellar regions Iria and Iriib, including a
 large non-coding region.";
 RL J. Gen. Microbiol. 139:1401-1407(1993).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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 CC -----
 DR EMBL; I01642; AAA23810.1; -.
 DR EMBL; AE000285; AAC74994.1; -.
 DR EMBL; D50833; BAA15755.1; -.
 DR EMBL; M85240; -; NOT ANNOTATED CDS.
 DR EMBL; L13279; AAA82575.1; -.
 DR PIR; D64956; A45738.
 DR HSSP; P06278; IVS.
 DR EcoGene; EG11387; AMYA.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR SMART; SM00642; Amy; 1.
 KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 KM Complete proteome.
 FT ACT_SITE 235 235 BY SIMILARITY.
 FT ACT_SITE 265 265 BY SIMILARITY.
 FT ACT_SITE 332 332 BY SIMILARITY.
 FT METAL 104 104 CALCIUM (BY SIMILARITY)
 FT METAL 239 239 CALCIUM (VIA CARBOXYL OXYGEN) (BY
 SIMILARITY).
 FT CONFLICT 19 20 KL -> SS (IN REF. 1).
 FT CONFLICT 109 109 A -> V (IN REF. 1).
 FT CONFLICT 149 149 Q -> E (IN REF. 1).
 FT CONFLICT 234 234 L -> I (IN REF. 1).
 SQ SEQUENCE 495 AA; 56639 MW; 26AF6797DDA54D6 CRC64;
 Query Match 38.0%; Score 996; DB 1; Length 495;
 Best Local Similarity 40.7%; Pred. No. 2,3e-63;
 Matches 200; Conservative 79; Mismatches 195; Indels 18; Gaps 6;
 QY 2 NGTLMQYFMYTPNDGQHKRLQNDAEHSDIGITAWTPPYKSLQSDN-GYGPYDLY 60
 DB 3 NPTLLCCFFMYPPDGKMPLEAERDGDNDGIMVWLPYKASGSGYSGYSDYDF 62
 QY DLGEFQOKGVTVTKYKTSKSELQDAIGSLSRNVQYGVVNLNHRKAGADATEDVAVEVP 120
 DB DLGEFQOKSIPKYGDKQGLAIDLAKNDIAVLDDVVVNHKAGADEKELIRQRYVA 122
 QY 121 ANNQETSEYQIKAWTDFRPFPGKNTYSDPKWHYHPDQADWDSKRSIFK----PR 176
 DB 123 DERTQIDEEIECEGRTYRTPPARQYQSQFTWDFCEGSHINPDEDGIFKIVNDT 182
 QY 177 GEGKAWDEVSSENGYDYLVADVDVDPVAETKKGIVYANBLSLDGFRIDAKHI 236
 DB 183 GEG--WMDQVDELDGPFYLMGENIDFRNATYERIKYARVMQTOCDGRLDVAKHI 240
 QY 237 KFSPLDWMYQAVRQATGKEMFVAEYVQNNACKLENYLNKTSFNQSVDPVPLHNLQAS 296
 DB 241 PAFVYKEMIEHVQEVAPKPLFIVAERYSHSVKLTQYIDQVGGKTMLPAPQMKHEHS 300
 QY 297 SOGGYDWRRLDGTVYSHPEKAVTFVENHDTOPQOSLESTVQTFKFLAYAFITRES 356
 DB 301 RMRGRDYMQITFGTLVEADPFPAVTLVANHDTQPLQALEAVEYEFKFLAYALILREN 360
 QY 357 GYPOVYGVDMYGTK-----GTSPEKIPSLKDNIEPLIKARKEVAYPQHDYIDHPV 408
 DB 361 GYPSVYFPLDYGAYHDVGAGDGYIDWPII-EQLDEILARQSFHAGVQTLFFDHPNC 419
 QY 409 TGTREGDSAAAGLALITGPGSKRMVYGLKAKAGTWDYDINRSDTYKIGSDGNG 468
 DB 420 IAFSGSTDEF--PGCVVMSNGSDSEKTHIGENTGKNTWDFLGNRGERVYTDENGSA 477
 QY 469 EFTVNDGSVSIY 480
 DB 478 TFFONGSVSVW 489
 RESULT 7
 AMYA_ORYSA STANDARD; PRT; 440 AA.

AC P27932; (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Alpha-amylase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-
 DE glucan glucanohydrolase).
 GN AMY1.2 OR AMY3A.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Japonica M202; TISSUE=Et:clated leaf;
 RX MEDLINE=91329692; PubMed=1714318;
 RA Sutcliffe T.D., Huang N., Lites J.C., Rodriguez R.L.;
 RL Plant Mol. Biol. 16:579-591(1991).
 CC -1- FUNCTION: Important for breakdown of endosperm starch during
 CC germination.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- TISSUE SPECIFICITY: Most abundant in embryo-derived callus tissue.
 CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
 CC in the aleurone cells under the control of the plant hormone
 CC gibberellic acid and in the developing grains at a low level.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, X56336; CAA39776.1; -
 CC PIR, S14958; S14958.
 CC HSP, P04063; IAVA.
 CC InterPro: P27932; -
 CC InterPro: IPR006589; Alp_amy1_cat_sub.
 CC InterPro: IPR006047; Alpha_amy1_cat.
 CC InterPro: IPR006046; Glyco_hydro_13.
 CC Pfam: PF00128; alpha-amylase; 1.
 CC PRINTS, PRO0110; ALPHAAMYLASE.
 CC SMART, SM00642; Amy; 1.
 CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 CC Signal; Multigene family.
 CC FT CHAIN 1 26 POTENTIAL.
 FT ACT_SITE 207 440 ALPHA-AMYLASE ISOZYM 3A.
 FT ACT_SITE 315 315 BY SIMILARITY.
 FT METAL 119 119 CALCIUM 1 (BY SIMILARITY).
 FT METAL 145 145 CALCIUM 2 (BY SIMILARITY).
 FT METAL 155 155 CALCIUM 3 (BY SIMILARITY).
 FT METAL 166 166 CALCIUM 3 (BY SIMILARITY).
 FT METAL 169 169 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
 FT SIMILARITY).
 FT METAL 170 170 CALCIUM 1 (BY SIMILARITY).
 FT METAL 171 171 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
 FT SIMILARITY).
 FT METAL 174 174 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
 FT SIMILARITY).
 FT METAL 176 176 CALCIUM 1 AND 3 (BY SIMILARITY).
 FT SEQUENCE 440 AA; 46872 MW; 5E9B78C29A91C2B CRC64;
 Query Match 13.2%; Score 346; DB 1; Length 440;
 Best Local Similarity 25.0%; Pred. No. 2.9e-17;
 Matches 128; Conservative 63; Mismatches 151; Indels 170; Gaps 21;

QY 5 LMQFEWYTPNDGQMKR-----LQNDAEHLSDIGITAVWIPPAKGLSQSDNGYGPY 57
 DB 31 LQGFNW-----DSMKQGGWYNNLKDQVGDIAAGVTHWLPPTH--SVSPGVMFG 82
 QY 58 DLYDGEFOQKGTVRKTKTSELQDAIGLSHRNVQYGVVNLNKKAGALATEDVTAVE 117
 DB 83 RLYDLN-----ASKYGTAKELKSLIAAFPAKIKCVADIVVHRC----- 122
 QY 118 VNPARNQGTSEHYQIKAWTDFRFGKNTYSDFKMWHYFEGADWDSEKRSIRIFKFRG 177
 DB 123 -----ADDKRGKGYCIFKGG 139
 QY 178 EGRKWD-----EVSSENG-----YDYLTADVDYDHPDVAETKMGWYANEL 223
 DB 140 PRGCLDWGSPMKCCDDTQYSDGTGHRDGAADPAAPADIDHINFLVQRELSDMLRLTRDV 199
 QY 224 SLDFRIDAKKHIKESFLRDWQAVRQATGKMEFVAEYQ-----NNAG--- 268
 DB 200 GFGWRLDPAKGYSAVARTTYQNAKPS-----FVAELWNSLSDGDKPRAANDGGRQ 254
 QY 269 KLENYLNTKTSFNQSVFVZELHFNLAASQGGGYDMRRLDGT---VSRHPEKAVTVE 325
 DB 255 ELVNWYKQVGPATAFDFTKGLQSA--VQGLWEMRD--KQKAPGMIGWYBEKAVTFVD 312
 QY 326 NHDTPQGSLSTVQTFWEK-----LAVAFILTRSGYQVGYDMYGTGKTSFKEIFSL 380
 DB 313 NHDT-----GSTQKMPFSDKVLIGVYLIT--HPGVCLFYDQVFM-----NL 356
 QY 381 KDNIEFILARKKRYAVGPHDYIDHPDVIGWTRBEDSSAAKGLAALITDGGGSKEMYA 440
 DB 357 KQELNALATRK-----RNGINAGSKRLVLAASD-----MYV 389
 QY 441 GLKNAETWYDITGRSPVTKIGSDMGFRHY 472
 DB 390 AM--VDERVITKIGPR--IEVGNIIISDFHI 416
 RESULT 8
 AMYA VIGMU
 ID AMYA VIGMU STANDARD, PRT; 421 AA.
 AC P17859;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase).
 GN AMY1.1.
 OS Vigna mungo (Black gram).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Orosidaceae; Papilionaceae; Phaseoleae; Vigna.
 OX NCBI_TaxID=3915;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cotyledon;
 RX MEDLINE=90332425; PubMed=2377468;
 RA Yamauchi D., Minamikawa T.;
 RT "Nucleotide sequence of cDNA for alpha-amylase from cotyledons of
 RT germinating Vigna mungo seeds".
 RL Nucleic Acids Res. 18:4250-4250(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=9120017; PubMed=8290640;
 RA Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
 RT "Nucleotide sequence of the alpha-amylase gene from Vigna mungo".;
 RL Plant Physiol. 103:1459-1459(1993).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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DR EMBL; X53049; CAA37217.1; -
DR EMBL; X73301; CAA51734.1; -
DR PIR; S10514; S10514.
DR HSSP; P04063; IAVA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.

KM Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;
KM Signal.

FT SIGNAL 1 23 PROBABLE.
FT CHAIN 24 421 ALPHA-AMYLASE.
FT ACT SITE 201 201 BY SIMILARITY.
FT ACT SITE 309 309 BY SIMILARITY.
FT METAL 113 113 CALCIUM 1 (BY SIMILARITY).
FT METAL 130 130 CALCIUM 2 (BY SIMILARITY).
FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).
FT METAL 135 135 CALCIUM 2 (BY SIMILARITY).
FT METAL 139 139 CALCIUM 2 (BY SIMILARITY).
FT METAL 149 149 CALCIUM 3 (BY SIMILARITY).
FT METAL 160 160 CALCIUM 3 (BY SIMILARITY).
FT METAL 168 168 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).

FT METAL 170 170 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 421 AA; 46888 MM; 15CA0DBADDB4656 CRC64;

Query Match 12.7%; Score 333.5; DB 1; Length 421;
Best Local Similarity 26.5%; Pred. No. 2.1e-16;
Matches 121; Conservative 55; Mismatches 166; Indels 115; Gaps 17;

QY 5 LQVFFWYTPNDGQHKRLQNDABHSDIGTRVWPPRAYKLSQSDNGYGYDYLDGE 64
DB 26 LFGGFWMSSKKGWNSLKNISIPDLANAGITHWLPSPSQSVSPESYLPGRLDLD 82
QY 65 FQCKGTVRYKTKSELDQAGSLHSRNVQVGVVLANHAGADATEDTAVEVNPANN 124
DB 83 ASKYGSKNELKSLIAFHEKIKCLADIVINR 115
QY 125 QETSEYQIKAMTDFPPRGNGTYSDFKMHVTFDQADMDSEKISRIKFRGEGKAMW 164
DB 116 TAE-----KDRG-----IYCFEGTDPDRDQSPSICD-----DT 150
QY 185 EVSEKNGNDV---YMYADVDYDHPVAVETKQKIWYANELSLDGFIDAKHIFSF 240
DB 151 AYSDGNGNDSGEGYDAAPDIDHNPQVRELSEMMWMLKTEIGFGMFPDVKGYAPSI 210
QY 241 LRDVQAVRQATKEMFTVAEW-----ONNAGLENLYNKTSPFNQSYVD 285
DB 211 SKTMEQT-----KPFVAVGEKWDISYGDGKPNYNOSHREALVWVESAGATTAD 265
QY 286 VPLHFNQASSGGGVDMRLDGT-----VSRPEKVFTEVNHDTOPGSLSTFQ 340
DB 266 FTKKGIQAA-VQ--ELMRLIDPNCKPGKMGVRENNAVITIDHDT-----GSTGR 315
QY 341 TWFRP-----LAAVAFITRESGYPVQVYGMGTGTSPELPSLKNIEPIIAKKEYA 395
DB 316 LMFPPSDKVMQVAYVILT-HPGTPISTFYDHFDM-----GLXKQIAKLSIRL 362
QY 396 YGPOHDIYDHPVIGWTRGSDSSAAKSGALALITDGP 432
DB 363 ---RNGINEXSYKYNASEGDLVYAKIDNKIMVIGP 396

RESULT 9

AM3C_ORYSA
ID AM3C_ORYSA STANDARD; PRT; 437 AA.
AC P27939;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amy1ase isozyme 3C precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
GN AMY1.7 OR AMY3B.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN (1)
RP SEQUENCE FROM N.A.
RC STEAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
RX MEDLINE=91329692; PubMed=1714318;
RA Sutcliffe T.D., Huang N., Lites J.C., Rodriguez R.L.;
RT "Characterization of an alpha-amy1ase multigene cluster in rice.";
RL Plant Mol. Biol. 15:579-591(1991).
CC -1- FUNCTION: Important for breakdown of endosperm starch during
germination.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: Germinating seeds.
CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
in the aleurone cells under the control of the plant hormone
gibberellic acid and in the developing grains at a low level.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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DR EMBL; X56338; CAA39778.1; -
DR PIR; S14956; S14956.
DR HSSP; P04063; IAVA.
DR Gramene; P27939; -
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;
KW Signal; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 437
FT ACT SITE 205 205
FT ACT SITE 313 313
FT ACT SITE 317 317
FT METAL 117 117
FT METAL 134 134
FT METAL 137 137
FT METAL 139 139
FT METAL 143 143
FT METAL 153 153
FT METAL 164 164
FT METAL 167 167
FT METAL 168 168
FT METAL 169 169
FT METAL 172 172
FT METAL 174 174
SQ SEQUENCE 437 AA; 48637 MM; BD04250840C7A8B CRC64;

Query Match 12.3%; Score 324; DB 1; Length 437;
 Best Local Similarity 24.9%; Pred. No. 1.1e-15;
 Matches 108; Conservative 56; Mismatches 140; Indels 130; Gaps 15;

QY 5 LMOYFMYWPNDOGHKR-LQNDAMHLSDIGTAVWIPAVYGLSGSDGYPDYLDLG 63
 DB 29 LFGGFWMESNKKQCGMYNPLHSHVDIATGVTHWLP--PSHSAVPGVIGGLYLD 86
 QY 64 EPOCKGTVRTKYGKSELQDAISLRSVYQYGVLDVNLHKAQADATEDVTAVEVNPANR 123
 DB 87 -----ASKYGTGLRELRLIAFHSKSIKVAADIVINRC----- 120
 QY 124 NQSTSEFYQIKAMTDRFRPKGNTYSGDFKHHWHFPGADWDESRKISRIFKRGSGKAMD 183
 DB 121 -----ADYKDSRGICYICFEGGTSPSRID 143
 QY 184 W--EVSSENGNY-----DYLMADVDYDHPDYVAETKMGIVYANELSIDGER 229
 DB 144 WGDPMICSDDTQYNSNGRHRDTGADPGARDIDHLNTRVQTELSDLMLKSDVGFQWR 203
 QY 230 IDAAKHKEFLDMYQAVQANGKEMFTAYEYQV-----NAGKLENYL 274
 DB 204 LDPAKGYSAVATVATYDNTDPS-----FVVAELTSMNRYDNGEPMNODGDEQELVNA 258
 QY 275 NKTSFNQSVFDPVPLHFNILQAASSQGGYDVRRLDGT-----VSSHPEKAVTFVENHDT 329
 DB 259 QAVGGRPASAFDFTTKGELQAA-VQG---ELMRKDKGKAPGMIGMLPEKAVTFIDNHD 314
 QY 330 QPGQSLSTVQYTFKP-----LAVAFILRESGYPVQYFIDMVGITGTSKELPSLXNDI 384
 DB 315 -----GSTONSWPFPSDKWQRYAYLLT-HPGVCFIFDYHVDW-----NIKOEI 358
 QY 385 EPIKARKEYAYGP 398
 DB 359 STLAAVSRNGIHP 372

RT "Sequence of an active fragment of B. polymyxa beta amylase.";
 RN Nucleic Acids Res. 15:3934-3934(1987).
 RP (4) DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES.
 RX MEDLINE=91215008; PubMed=1827035;
 RA Uozumi N., Matsuda T., Tsukagoshi N., Ueda S.;
 RT "Structural and functional roles of cysteine residues of Bacillus
 polymyxa beta-amylase.";
 RL Biochemistry 30:4594-4599(1991).
 CC -1- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO
 CC PRODUCE MULTIFORM BETA-AMYLASES AND A 48 kDa ALPHA-AMYLASE AFTER
 CC SECRETION.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in
 CC polysaccharides so as to remove successive maltose units from the
 CC non-reducing ends of the chains.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: In the N-terminal section; belongs to family 14 of
 CC glycosyl hydrolases.
 CC -1- SIMILARITY: In the C-terminal section; belongs to family 13 of
 CC glycosyl hydrolases.
 CC -----
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 CC -----
 CC EMBL: M15817; AA85446.1; -;
 CC EMBL: Y00150; CA86344.1; -;
 CC PIR: A29130; A29130.
 CC HSP: P36924; 1B92.
 CC InterPro: IPR005589; Alp_amy1_cat_sub.
 CC InterPro: IPR005048; Alpha_amy1_C.
 CC InterPro: IPR005047; Alpha_amy1_cat.
 CC InterPro: IPR005085; Cbm 25.
 CC InterPro: IPR005046; Glyco_hydro_13.
 CC InterPro: IPR001554; Glyco_hydro_14.
 CC Pfam: PF02806; alpha-amylase_1.
 CC Pfam: PF03423; Cbm 25; 2.
 CC Pfam: PF01373; Glyco_hydro_14; 1.
 CC PRINTS: PRO0110; ALPHAMYLASE.
 CC PRINTS: PRO0750; BETRAYLASE.
 CC SMART: SM00642; Amy1; 1.
 CC SMART: SM00632; Amy_C; 1.
 CC PROSITE: PS00506; BETA_AMYLASE_1; 1.
 CC PROSITE: PS00679; BETA_AMYLASE_2; 1.
 CC Multi-functional enzyme; Hydrolase; Glycosidase; signal;
 CC KM Polysaccharide degradation; Repeat.
 CC STGNL 1 35
 CC CHAIN 36 1196
 CC DOMAIN 36 454
 CC REPEAT 455 558
 CC REPEAT 565 668
 CC DOMAIN 669 1196
 CC DISULFID 118 126
 CC ACT_SITE 198 198
 CC ACT_SITE 394 394
 CC MUTAGEN 118 118
 CC MUTAGEN 126 126
 CC MUTAGEN 358 358
 CC CONFLICT 1 1
 CC CONFLICT 67 67
 CC CONFLICT 100 100
 CC CONFLICT 154 154
 CC CONFLICT 177 177
 CC CONFLICT 227 228
 CC CONFLICT 330 330
 CC CONFLICT 425 425
 CC -----
 CC BETA/ALPHA-AMYLASE.
 CC BETA-AMYLASE.
 CC -----
 CC ALPHA-AMYLASE.
 CC BY SIMILARITY.
 CC C->S: 5-FOLD DECREASE IN ACTIVITY.
 CC C->V: 20-FOLD DECREASE IN ACTIVITY.
 CC C->S: 60-FOLD DECREASE IN ACTIVITY.
 CC M->S: MIGL (IN REF. 3).
 CC N->S (IN REF. 3).
 CC N->D (IN REF. 3).
 CC S->N (IN REF. 3).
 CC E->O (IN REF. 3).
 CC NA->KS (IN REF. 3).
 CC G->S (IN REF. 3).
 CC N->S (IN REF. 3).

```

FT CONFLICT 493 493 D -> A (IN REF. 3)
FT CONFLICT 532 532 S -> L (IN REF. 3)
FT CONFLICT 559 559 A -> T (IN REF. 3)
FT CONFLICT 665 665 A -> T (IN REF. 3)
FT CONFLICT 681 681 D -> A (IN REF. 3)
FT CONFLICT 686 686 T -> A (IN REF. 3)
FT CONFLICT 725 728 APTS -> VESP (IN REF. 3)
FT CONFLICT 736 736 N -> K (IN REF. 3)
FT CONFLICT 741 741 N -> S (IN REF. 3)
FT CONFLICT 758 758 S -> N (IN REF. 3)
SQ SEQUENCE 1196 AA, 130893 MW, A41EA6B70F257064 CRC64;

Query Match 12.3%; Score 323; DB 1; Length 1196;
Best Local Similarity 21.5%; Pred. No. 4,4e-15;
Matches 112; Conservative 82; Mismatches 162; Indels 164; Gaps 24;

OY 10 EMTYNDQHWKRLQNDAEHLSDIGITAVWIPRAYKGLSQSDNGYGPYDLUDGEPQOK 68
DB 779 KWH---GGDFQGIINKLDYIKMGFTAWITPTMQSEYAYGHTYDFY----- 826
OY 69 GTVTRKYGTSKSELDAIGLSLRVQYGVYDLVHNKAGADATEDVTAVERNANQETS 128
DB 827 -AVDGHGTMKDLQGLVYKAKDKNIAYVVDVYVNHGT----- 862
OY 129 EYQIKANTDPRFGKNTYSDF-KMHYHFDG---ADMDESKISRIKFRGEGKAMD 183
DB 863 -----DFQ-PGNGFAPKAPFDADYVHNGITDGVYNNQ----- 897
OY 184 WEVSENGNYDYLMADYDHPVVAETKKGWYANELSLDFRIDAAGHINSELRD 243
DB 898 WKI---ENG--DVAAGLDLHNENPANELKMWIKMLNETGIDGLRDLTVGVFKGLTD 953
OY 244 WVQAVRQATGKEMFTVAEYWMONNAGKLENYLNKTSFNOSVDPVPLEHNLQAASQGGCYD 303
DB 954 FDOAA-----NFTMGELIFHGDPAYVGDY--TRYDLAALDFPMYIYIKVVF--GHDQS 1002
OY 304 MRRLIDGTIVSRHPEKAVT---FVENHDT-----OPQSLESTQVTFKPLAVAFI 351
DB 1003 MRKICDRSDRYDAQTNQVFIQNHVYKFLNDASKPGANDKMPOL---KALGFT 1059
OY 352 LTRSGYQVYVGYDMYGTGTSPEKIPSLKDNIEPILAKREYAVGPOHDYIDHPVIGW 411
DB 1060 LT-SRGIPIIYQGTQGYSG---GDDPANRENN-----FNANHDLVYQYIAKLNY 1105
OY 412 TREGSSAAKSGLALITDGPQSGKRWYAGLKNGETYD-----ITGRSPDTVKG 464
DB 1106 VRANHPAL-----QNGSOR-----EKWVDSFYSFGRSKXGDAIYF 1144
OY 465 DGM-----GEF-----HVNDGSYSI 479
DB 1145 NSMNSQTRTIGNFDLNSGTRLTNQLSNDVSQINNYSITV 1184

RESULT 11
AM3B_ORYSA STANDARD; PRT; 438 AA.
ID AM3B_ORYSA P27937;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase isozyme 3B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase)
GN AMY1.6 OR AMY3B.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhacroidae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RX MEDLINE=91329692; PubMed=1714318;
RX Sutcliffe T.D., Huang N., Lites J.C., Rodriguez R.L.;

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RT "Characterization of an alpha-amylase multi-gene cluster in rice."
RL Plant Mol. Biol. 16:579-591(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Sutcliffe T.D., Huang N., Rodriguez R.L.
Submitted (May-1993) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: Germinating seeds.
CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurone cells under the control of the plant hormone
CC gibberellic acid and in the developing grains at a low level.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: X56337; CAA39777.1; -
DR EMBL: X24941; AAA3897.1; -
DR PIR: S14957; S14957.
DR HSSP: P04063; IAVA.
DR Gramene; P27937; -.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006046; Glyco_Hydro_13.
DR Pfam: PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW signal; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 438 ALPHA-AMYLASE ISOZYME 3B.
FT ACT SITE 205 205 BY SIMILARITY.
FT ACT SITE 313 313 BY SIMILARITY.
FT METAL 117 117 CALCIUM 1 (BY SIMILARITY).
FT METAL 134 134 CALCIUM 2 (BY SIMILARITY).
FT METAL 137 137 CALCIUM 2 (BY SIMILARITY).
FT METAL 139 139 CALCIUM 2 (BY SIMILARITY).
FT METAL 143 143 CALCIUM 3 (BY SIMILARITY).
FT METAL 153 153 CALCIUM 3 (BY SIMILARITY).
FT METAL 164 164 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 167 167 SIMILARITY).
FT METAL 168 168 CALCIUM 1 (BY SIMILARITY).
FT METAL 169 169 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 172 172 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 174 174 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SQ SEQUENCE 438 AA, 48591 MW, B9DE0D5ABC63F9C CRC64;
Query Match 12.2%; Score 319; DB 1; Length 438;
Best Local Similarity 24.5%; Pred. No. 2,4e-15;
Matches 108; Conservative 54; Mismatches 136; Indels 142; Gaps 16;

OY 5 LMOYFMYTNDQHWKRLQNDAEHLSDIGITAVWIPRAYKGLSQSDNGYGPY 57
DB 29 LPOGFNW-----ESWKQGGWYTFHGHVDDIAATGVTHWLP--PSHSAVAPQGYMG 80
OY 58 DLVYDLGEPQOKGVRTRKYGTSKSELDAIGLSLRVQYGVYDLVHNKAGADATEDVTA 117
DB 81 RLVDLD-----ASKYTGALRLSLIAFSGKIKVADIVNRC----- 120
OY 118 VNPANNOETSEYQIKAWTDFRFGKNTYSDFKMHYHFDGADWDSEKISRIFKRG 177

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Db 121 -----DYMADVDYDHPVVAETKKGWVANEL 223
OY 178 ESKAMW---EVSSNGNY-----ADYDSNGIYCFEGGT 137
Db 138 PDSRLDWPDMICSDDTQYSGNRGDRDTGADFGAAPDIDHINTVOTELSDMLWMLKSDV 197
OY 224 SLDGRFLDAHAIKFSFLRDVQAVRQATGKEMFTVAEYMN-----NAG 268
Db 198 GFDGRFLDFAKGYSAVAKTYVDNTPDS-----FVAELINSMKMYDNGSPSWNQDGRQ 252
OY 269 KLENTLNTSFRQSVFDPPLHFNLOAASGGGVDMLDGT-----VSRHEKAVTF 323
Db 253 ELVWMAQAVGPASAFDFTTKGELQAA-VQG--ELWEMKDKNGKAPGMIGWPEKAVTF 308
OY 324 VENHDTQPGQSLSTVQTFKRP-----LAVAFILTRSGYPQVFGDMYGTGTSPEKIP 378
Db 309 IDNHT-----GSTQNSMFPSPDKVMQGVAVILT-HGQVCFIYDHFVK----- 352
OY 379 LKDNIEPILKRRKAYANP 398
Db 353 NLKQELSTLAARSRNEIHP 372

RESULT 12
AM3D_ORYSA STANDARD; PRT; 435 AA.
AC P27933;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylose isozyme 3D precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
  glucanohydrolase).
GN AM1.3 OR AM3D.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_Taxid=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
RX MEDLINE=91088278; PubMed=2263460;
  Huang N., Kozumi N., Reini S., Rodriguez R.L.;
  "Structural organization and differential expression of rice alpha-
  amylose genes";
  Nucleic Acids Res. 18:7007-7014 (1990).
RN [2]
RP SEQUENCE FROM N.A. (CLONE POS137).
RX MEDLINE=9018322; PubMed=2370848;
  O'Neill S.D., Kumagai M.H., Majumdar A., Huang N., Sutcliffe T.D.,
  Rodriguez R.L.;
  "The alpha-amylose genes in Oryza sativa: characterization of cDNA
  clones and mRNA expression during seed germination.";
  Mol. Genet. 221:235-244 (1990).
RT Mol. Genet. 221:235-244 (1990).
RL
CC -1- FUNCTION: Important for breakdown of endosperm starch during
  germination.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
  linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: Is expressed in all tissues, except in
  immature seeds. Is the most abundant alpha-amylose isozyme in
  callus.
CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
  in the aleurone cells under the control of the plant hormone
  gibberellic acid and in the developing grains at a low level.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CC or send an email to license@1sb-sib.ch).
CC -----
DR EMBL: M59351; AAA33895.1; -.
DR EMBL: M24287; AAA33886.1; -.
DR FIR: S12625; S12625.
DR HSSP: P04063; IAVA.
DR Gramene; P27933; -.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amylose; 1.
DR PRINTS: PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;
  KW signal; Multigene family.
FT SIGNAL 1 25
FT CHAIN 26 435
FT ACT_SITE 203 203
FT ACT_SITE 311 311
FT METAL 116 116
FT METAL 133 133
FT METAL 136 136
FT METAL 138 138
FT METAL 141 141
FT METAL 151 151
FT METAL 162 162
FT METAL 167 167
FT METAL 170 170
FT METAL 172 172
FT CONFLICT 73 74
FT CONFLICT 137 137
FT SEQUENCE 435 AA; 47911 MW; 1BBDA6195BAD6E CRC64;
SQ
Query Match 12.1%; Score 318; DB 1; Length 435;
Best Local Similarity 28.0%; Pred. No. 2.8e-15;
Matches 111; Conservative 42; Mismatches 134; Indels 110; Gaps 17;
OY 5 LMOYFETWYTPNDGQHKR-----LQNDAGELSDIGTAVWIPRXYGSLGSDNGYGPY 57
Db 28 LFGGFW-----ESKKQGGWYNMLKQVDDIAAGVHWLP--DSHVAFGYMG 79
OY 58 DLYDLGFQKQGVTVTKYGTSELDQAGLSLRNVQVGVVNLHKG--ADATEDVYA 115
Db 80 RLVDLD-----ASKGTAEIKSLIAFPGKGVQCVADVIVHRCAEKKDARGYCV 131
OY 116 VEVPANRQNETSEYQIATWDFPFGKNTYSPFKMWHYFDGADMDSEKIRIRKF 175
Db 132 FEGGTDRD-----WPGMVICSDDTQYSGTGH-----RD 162
OY 176 RGGKAMDEVSSENGNYDYLAVADVDYDHPVVAETKKGWVANELSLDGRFLDAH 235
Db 163 TSGR-----FGAAPDIDHINTVQELDMLWMLSDVGFDDWRDLDFKAG 207
OY 236 IKFSFLRDVQAVRQATGKEMFTVAEYQ-----NNAG-----LENTLNTSPN 280
Db 208 YSTDIAKMYVESC-----KPGFVAEIMVNSLSYNGKGPANQDGRDELVMVAVAGSP 262
OY 281 QSVFDPPLHFNLOAASGGGVDMLDGT-----VSRHEKAVTFVENHDTQPGQSL 335
Db 263 AMTFDFTTKGLD-AVQG--ELWRLRNGKARGMIGWPEKAVTFVDNHT----- 312
OY 336 ESTVQTFKRP-----LAVAFILTRSGYPQVFGDMY 367
Db 313 GSTQKLMFPSPDKVMQGVAVILT-HGQVCFIYDHF 348

RESULT 13
AM3E_ORYSA STANDARD; PRT; 437 AA.

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AC P27934; 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase isozyme 3B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
GN AM1.4 OR AM13E.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhacidae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etisolated leaf;
RX MEDLINE=9108278; PubMed=2263460;
RA Huang N., Koizumi N., Reini S., Rodriguez R.L.;
RT "Structural organization and differential expression of rice alpha-
amylase genes.";
RU Nucleic Acids Res. 18:7007-7014 (1990).
CC -1- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: More abundant in germinating seeds than in
CC young roots, young leaves and callus.
CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurone cells under the control of the plant hormone
CC gibberellic acid and in the developing grains at a low level.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: M59352; AAA33896.1; -
CC PIR: J0946; J0946.
CC HSSP: P04063; J0946.
DR Gramene; P27934; -
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amylase_1.
DR PRINTS: PR00110; ALPHAMYLASE.
DR SMART: SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;
KW Signal; Multigene family.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 437 ALPHA-AMYLASE ISOZYME 3B.
FT ACT_SITE 204 204 BY SIMILARITY.
FT ACT_SITE 312 312 BY SIMILARITY.
FT METAL 116 116 CALCIUM 1 (BY SIMILARITY).
FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).
FT METAL 136 136 CALCIUM 2 (BY SIMILARITY).
FT METAL 138 138 CALCIUM 2 (BY SIMILARITY).
FT METAL 142 142 CALCIUM 2 (BY SIMILARITY).
FT METAL 152 152 CALCIUM 3 (BY SIMILARITY).
FT METAL 153 153 CALCIUM 3 (BY SIMILARITY).
FT METAL 163 163 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 166 166 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 168 168 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 171 171 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 173 173 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 437 AA; 48707 MW; C088276CCEA16602 CRC64;

Query Match 12.0%; Score 315.5; DB 1; Length 437;
Best Local Similarity 24.9%; Pred. No. 4.2e-15;
Matches 122; Conservative 54; Mismatches 146; Indels 167; Gaps 21;
QY 5 LMGFEWTPNQGHWK-----LQNDAEHLSDIGTAWVIPPAYKSLQSQDNQGY 57
DB LFGQFW-----ESRKQGGWTFHEKVEELASGATHWLP--BSHSVPGQYMG 79
QY 58 DLYDLGFOQKGTVRTKYGKSELDQAGSLHSRVQYGVYLVNKKAGADATEDVTA 117
DB RLYDL-----ASKYGTAEELKELIDAFHDKNVECLADIVNRC----- 119
QY 118 VNPANNQETSESEYQKATDPRFPGNGTYSDFKHWVHPDQADMDSEKXSRJFKFRG 177
DB 120 -----ADYKDRGYCYVFEGET 136
QY 178 EGRKAWD-----EVSSENGND-----YLMADVDYDHPVVAETKKGWYANBL 223
DB 137 PGRLLDWGPDWICSDDTQYNSNGRHRDTGAGCAAPDIDHLPVQRELTDWLNLRD 196
QY 224 SLGFRIDAKKIKFELDWQAVRQATGKEMFYAEYQ-----NNAK----- 269
DB 197 GFDGMRUDFPAKGYSAFLARIYDNTNPT-----FVGEIWSLLYNGDEPSTNDADRQ 251
QY 270 -LENYLNTKTSFNQSVDFVPLHFNLAASQGGYDMRLLDGT-----VSSHPEKAVTF 323
DB 252 ELVNVWEGVGPATAFDFTTKGLQAA-VQG--ELMRLLDNGKAPGLMGMPPQAVTF 307
QY 324 VEHNDTPQSGLESTVQWFKP-----LAYFLTRRESYPOYFGDMYGTGSEKPE 378
DB 308 VDMHDGTSQSL-----WPFSDKVMQGYAVILT-HPDIFCFYDHF--DMNLQHELA 358
QY 379 SL-----KNTPEILKARKE-----AGPOHD-----YIDH-P 406
DB 359 TLEFISRNKHAESLIDLKAGDLYVAMIDKATYTKGPRYDAGGILPSDFHVAHGN 418
QY 407 DVIGWTRREG 415
DB 419 DYCWEKEG 427
RESULT 14
AM13_WHEAT STANDARD; PRT; 413 AA.
ID AM13_WHEAT
AC P08117;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase AMY3 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
GN AMY1.1 OR ALPHA-AMY3.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Chinese Spring;
RA Baillcombe D.C., Huttly A.K., Martienssen R.A., Barker R.F.,
RA Jarvis M.G.;
RT "A novel wheat alpha-amylase gene (alpha-Amy1)." ;
RI Mol. Gen. Genet. 209:33-40 (1987).
CC -1- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurone cells under the control of the plant hormone
CC gibberellic acid and in the developing grains at a low level.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X05809; CAA29252.1; -
DR EMBL; M16991; AAA34259.1; -
DR PIR; S06357; ALMT3.
DR HSSP; P04063; IAVA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR PRINTS; PR00110; ALPHAAMYLAASE.
DR SMART; SM00642; Amy; 1.
KW Germination; Carbohydrate metabolism; Hydrolyase; Glycosidase; Seed;
KW Calcium-binding; Signal; Multigene family.
FT SIGNAL 1 24
FT CHAIN 1 25
FT ACT_SITE 203 413
FT METAL 115 413
FT METAL 115 413
FT METAL 132 413
FT METAL 132 413
FT METAL 135 413
FT METAL 137 413
FT METAL 141 413
FT METAL 151 413
FT METAL 151 413
FT METAL 162 413
FT METAL 167 413
FT METAL 170 170
FT METAL 170 170
FT METAL 172 172
FT METAL 172 172
FT SEQUENCE 413 AA; 45370 MW; C262ECALC54FCE4 CRC64;
SQ
Query Match 12.0%; Score 315; DB 1; Length 413;
Best Local Similarity 24.7%; Pred. No. 4.2e-15;
Matches 110; Conservative 52; Mismatches 158; Indels 126; Gaps 16;
CC -----
QY 5 LKQYFEMWT-PNDGQKRLQNDALHSLDIGTAVVIPPAYKGLSQSDNGGCPYLYPLG 63
DB 28 LQGFWMESWKTQGGKFKMKGKVEIAGTATWMLPPSQ-SVSEGGIPLGLYTL- 84
QY 64 EFOQKGTATKTYGSELODAIGSLHSRNQYGVVNLHKAQADATEDVTAVEVNPANR 123
DB 85 -----NSKYSGADLKSLIOAFRGKNIQSCADIVINHC----- 118
QY 124 NQSTSEYVIXAMTDRPFRGNTYSDPFMHWYHFDGADMDSRKISIFKRGEGKAMD 183
DB 119 -----ADKDGREYVCLFEGSTDAEFLD 141
QY 184 W---EVSSENGVND-----YLMYADVDYHPDVVAETKKGWIMYANESLDFPR 229
DB 142 WGDDEICSDDTKYSNGRGHDTGGGDDAPDIDHNPVQRELSAMLWLKTDLGDDMR 201
QY 230 IDAAKIKRSPLRDWAQVRAQTGKEMFVAAYVQNNKGLKENTYKNSFNQSVFVDFLH 289
DB 202 LDFAKSYSAAMAKIYD-----NSKRAFVGLYDRLDRLANWVRGVGGPATADDFTK 256
QY 290 FNLQAASQGGGVDMRLLDGT---VVSHPPEKAVTPVENHDTOPGOSLESTVQTFXP- 345
DB 257 GVLQGEAVQ--GDLGRVRGSDGKAPGMIQWPEKTVFIDNHT-----GSTORLWPPS 308
QY 346 ----LAVAFILTRRESGVPGVGDWYGTGSPKELPSIKDNIIEPLAKRKRYAAGPQHD 401
DB 309 DKVMGQYAVILR-HPGIPCLFYDHFVDMK-----LKQBITALATVRSNGI----- 353
QY 402 YIDHP-----DVIQWTRGDSAAKSG 423
DB 354 ---HPGSTLDIL--KAEGLVYAKIG 374

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RESULT 15
ID AMY1_HORVU STANDARD; PRT; 438 AA.
AC P06593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amy1ase type A isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-
DE glucan glucanohydrolase) (AMY1) (low pI alpha-amy1ase).
GN AMY1.1.
OS Hordeum vulgare (barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A. -
RC STRAIN=cv. Himalaya;
RX MEDLINE=83238423; PubMed=6190808;
RA Rogers J.C., Millman C.;
RT "Isolation and sequence analysis of a barley alpha-amy1ase cDNA
RT clone."
RL J. Biol. Chem. 258:8169-8174(1983).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- DEVELOPMENTAL STAGE: Production of alpha-amy1ase is hormonally
CC regulated. Germinating embryos produce the hormone gibberellic
CC acid, which within 10 hours stimulates the aleurone cells covering
CC the endosperm of the seed to produce alpha-amy1ase. The enzyme
CC then degrades the starch within the endosperm for use by the
CC developing plant embryo.
CC -1- MISCELLANEOUS: There are at least 4 types of alpha-amy1ase in
CC barley.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J01236; AAA32929.1; -
DR PIR; A00846; ALBH.
DR HSSP; P04063; IAVA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR PRINTS; PR00110; ALPHAAMYLAASE.
DR SMART; SM00642; Amy; 1.
KW Germination; Carbohydrate metabolism; Hydrolyase; Glycosidase; Seed;
KW Calcium-binding; Signal; Multigene family.
FT SIGNAL 1 24
FT CHAIN 1 25
FT ACT_SITE 204 438
FT ACT_SITE 204 438
FT ACT_SITE 229 438
FT ACT_SITE 229 438
FT ACT_SITE 315 438
FT METAL 116 438
FT METAL 133 438
FT METAL 133 438
FT METAL 136 438
FT METAL 138 438
FT METAL 142 438
FT METAL 142 438
FT METAL 152 438
FT METAL 163 438
FT METAL 166 438

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FT METAL 167 167 CALCIUM 1 (BY SIMILARITY).
FT METAL 168 168 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 171 171 SIMILARITY).
FT METAL 171 171 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 173 173 SIMILARITY).
FT METAL 173 173 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 438 AA; 47796 MW; 2393FDAC51E80F51 CRC64;

Query Match 11.7%; Score 307.5; DB 1; Length 438;
Best Local Similarity 25.2%; Pred. No. 1.6e-14;
Matches 110; Conservative 51; Mismatches 131; Indels 145; Gaps 18;

QY 5 LMOVPEWYTPNDGQHMKR-----LQNDAEHLSDIGTAVWIPPAKGLSQSDNGYGPY 57
DB 28 LFOGPNW-----ESMKSGGMNMMGKVDIAAGVTHVWLP--PSHSVSNEGIMPG 79
QY 58 DLYDIGEPQOKGTATKTKGTSELODAIGLSHRNVQYGVYLNHKAQADATEDVTAVE 117
DB 80 RLYDID-----ASKYGNAAELKSLIGALHGKGVQAIADIVINHRC----- 119
QY 118 VNPANRQETSEBYQIKAMTDFRFGNGNTYSDFKHWYHFDGADWDESRSRIFKFRG 177
DB 120 -----ADYKDSRGICYCFEGGT 136
QY 178 EGRKAWD-----EVSSSENGY---DYLMTADVDYDHPDVVAETKKGIWYANEL 223
DB 137 SDGRLDWGPBHMICRDDTKYSDGTANLDGADPFAAPDIDHLDNRVORELKEMLLMKSDL 196
QY 224 SLDGFRIDAAKHIKESFLBDWQAVROATGKEMFTVAEYMNNA-----GK----- 269
DB 197 GFDANRLDPARGYSPEMAKVYIDGTSFS-----LAAYEYMDMAVGGDGKENVYDQDAHQ. 251
QY 270 -LENYLNKTSFNQS---VEDVPLHFNLOAASQGGGYDMRLLDGT-----VSRHPEKA 320
DB 252 NLVNVVDKVGGAASAGWVPDFTTKGILNNA--VEG---ELMRLIDPQKAPGVMGWMPAKA 307
QY 321 VTFVENHDTQPGQSLESTVGTWFKP-----LAYAFILTRSGYPOVFYGDWYGTGTSBK 375
DB 308 ATFVVDNHDY-----GSTQAMPFPSPDKWQGYAYILT-HPGIFCLTFIDHFFNW----- 354
QY 376 SIPSLEKNIEPIIKARK 392
DB 355 ---GFKDQIAALVALIRK 368
```

Search completed: May 3, 2004, 20:51:14
Job time : 12.3995 secs

Query Match 100.0%; Score 2847; DB 2; Length 514;
 Best Local Similarity 100.0%; Pred. No. 3.8e-245;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFNGTMMQYFEMWLPDDGTLMTKVANEANNSLSLGTALMLPAPYKGTSRSDVGYGY 60
 DB 1 AAFNGTMMQYFEMWLPDDGTLMTKVANEANNSLSLGTALMLPAPYKGTSRSDVGYGY 60
 QY 61 DLYDGEFNQKGTATKGTATQYLOAIOAAHAAQYVADVFDHKGADGTEWDAVE 120
 DB 61 DLYDGEFNQKGTATKGTATQYLOAIOAAHAAQYVADVFDHKGADGTEWDAVE 120
 QY 121 VNPSDRNOEISGTQIOAWTKFDPFGNGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
 DB 121 VNPSDRNOEISGTQIOAWTKFDPFGNGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
 QY 181 IGRAMWEVDTENGNYDYLMYADLMDHPEVVTTELKMGKMYVNTNIDGFRDLAVHAIK 240
 DB 181 IGRAMWEVDTENGNYDYLMYADLMDHPEVVTTELKMGKMYVNTNIDGFRDLAVHAIK 240
 QY 241 FSPFPDMLSYRSQTKPLFTVGEWYSYDINKLHNYITKDTGMSLFPAPLNKRYTASK 300
 DB 241 FSPFPDMLSYRSQTKPLFTVGEWYSYDINKLHNYITKDTGMSLFPAPLNKRYTASK 300
 QY 301 SGGAFDMRTLMNTLMKQOPTLAVTFVNDHDEPQALQSWDPMFKPLAVAFILTRQEG 360
 DB 301 SGGAFDMRTLMNTLMKQOPTLAVTFVNDHDEPQALQSWDPMFKPLAVAFILTRQEG 360
 QY 361 YPCVFYGDYGYIPQYNIPSLKSKIDPLIARDYAVGTQHDYLDHSDIIGMTRREGTEKP 420
 DB 361 YPCVFYGDYGYIPQYNIPSLKSKIDPLIARDYAVGTQHDYLDHSDIIGMTRREGTEKP 420
 QY 421 GSGIALALITDGGSGKMYVQKQHAKGYFDLTGNSDVTIINSOGWGEFKNVGSVSW 480
 DB 421 GSGIALALITDGGSGKMYVQKQHAKGYFDLTGNSDVTIINSOGWGEFKNVGSVSW 480
 QY 481 VPRKTTVSTIARPIITRPWTGFEVWTEBRLVAM 514
 DB 481 VPRKTTVSTIARPIITRPWTGFEVWTEBRLVAM 514

RESULT 2

AAR72449
 ID AAR72449 standard; protein; 515 AA.

AC AAR72449;
 XX
 XX 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 01-DEC-1995 (first entry)
 XX
 XX Bacillus stearothermophilus alpha amylase (mature protein).
 DE
 XX Alpha amylase; variant; enzyme; detergent; additive; dishwashing;
 KW washing; Bacillus licheniformis; Bacillus amyloliquefaciens;
 KW Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
 KW chemostable.
 XX
 XX Geobacillus stearothermophilus.
 OS
 XX WO95.0603-A1.
 PN
 XX 20-APR-1995.
 PD
 XX
 PF 05-OCT-1994; 94WO-DK000370.
 XX
 XX 08-OCT-1993; 93DK-00001133.
 PR 02-FEB-1994; 94DK-00000140.
 XX
 XX (NOVO) NOVO-NORDISK AS.
 PA
 XX Borchert TV, Bisgard-Frantzen H, Sverdsen A, Thelersen M;

PI Van Der Zee P;
 XX WPI, 1995-161790/21.
 DR N-PSDB; AAQ8068.
 DR
 XX
 PT New Bacillus derived alpha-amylase variants - having amino acid
 PT modifications to improve washing and/or dishwashing performance.
 XX
 PS Claim 34; Page 11-12; 105pp; English.

CC Variant alpha amylase enzymes which have improved washing and/or as
 CC detergent additives. The enzymes have one or more amino acid residues
 CC added, deleted or substituted. The variants can also be used for textile
 CC desizing prior to scouring, bleaching and dyeing. The variants have
 CC improved thermostability, acid/alkaline stability, low temperature
 CC optimum; pH optimum; higher hydrolysis velocity and improved tolerance
 CC other composition constituents, e.g. oxidation agents. (updated on 25-MAR
 CC -2003 to correct PN field.) (updated on 25-MAR-2003 to correct PI field.)
 CC (updated on 16-OCT-2003 to standardise OS field)
 CC
 XX Sequence 515 AA;

Query Match 100.0%; Score 2847; DB 2; Length 515;
 Best Local Similarity 100.0%; Pred. No. 3.8e-245;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFNGTMMQYFEMWLPDDGTLMTKVANEANNSLSLGTALMLPAPYKGTSRSDVGYGY 60
 DB 1 AAFNGTMMQYFEMWLPDDGTLMTKVANEANNSLSLGTALMLPAPYKGTSRSDVGYGY 60
 QY 61 DLYDGEFNQKGTATKGTATQYLOAIOAAHAAQYVADVFDHKGADGTEWDAVE 120
 DB 61 DLYDGEFNQKGTATKGTATQYLOAIOAAHAAQYVADVFDHKGADGTEWDAVE 120
 QY 121 VNPSDRNOEISGTQIOAWTKFDPFGNGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
 DB 121 VNPSDRNOEISGTQIOAWTKFDPFGNGNTYSSFKRWYHFDGVWDESRKLSRIYKFRG 180
 QY 181 IGRAMWEVDTENGNYDYLMYADLMDHPEVVTTELKMGKMYVNTNIDGFRDLAVHAIK 240
 DB 181 IGRAMWEVDTENGNYDYLMYADLMDHPEVVTTELKMGKMYVNTNIDGFRDLAVHAIK 240
 QY 241 FSPFPDMLSYRSQTKPLFTVGEWYSYDINKLHNYITKDTGMSLFPAPLNKRYTASK 300
 DB 241 FSPFPDMLSYRSQTKPLFTVGEWYSYDINKLHNYITKDTGMSLFPAPLNKRYTASK 300
 QY 301 SGGAFDMRTLMNTLMKQOPTLAVTFVNDHDEPQALQSWDPMFKPLAVAFILTRQEG 360
 DB 301 SGGAFDMRTLMNTLMKQOPTLAVTFVNDHDEPQALQSWDPMFKPLAVAFILTRQEG 360
 QY 361 YPCVFYGDYGYIPQYNIPSLKSKIDPLIARDYAVGTQHDYLDHSDIIGMTRREGTEKP 420
 DB 361 YPCVFYGDYGYIPQYNIPSLKSKIDPLIARDYAVGTQHDYLDHSDIIGMTRREGTEKP 420
 QY 421 GSGIALALITDGGSGKMYVQKQHAKGYFDLTGNSDVTIINSOGWGEFKNVGSVSW 480
 DB 421 GSGIALALITDGGSGKMYVQKQHAKGYFDLTGNSDVTIINSOGWGEFKNVGSVSW 480
 QY 481 VPRKTTVSTIARPIITRPWTGFEVWTEBRLVAM 514
 DB 481 VPRKTTVSTIARPIITRPWTGFEVWTEBRLVAM 514

RESULT 3

AAM31406
 ID AAM31406 standard; protein; 515 AA.

AC AAM31406;
 XX
 XX 17-OCT-2003 (revised)
 DT 11-MAY-1998 (first entry)
 XX
 XX Bacillus stearothermophilus Teramyl-1-like alpha-amylase.

XX Termamyl; alpha-amylase; enzyme engineering; protein engineering; starch;
 KW liquefaction; saccharification; sweetener; textile desizing;
 KW detergent additive; ss.
 XX Geobacillus stearothermophilus.
 XX WO9741213-A1.
 XX 06-NOV-1997.
 XX 30-APR-1997; 97WO-DK000197.
 XX 30-APR-1996; 96DK-00000515.
 XX 28-JUN-1996; 96DK-00000712.
 XX 11-JUL-1996; 96DK-00000775.
 XX 08-NOV-1996; 96DK-00001263.
 XX (NOVO) NOVO-NORDISK AS.
 XX Svendsen A, Borchert TV, Bisgard-Frantzen H;
 XX WPI, 1997-549718/50.
 XX N-PSDB; AAV02473.
 XX Termamyl-like alpha-amylase variants with improved properties - e.g.
 PT increased stability at low pH and low calcium, useful as detergent
 PT additives and in industrial starch processing e.g. liquefaction.
 XX Disclosure, Page 86; 101pp; English.
 XX This protein comprises the Termamyl-like alpha-amylase of Bacillus
 CC steothermophilus. The invention relates to novel variants of Termamyl-
 CC like alpha-amylases that have alpha-amylase activity and exhibit an
 CC alteration in at least one property selected from: substrate specificity;
 CC binding or cleavage pattern; thermal stability; pH/activity or
 CC pH/stability profile; stability towards oxidation; Ca²⁺ dependency and
 CC specific activity. The variant has one or more mutations from those
 CC listed in the specification in relation to Bacillus licheniformis
 CC Termamyl (see AAV01404). Also claimed are constructs comprising DNA
 CC encoding the variant (see AAV02471-73), and recombinant expression
 CC vectors and transformed cells containing the DNA. The Termamyl-like alpha
 CC in industrial starch processing e.g. liquefaction (claimed) or
 CC saccharification to produce sweeteners, and in textile desizing
 CC (claimed). (Updated on 17-OCT-2003 to standardise OS field)
 CC
 XX Sequence 515 AA:
 SQ

Query Match 100.0%; Score 2847; DB 2; Length 515;
 Best Local Similarity 100.0%; Pred. No. 3.8e-245;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 1 AAFNGTMMQYFEWYLPDDGLMTKVAENNNLSIGITATLWLPAYKGTSSDVGCVY 60
 DB 1 AAFNGTMMQYFEWYLPDDGLMTKVAENNNLSIGITATLWLPAYKGTSSDVGCVY 60
 XX 61 DLYDGEFNGKTVTKYTKYQAOYQAOAAHAGMAYADVPHKGGAGDTEWDAVE 120
 DB 61 DLYDGEFNGKTVTKYTKYQAOYQAOAAHAGMAYADVPHKGGAGDTEWDAVE 120
 XX 121 VNPSPRNDIEISGTYOQAWTKFDPGRGNTYSSPFKRWYHFDGVMDSRKLRIYKFRG 180
 DB 121 VNPSPRNDIEISGTYOQAWTKFDPGRGNTYSSPFKRWYHFDGVMDSRKLRIYKFRG 180
 XX 181 ICKADWEDVTENGNYDYIMYADLMDHDEEVTTELKNGKRYVNTTNDGFFLDVVKIK 240
 DB 181 ICKADWEDVTENGNYDYIMYADLMDHDEEVTTELKNGKRYVNTTNDGFFLDVVKIK 240
 XX 241 FSEFDMLSYVRSQGTGKPLFTVGEYMSYDINKLHNYITKTDGTSGLFPAFLNKFYASK 300
 DB 241 FSEFDMLSYVRSQGTGKPLFTVGEYMSYDINKLHNYITKTDGTSGLFPAFLNKFYASK 300

XX 301 SGGAFFMRITMTMTLTKKQPTLAVTFVDNHDTEFGQALOSWVDPKPKPLAFAFILTRQEG 360
 DB 301 SGGAFFMRITMTMTLTKKQPTLAVTFVDNHDTEFGQALOSWVDPKPKPLAFAFILTRQEG 360
 XX 361 YPCVFYGDYIGIPQYNIPLSKSKIDPDLIARRDYAGTQHDYLDHSDIIGMREGGTEKP 420
 DB 361 YPCVFYGDYIGIPQYNIPLSKSKIDPDLIARRDYAGTQHDYLDHSDIIGMREGGTEKP 420
 XX 421 GSGIALLITDGPQSGSKMVTYKQAGKRYFDLTGNRSDPTVTINSDCWGEFKNGSSVSW 480
 DB 421 GSGIALLITDGPQSGSKMVTYKQAGKRYFDLTGNRSDPTVTINSDCWGEFKNGSSVSW 480
 XX 481 VPKRTVSTIARPIITRPMTGEFVFRWTEPRLVAM 514
 DB 481 VPKRTVSTIARPIITRPMTGEFVFRWTEPRLVAM 514

RESULT 4
 ID AAY9770 standard; protein; 515 AA.
 XX AAY9770.
 XX AAY9770.
 XX 12-SEP-2003 (revised)
 DT 04-SEP-2000 (first entry)
 XX Bacillus stearothermophilus Termamyl-like alpha-amylase #2.
 DE Bacillus stearothermophilus Termamyl-like alpha-amylase #2.
 XX Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
 KW saccharification; muten; mutant; enzyme stability; hybrid.
 XX Geobacillus stearothermophilus.
 OS WO200029560-A1.
 XX 25-MAY-2000.
 PD 16-NOV-1999; 99WO-DK000628.
 PF 16-NOV-1998; 98DK-00001495.
 XX 16-NOV-1998; 98DK-00001495.
 PR (NOVO) NOVO-NORDISK AS.
 XX Svendsen A, Kjærulff S, Bisgard-Frantzen H, Andersen C;
 FI WPI, 2000-387777/33.
 DR N-PSDB; AAA48482.
 XX Variant of parent termamyl-like alpha amylase useful for washing, textile
 PT desizing and starch liquefaction, comprising alterations in one or more
 PT solvent exposed amino acid residues.
 XX Claim 8; Fig 1; 80pp; English.
 PS The present sequence is a parent alpha-amylase from which mutants with
 XX increased stability at acidic pH, low calcium concentration and high
 XX temperatures have been derived. A variant may contain mutations in one or
 XX more solvent exposed amino acid residues to increase the overall
 CC hydrophobicity of the enzyme or the overall number of methyl groups in
 CC the side chains of exposed residues may be increased. The mutations can
 CC be incorporated by site-directed mutagenesis or by random mutagenesis. As
 CC a result of their increased stability, the variants are suitable for the
 CC industrial processing of starch, i.e. starch liquefaction and
 CC saccharification. They may also be useful for washing, dishwashing and
 CC textile desizing. Hybrid alpha-amylases comprising partial amino acid
 CC sequences derived from two or more alpha-amylases have also been created
 CC in order to increase enzyme stability. Note: According to the
 CC specification, the present sequence and the sequence shown in AAY9604
 CC are the same. (Updated on 12-SEP-2003 to standardise OS field)
 XX
 XX Sequence 515 AA:
 SQ

Query Match 100.0%; Score 2847; DB 3; Length 515;

Tue May 4 14:34:48 2004

us-10-644-187-6.rag

Page 4

Best Local Similarity 100.0%; Pred. No. 3.8e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAFNGTMMQYFEMWLPDDGTLMTKVAANEANLSSIGITLALMPAYKGSRSDDVGYVY 60
Db 1 AAFNGTMMQYFEMWLPDDGTLMTKVAANEANLSSIGITLALMPAYKGSRSDDVGYVY 60
QY 61 DLYDLGEFNOGKTVTKYGTAKYLOAIOAANAAGMUYADVDPHKGADGTEWDAVE 120
Db 61 DLYDLGEFNOGKTVTKYGTAKYLOAIOAANAAGMUYADVDPHKGADGTEWDAVE 120
QY 121 VNPSDRNOEISGTYOIQAMTKFDPFGKNTYSSFKRMWHPGVMDSEKLSRIYKFRG 180
Db 121 VNPSDRNOEISGTYOIQAMTKFDPFGKNTYSSFKRMWHPGVMDSEKLSRIYKFRG 180
QY 181 IGKAMDEVDTENGNDYDLYADLMDHDEVTTELKMGKMYVNTNIDGFRDLAVKAIK 240
Db 181 IGKAMDEVDTENGNDYDLYADLMDHDEVTTELKMGKMYVNTNIDGFRDLAVKAIK 240
QY 241 FSFFPDLSTYRSOTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFPAPLHNKRYTASK 300
Db 241 FSFFPDLSTYRSOTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFPAPLHNKRYTASK 300
QY 301 SGGAPEMRITMTNTLMKQPTLAVTFVNDHDEPQALOSWVDPWFKPLAVAFILTRQEG 360
Db 301 SGGAPEMRITMTNTLMKQPTLAVTFVNDHDEPQALOSWVDPWFKPLAVAFILTRQEG 360
QY 361 YPCVFYGDYVYGIPOYNIPLSKIKIDPLLIARSDYAGTQHDYLDSDIIGWTRGEGTEKP 420
Db 361 YPCVFYGDYVYGIPOYNIPLSKIKIDPLLIARSDYAGTQHDYLDSDIIGWTRGEGTEKP 420
QY 421 GSGLAALITDGPGGSKMYVKGKQAKGVYDITGNRSDVTYVINSOGKEFKVNGGSVSW 480
Db 421 GSGLAALITDGPGGSKMYVKGKQAKGVYDITGNRSDVTYVINSOGKEFKVNGGSVSW 480
QY 481 VPKRTVSTIARPIITRPWTGSEFVWTEPRLVAM 514
Db 481 VPKRTVSTIARPIITRPWTGSEFVWTEPRLVAM 514
RESULT 5
ID AAY97547 standard; protein; 515 AA.
XX AAY97547;
XX AC AAY97547;
DT 11-SEP-2003 (revised)
DT 12-FEB-2001 (first entry)
XX B. steaerotherophilus termamyl-like alpha amylase.
XX Termamyl-like alpha-amylase; variant; starch liquefaction; fuel;
XX detergent composition; laundry cleaning composition; ethanol production;
XX dish washing cleaning composition; hard surface cleaning composition;
XX industrial ethanol production; textile desizing.
XX Geobacillus steaerotherophilus.
XX WO200060059-A2.
XX 12-OCT-2000.
XX 28-MAR-2000; 2000WO-DK000148.
XX 30-MAR-1999; 99DK-00000437.
XX (NOVO) NOVO NORDISK AS.
XX Andersen C, Jorgensen CT, Bisgard-Frantzen H, Svendsen A;
XX PI Kjaerulff S;
XX WPI; 2001-015656/02.
XX DR N-PSDB; AAA37851.

XX New variants of parent Termamyl-like alpha-amylase, useful in starch
PT liquefaction, in detergent compositions and in ethanol production,
PT exhibit altered cleavage pattern relative to the parent.
PS Claim 17; Page 69-70; 78pp; English.
XX This sequence represents a termamyl-like alpha amylase. The invention
CC relates to a variant (1) of parent termamyl-like alpha-amylase comprising
CC alteration at one or more of the positions W13, G48, T49, S50, Q51, A52,
CC D53, V54, G57, G107, G108, A111, S168 and M197. The alterations in (1)
CC are independently an insertion of an amino acid downstream of the amino
CC acid which occupies the position of deletion or substitution of the amino
CC acid which occupies the position with a different amino acid. The variant
CC has alpha-amylase activity, (1) or compositions containing it are useful
CC in starch liquefaction, in detergent compositions such as laundry, dish
CC washing and hard surface cleaning compositions, ethanol production, desizing of
CC as fuel, drinking and industrial ethanol production, desizing of
CC textiles, fabrics or garments. (1) exhibits a reduced capability of
CC cleaving a substrate close to the branching point, and further exhibits
CC improved substrate specificity and/or improved specific activity relative
CC to the parent alpha-amylase. (updated on 11-SEP-2003 to standardise OS
CC field)
XX . Sequence 515 AA;
XX SQ
Query Match 100.0%; Score 2847; DB 4; Length 515;
Best Local Similarity 100.0%; Pred. No. 3.8e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAFNGTMMQYFEMWLPDDGTLMTKVAANEANLSSIGITLALMPAYKGSRSDDVGYVY 60
Db 1 AAFNGTMMQYFEMWLPDDGTLMTKVAANEANLSSIGITLALMPAYKGSRSDDVGYVY 60
QY 61 DLYDLGEFNOGKTVTKYGTAKYLOAIOAANAAGMUYADVDPHKGADGTEWDAVE 120
Db 61 DLYDLGEFNOGKTVTKYGTAKYLOAIOAANAAGMUYADVDPHKGADGTEWDAVE 120
QY 121 VNPSDRNOEISGTYOIQAMTKFDPFGKNTYSSFKRMWHPGVMDSEKLSRIYKFRG 180
Db 121 VNPSDRNOEISGTYOIQAMTKFDPFGKNTYSSFKRMWHPGVMDSEKLSRIYKFRG 180
QY 181 IGKAMDEVDTENGNDYDLYADLMDHDEVTTELKMGKMYVNTNIDGFRDLAVKAIK 240
Db 181 IGKAMDEVDTENGNDYDLYADLMDHDEVTTELKMGKMYVNTNIDGFRDLAVKAIK 240
QY 241 FSFFPDLSTYRSOTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFPAPLHNKRYTASK 300
Db 241 FSFFPDLSTYRSOTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFPAPLHNKRYTASK 300
QY 301 SGGAPEMRITMTNTLMKQPTLAVTFVNDHDEPQALOSWVDPWFKPLAVAFILTRQEG 360
Db 301 SGGAPEMRITMTNTLMKQPTLAVTFVNDHDEPQALOSWVDPWFKPLAVAFILTRQEG 360
QY 361 YPCVFYGDYVYGIPOYNIPLSKIKIDPLLIARSDYAGTQHDYLDSDIIGWTRGEGTEKP 420
Db 361 YPCVFYGDYVYGIPOYNIPLSKIKIDPLLIARSDYAGTQHDYLDSDIIGWTRGEGTEKP 420
QY 421 GSGLAALITDGPGGSKMYVKGKQAKGVYDITGNRSDVTYVINSOGKEFKVNGGSVSW 480
Db 421 GSGLAALITDGPGGSKMYVKGKQAKGVYDITGNRSDVTYVINSOGKEFKVNGGSVSW 480
QY 481 VPKRTVSTIARPIITRPWTGSEFVWTEPRLVAM 514
Db 481 VPKRTVSTIARPIITRPWTGSEFVWTEPRLVAM 514
RESULT 6
ID ABB06935 standard; protein; 515 AA.
XX ABB06935;
XX AC ABB06935;

DT 29-AUG-2003 (revised)
 DT 19-JUN-2002 (first entry)
 XX
 DE B. steaerothermophilus termamyl-like alpha-amylase protein SEQ ID NO:6.
 XX
 KM Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
 KM variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
 KM washing; sweetener; ethanol; starch.
 XX
 OS Geobacillus steaerothermophilus.
 XX
 PN MO20016712-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 07-MAR-2001; 2001WO-DK000144.
 XX
 PR 08-MAR-2000; 2000DK-00000376.
 PR 15-MAR-2000; 2000US-0189857P.
 PR 23-FEB-2001; 2001DK-00000303.
 PR 26-FEB-2001; 2001US-0271382P.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Andersen C, Borchert TV, Nielsen BR;
 XX
 DR WPI; 2002-239612/29.
 DR N-PSDB; ABL50566.
 XX
 PT Novel variant of parent termamyl-like alpha-amylase useful as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 PS Claim 8; Page 138-139; 153pp; English.
 XX
 CC The present invention describes a variant of a parent termamyl-like alpha
 CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
 CC positions of a group of 31 possible amino acid positions. The alteration
 CC in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,
 CC Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,
 CC Arg310, Asn314, Arg320, His324, Gly345, Tyr396, Arg400, Trp439, Arg444,
 CC Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
 CC washing and/or dishwashing, textile desizing, and starch liquefaction.
 CC (1) is useful as a component in hard surface cleaning detergent
 CC composition, and for producing sweeteners and ethanol from starch. (I)
 CC has altered solubility, preferably increased solubility, in particular
 CC under washing, dish washing or hard surface cleaning conditions. The
 CC present sequence represents a Bacillus steaerothermophilus termamyl-like
 CC alpha-amylase which is used in the exemplification of the present
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 515 AA;
 XX
 QY Query Match 100.0%; Score 2847; DB 5; Length 515;
 DB Best Local Similarity 100.0%; Pred. No. 3,8e-245;
 DB Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPNGTMMQYFEWYLPDDGLTKVANEANNISLGLTLMTPRAYKTSRSDVGYGY 60
 DB 1 AAPNGTMMQYFEWYLPDDGLTKVANEANNISLGLTLMTPRAYKTSRSDVGYGY 60
 QY 61 DLVLDGFNKGATVTKTKAQLQAIQAAHAGMOVADVVDHKGADGTEWDAVE 120
 DB 61 DLVLDGFNKGATVTKTKAQLQAIQAAHAGMOVADVVDHKGADGTEWDAVE 120
 QY 121 VNPEDNQEISGTYQIQAMTKFDPFGKNTYSSFKRWYHFDGVDDESKLSRIYKFRG 180
 DB 121 VNPEDNQEISGTYQIQAMTKFDPFGKNTYSSFKRWYHFDGVDDESKLSRIYKFRG 180
 QY 181 IGMAMDEVDTENGNVDYLAADJDMHDEVTETLKNMGKMYVYTTNIDGFRLDAYVHK 240
 DB 181 IGMAMDEVDTENGNVDYLAADJDMHDEVTETLKNMGKMYVYTTNIDGFRLDAYVHK 240

QY 241 FSPFPDLSTVRSQTKPLFTVGEYMSYDINKLHNTYTKDGTMSLFDAPLHNKFTYAK 300
 DB 241 FSPFPDLSTVRSQTKPLFTVGEYMSYDINKLHNTYTKDGTMSLFDAPLHNKFTYAK 300
 QY 301 SGCAFDMRTIMTNTLMKDOPTLAVTFVDNHDTEPGQALOSWDPMFKPLAYAFILTRQGG 360
 DB 301 SGCAFDMRTIMTNTLMKDOPTLAVTFVDNHDTEPGQALOSWDPMFKPLAYAFILTRQGG 360
 QY 361 YPCVFYDDYGIPOYNIPSLKSKIDPLIARRYAGTODYLDHSIIIGMTREGTEK 420
 DB 361 YPCVFYDDYGIPOYNIPSLKSKIDPLIARRYAGTODYLDHSIIIGMTREGTEK 420
 QY 421 GSGIALLITDGPSSKMYVKQKQKGFYDLTGNSDPTVTINSDGWGEFRVNGSSVSVM 480
 DB 421 GSGIALLITDGPSSKMYVKQKQKGFYDLTGNSDPTVTINSDGWGEFRVNGSSVSVM 480
 QY 481 VPKRTVSTIARPTTTPWTGEPVWTEPRLVAM 514
 DB 481 VPKRTVSTIARPTTTPWTGEPVWTEPRLVAM 514
 RESULT 7
 ID AAU12151 standard; protein: 515 AA.
 XX
 XX AAU12151;
 XX
 AC 29-AUG-2003 (revised)
 DT 09-APR-2002 (first entry)
 XX
 XX
 DE Bacillus TERMAMYL-like alpha-amylase BSG.
 XX
 KM TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing;
 KM starch liquefaction; ethanol production; hard surface cleaner; sweetener;
 KM amylopectin; limit dextrin; NOVAMYL; BSG.
 XX
 OS Geobacillus steaerothermophilus.
 XX
 PN WO20018107-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 10-MAY-2001; 2001WO-DK000223.
 XX
 PR 12-MAY-2000; 2000DK-00000779.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Svendsen A, Jorgensen CT, Nielsen BR;
 XX
 DR WPI; 2002-106123/14.
 DR N-PSDB; AAS20024.
 XX
 PT New variant of parent Termamyl-like alpha-amylase for use as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 PS Claim 5; Fig 1; 84pp; English.
 XX
 CC The invention relates to a variant of parent TERMAMYL-like alpha- amylase
 CC comprising an alteration at regions 186-193, 261-275, 283-293 or 334-339,
 CC or at position 234, where the variant has alpha-amylase activity and each
 CC position corresponds to a position of a parent Termamyl-like alpha-
 CC amylase sequence having a Bacillus licheniformis alpha-amylase sequence
 CC of 483 amino acids, given in specification. The variant alpha- amylase, a
 CC detergent additive, comprising the variant or a detergent composition
 CC comprising the variant, is useful for washing and/or dishwashing or
 CC textile desizing. The alpha-amylase is useful for starch liquefaction or
 CC ethanol production and as a component in a hard surface cleaning
 CC detergent composition, and for producing sweeteners from starch. The
 CC variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage
 CC activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic
 CC branch linkage cleavage activity of amylopectin or a limit dextrin

CC prepared by TERAMYL (RTM) or NOVAMYL (RTM). The present sequence is a
 CC natural variant of the TERAMYL alpha-amylase, BSG. (Updated on 29-AUG-
 CC 2003 to standardise OS field)

SC Sequence 515 AA;

Query Match 100.0%; Score 2847; DB 5; Length 515;
 Best Local Similarity 100.0%; Pred. No. 3.8e-245;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 AAFNGTMOYFEMWLPDDGTLMTKVAEANNLSLGLTALMLPAYKGRSDVGYGY 60
 DB 1 AAFNGTMOYFEMWLPDDGTLMTKVAEANNLSLGLTALMLPAYKGRSDVGYGY 60
 CC 61 DLYDGEFNOKGTVRTKGTAKQYLOAIQAHAAGMOYADVDFHKGADGTEWDAVE 120
 DB 61 DLYDGEFNOKGTVRTKGTAKQYLOAIQAHAAGMOYADVDFHKGADGTEWDAVE 120
 CC 121 VNPDRNOISGTYQIOAMTKFDFPGRGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 180
 DB 121 VNPDRNOISGTYQIOAMTKFDFPGRGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 180
 CC 181 IGRAMDWEVDTENGNYDYLMYADLMDHPEVTELEKMGKRYVNTNIDGFRLDVYHIK 240
 DB 181 IGRAMDWEVDTENGNYDYLMYADLMDHPEVTELEKMGKRYVNTNIDGFRLDVYHIK 240
 CC 241 FSPFPDLSTYRSQGTGKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHNFYASK 300
 DB 241 FSPFPDLSTYRSQGTGKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHNFYASK 300
 CC 301 SGGAFAFRMLTMTNLMKQPTLAVTFVDNHDTEPGALQSWDPMFKPLAVAFILTRQEG 360
 DB 301 SGGAFAFRMLTMTNLMKQPTLAVTFVDNHDTEPGALQSWDPMFKPLAVAFILTRQEG 360
 CC 361 YPCVFYGDYGYLPQYNISLSKIDPLLIARDYAVGTHDYLDHSDITGTRGTEKXP 420
 DB 361 YPCVFYGDYGYLPQYNISLSKIDPLLIARDYAVGTHDYLDHSDITGTRGTEKXP 420
 CC 421 GSGLAALITDGPQSGKMYGKQAGKVFYDLTGNSDVTITNSDQMGSEFKNGSVSVW 480
 DB 421 GSGLAALITDGPQSGKMYGKQAGKVFYDLTGNSDVTITNSDQMGSEFKNGSVSVW 480
 CC 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514
 DB 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514

RESULT 8

ID AAB47852 standard; protein; 515 AA.

AC AAB47852;

DT 29-AUG-2003 (revised)

DT 02-APR-2002 (first entry)

DE Bacillus alpha amylase BSG.

XX Alpha amylase, Bacillus; Termamyl-like; maltodextrin; glucose syrup;
 KW starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;
 KW bakery; cereal bar; ice cream; coffee whitener; salad dressing;
 KW cured meat; fermented meat; spice.

OS Geobacillus stearothermophilus.

XX MO200196537-A2.

XX 20-DEC-2001.

XX 13-JUN-2001; 2001MO-DK000404.

XX 14-JUN-2000; 2000DK-0000917.

PR 20-JUN-2000; 2000US-0212852P.

XX (NOVO) NOVOZYMES AS.
 PA Nielsen BR, Welbye M;
 XX WPI/ 2002-098064/13.
 DR N-PSDB; AAI72213.
 XX New modified alpha-amylase derived from the genus Bacillus and/or is a
 PT Termamyl-like alpha-amylase, which has been pre-oxidized for producing
 PS maltodextrin or glucose syrup.
 XX Claim 5; Page 32-33; 47pp; English.

CC The sequences given in AAB47850-56 show modified alpha-amylases derived
 CC from the genus Bacillus. These alpha amylases are Termamyl-like alpha-
 CC amylase and they have been pre-oxidized. The alpha amylase is useful for
 CC producing a maltodextrin or glucose syrup, by treating starch with a pre-
 CC oxidized alpha-amylase until a product with a DE between 5-45 has been
 CC provided and/or until a product with a molecular weight of between 5-30
 CC kDa has been provided. The product comprises a maltodextrin with a DE of
 CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kDa. The
 CC alpha amylase is useful for producing a maltodextrin or glucose syrup,
 CC where the glucose syrup is useful as an ingredient in food, feed or
 CC pharmaceuticals. Glucose syrup is useful in confectionery such as
 CC candies, beverages such as isotonic drinks, bakery such as cereal bars,
 CC dairy and ice cream such as coffee whiteners, conventional foods such as
 CC salad dressings, and food ingredients and preparations such as cured
 CC meat, fermented meat, spices and seasoning encapsulated flavours.
 CC (Updated on 29-AUG-2003 to standardise OS field)

SC Sequence 515 AA;

Query Match 100.0%; Score 2847; DB 5; Length 515;
 Best Local Similarity 100.0%; Pred. No. 3.8e-245;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 AAFNGTMOYFEMWLPDDGTLMTKVAEANNLSLGLTALMLPAYKGRSDVGYGY 60
 DB 1 AAFNGTMOYFEMWLPDDGTLMTKVAEANNLSLGLTALMLPAYKGRSDVGYGY 60
 CC 61 DLYDGEFNOKGTVRTKGTAKQYLOAIQAHAAGMOYADVDFHKGADGTEWDAVE 120
 DB 61 DLYDGEFNOKGTVRTKGTAKQYLOAIQAHAAGMOYADVDFHKGADGTEWDAVE 120
 CC 121 VNPDRNOISGTYQIOAMTKFDFPGRGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 180
 DB 121 VNPDRNOISGTYQIOAMTKFDFPGRGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 180
 CC 181 IGRAMDWEVDTENGNYDYLMYADLMDHPEVTELEKMGKRYVNTNIDGFRLDVYHIK 240
 DB 181 IGRAMDWEVDTENGNYDYLMYADLMDHPEVTELEKMGKRYVNTNIDGFRLDVYHIK 240
 CC 241 FSPFPDLSTYRSQGTGKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHNFYASK 300
 DB 241 FSPFPDLSTYRSQGTGKPLFTVGEYWSYDINKLHNYITKTGMSLFDAPLHNFYASK 300
 CC 301 SGGAFAFRMLTMTNLMKQPTLAVTFVDNHDTEPGALQSWDPMFKPLAVAFILTRQEG 360
 DB 301 SGGAFAFRMLTMTNLMKQPTLAVTFVDNHDTEPGALQSWDPMFKPLAVAFILTRQEG 360
 CC 361 YPCVFYGDYGYLPQYNISLSKIDPLLIARDYAVGTHDYLDHSDITGTRGTEKXP 420
 DB 361 YPCVFYGDYGYLPQYNISLSKIDPLLIARDYAVGTHDYLDHSDITGTRGTEKXP 420
 CC 421 GSGLAALITDGPQSGKMYGKQAGKVFYDLTGNSDVTITNSDQMGSEFKNGSVSVW 480
 DB 421 GSGLAALITDGPQSGKMYGKQAGKVFYDLTGNSDVTITNSDQMGSEFKNGSVSVW 480
 CC 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514
 DB 481 VPKRTVSTIARPIITRPWTGEFVWTEPRLVAM 514

RESULT 9
 ABB76588
 ID ABB76588 standard; protein; 515 AA.
 AC ABB76588;
 DT 29-AUG-2003 (revised)
 DT 19-AUG-2002 (first entry)
 DE Termamy1-like-alpha-amy1ase #3.
 KW Termamy1; alpha amy1ase; starch liquefaction; ethanol production;
 KW textile desizing; detergent; enzyme.
 OS Geobacillus stearothermophilus.
 XX WO200210355-A2.
 PN 07-FEB-2002.
 PD 12-JUL-2001; 2001WO-DK000488.
 PF 01-AUG-2000; 2000DK-00001160.
 PR 12-SEP-2000; 2000DK-00001354.
 PR 10-NOV-2000; 2000DK-00001887.
 PR 26-APR-2001; 2001DK-00000655.
 XX (NOVO) NOVOZYMES AS.
 PA Thisted T, Kjaerulff S, Andersen C, Englaug CC;
 XX WPI: 2002-280633/32.
 DR N-PSDB; ABL86209.
 PT Variant of parent Termamy1-like alpha amy1ase, useful in detergent
 PT compositions, for starch liquefaction, ethanol production, washing and/or
 PT dish washing, and textile desizing.
 XX Claim 4; Fig 5; 90pp; English.
 CC This invention relates to variants of a parent Termamy1-like alpha-
 CC amy1ase. These are used for starch liquefaction, ethanol production,
 CC detergent, and textile desizing. The amy1ases have altered stability,
 CC particularly at high temperatures from 70-120plusoc and low pH in the
 CC range from pH 4.0-6.0. The present sequence is a termamy1-like-alpha-
 CC amy1ase. (Updated on 29-AUG-2003 to standardise OS field)
 CC
 SO Sequence 515 AA.
 Query Match 100.0%; Score 2847; DB 5; Length 515;
 Best Local Similarity 100.0%; Pred. No. 3,8e-245;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
 AEU03090
 ID AEU03090 standard; protein; 549 AA.
 AC AEU03090;
 DT 21-JAN-2003 (first entry)
 DE Alpha amy1ase polypeptide #51.
 KW Alpha amy1ase; enzyme; starch linkage hydrolysis; starch liquefaction;
 KW starch breakdown catalysis; textile desizing; lignocellulosic fibre;
 KW enzymatic de-linking; recycled paper; high-maltose syrup; dough;
 KW high glucose syrup; corn-wet milling process; detergent; baking process;
 KW beverage; oil field; fuel ethanol; brewing process; scaling;
 KW starch modification.
 XX Unidentified.
 XX WO200268589-A2.
 PD 06-SEP-2002.
 PF 21-FEB-2002; 2002WO-US005068.
 PR 21-FEB-2001; 2001US-0270495P.
 PR 21-FEB-2001; 2001US-0270496P.
 PR 14-MAY-2001; 2001US-0291122P.
 XX (DIVE-) DIVERSA CORP.
 PA Callen W, Richardson T, Frey G;
 XX WPI: 2003-018656/01.
 DR N-PSDB; ABX08461.
 PT Novel purified polypeptide with alpha-amy1ase activity, useful e.g. for
 PT liquefying starch, for textile desizing, for creating lignocellulosic
 PT fibers, and for producing high-maltose or high-glucose syrup.
 XX Claim 30; Fig 16; 301pp; English.
 PS The invention relates to a purified polypeptide with alpha-amy1ase
 PS activity and the polynucleotide encoding it. The polypeptide is useful
 PS for hydrolyzing starch linkages, for catalyzing the breakdown of a
 PS starch, for modifying small molecules, for liquefying starch, for washing
 PS an object, for textile desizing, for creating lignocellulosic fibers, for
 PS improving fibre properties, for enzymatic de-linking of recycled paper
 PS pulp, for producing a high-maltose or high-glucose syrup or a mixed
 PS syrup, and for increasing the flow of production fluids from a
 PS subterranean formation by removing a viscous, starch-containing
 PS fluid formed during production operations and found within the
 PS subterranean formation which surrounds a completed well bore. The
 PS polypeptide is also useful for preparing a dough or a baked product
 PS prepared from the dough and in corn-wet milling processes, detergents,

CC baking processes, beverages, oil fields (fuel ethanol), brewing processes
 CC and starch modification in the paper and pulp industry, for removing
 CC starch containing stains from a material and for reducing staining of
 CC bakery products. Sequences AB003040-AB003144 represent alpha amylase
 CC polypeptides of the invention
 CC
 XX
 SQ Sequence 549 AA;
 Query Match 99.4%; Score 2829; DB 6; Length 549;
 Best Local Similarity 99.4%; Pred. No. 1.7e-243; Indels 0; Gaps 0;
 Matches 511; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AAPFNGTMMQYFEWYLPDDGTLMTKVAEANNLSLGLTALWLPAYKGTSSRDVGIVY 60
 DB 35 AAPFNGTMMQYFEWYLPDDGTLMTKVAEANNLSLGLTALWLPAYKGTSSRDVGIVY 94
 QY 61 DLYDLGEFNQKGTAVRTKTKGTAKYLOALQAAHAGMOYVADVDPDHKGADGTEWDAVE 120
 DB 95 DLYDLGEFNQKGTAVRTKTKGTAKYLOALQAAHAGMOYVADVDPDHKGADGTEWDAVE 154
 QY 121 VNPSDRNOEISGTQYIOAMTKFDFPGRGNTYSSEFKMWYHFDGYWDESRKLSRIYKFRG 180
 DB 155 VNPSDRNOEISGTQYIOAMTKFDFPGRGNTYSSEFKMWYHFDGYWDESRKLSRIYKFRG 214
 QY 181 IGAAMDMEVDTEENGNDYDLYMTADLDMDHPEVYTELKMGKMYVNTTNIIDGFRDLDAVGHK 240
 DB 215 IGAAMDMEVDTEENGNDYDLYMTADLDMDHPEVYTELKMGKMYVNTTNIIDGFRDLDAVGHK 274
 QY 241 FSFFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNFYTASK 300
 DB 275 FSFFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNFYTASK 334
 QY 301 SGGAFDVRLTMTNTLMKQOPTLAVTFVNDHDETPGQALQSVWDPWFKPLAYAFILTRQEG 360
 DB 335 SGGAFDVRLTMTNTLMKQOPTLAVTFVNDHDETPGQALQSVWDPWFKPLAYAFILTRQEG 394
 QY 361 YPCVFGDYGYGIPQVNIPLSKSIDPLLIARDVAVGTQHDYLDHSDIIGTRGVTEKP 420
 DB 395 YPCVFGDYGYGIPQVNIPLSKSIDPLLIARDVAVGTQHDYLDHSDIIGTRGVTEKP 454
 QY 421 GSGLAALITDGPQSKMYVQKQAGKVFYDLTGNSDPTVTINSDGWGEFKNQGSVSVW 480
 DB 455 GSGLAALITDGPQSKMYVQKQAGKVFYDLTGNSDPTVTINSDGWGEFKNQGSVSVW 514
 QY 481 VPRKTTVSTIARPIITRPMTGFEFVWTEPRLVAV 514
 DB 515 VPRKTTVSTIARPIITRPMTGFEFVWTEPRLVAV 548
 RESULT 11
 AB003084
 ID AB003084 standard; protein; 549 AA.
 AC AB003084;
 XX
 XX 21-JAN-2003 (first entry)
 XX
 XX Alpha amylase polypeptide #45.
 XX
 XX Alpha amylase; enzyme; starch linkage hydrolysis; starch liquefaction;
 XX starch breakdown catalysis; textile desizing; lignocellulosic fibres;
 XX enzymatic de-linking; recycled paper; high-maltose syrup; dough;
 XX high glucose syrup; corn-wet milling process; detergent; baking process;
 XX beverages; oil fields; fuel ethanol; brewing process; staling;
 XX starch modification.
 OS Unidentified.
 XX
 XX WO200268589-A2.
 XX
 XX 06-SEP-2002.
 XX
 XX 21-FEB-2002; 2002WO-US005068.
 PF

XX
 PR 21-FEB-2001; 2001US-0270495P.
 PR 21-FEB-2001; 2001US-0270496P.
 PR 14-MAY-2001; 2001US-0291122P.
 XX
 XX (DIVE-) DIVERSA CORP.
 XX
 XX Callen W, Richardson T, Frey G;
 DR WPI; 2003-018656/01.
 XX N-PSDB; ABX08455.
 PT Novel purified polypeptide with alpha-amylase activity, useful e.g. for
 PT liquefying starch, for textile desizing, for treating lignocellulosic
 PT fibers, and for producing high-maltose or high-glucose syrup.
 XX
 XX Claim 30; Fig 16; 301pp; English.
 CC The invention relates to a purified polypeptide with alpha-amylase
 CC activity and the polynucleotide encoding it. The polypeptide is useful
 CC for hydrolysing starch linkages, for catalysing the breakdown of a
 CC starch, for modifying small molecules, for liquefying starch, for washing
 CC an object for textile desizing, for treating lignocellulosic fibers, for
 CC improving fibre properties, for enzymatic de-linking of recycled paper
 CC pulp, for producing a high-maltose or high-glucose syrup or a mixed
 CC syrup, and for increasing the flow of production fluids from a
 CC substrate during production operations and found within the
 CC fluid formed during production operations and found within the
 CC substrate; a formulation which surrounds a completed well bore. The
 CC polypeptide is also useful for preparing a dough or a baked product
 CC prepared from the dough and in corn-wet milling processes, detergents,
 CC baking processes, beverages, oil fields (fuel ethanol), brewing processes
 CC and starch modification in the paper and pulp industry, for removing
 CC starch containing stains from a material and for reducing staining of
 CC bakery products. Sequences AB003040-AB003144 represent alpha amylase
 CC polypeptides of the invention
 CC
 XX
 SQ Sequence 549 AA;
 Query Match 99.2%; Score 2825; DB 6; Length 549;
 Best Local Similarity 99.4%; Pred. No. 3.9e-243; Indels 0; Gaps 0;
 Matches 511; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAPFNGTMMQYFEWYLPDDGTLMTKVAEANNLSLGLTALWLPAYKGTSSRDVGIVY 60
 DB 35 AAPFNGTMMQYFEWYLPDDGTLMTKVAEANNLSLGLTALWLPAYKGTSSRDVGIVY 94
 QY 61 DLYDLGEFNQKGTAVRTKTKGTAKYLOALQAAHAGMOYVADVDPDHKGADGTEWDAVE 120
 DB 95 DLYDLGEFNQKGTAVRTKTKGTAKYLOALQAAHAGMOYVADVDPDHKGADGTEWDAVE 154
 QY 121 VNPSDRNOEISGTQYIOAMTKFDFPGRGNTYSSEFKMWYHFDGYWDESRKLSRIYKFRG 180
 DB 155 VNPSDRNOEISGTQYIOAMTKFDFPGRGNTYSSEFKMWYHFDGYWDESRKLSRIYKFRG 214
 QY 181 IGAAMDMEVDTEENGNDYDLYMTADLDMDHPEVYTELKMGKMYVNTTNIIDGFRDLDAVGHK 240
 DB 215 IGAAMDMEVDTEENGNDYDLYMTADLDMDHPEVYTELKMGKMYVNTTNIIDGFRDLDAVGHK 274
 QY 241 FSFFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNFYTASK 300
 DB 275 FSFFPDMLSYRSQTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNFYTASK 334
 QY 301 SGGAFDVRLTMTNTLMKQOPTLAVTFVNDHDETPGQALQSVWDPWFKPLAYAFILTRQEG 360
 DB 335 SGGAFDVRLTMTNTLMKQOPTLAVTFVNDHDETPGQALQSVWDPWFKPLAYAFILTRQEG 394
 QY 361 YPCVFGDYGYGIPQVNIPLSKSIDPLLIARDVAVGTQHDYLDHSDIIGTRGVTEKP 420
 DB 395 YPCVFGDYGYGIPQVNIPLSKSIDPLLIARDVAVGTQHDYLDHSDIIGTRGVTEKP 454
 QY 421 GSGLAALITDGPQSKMYVQKQAGKVFYDLTGNSDPTVTINSDGWGEFKNQGSVSVW 480

Db 455 GGGAAALITDGGGSKMAYVGHQKQAKVFDLTGNRSDTWTINSDDMGGEFKVNGSVSW 514

QY 481 VPRKTTVSTIARPIITRPWTGFEFVWTEPRLVAM 514

Db 515 VPRKTTVSTIARPIITRPWTGFEFVWTEPRLVAM 548

RESULT 12

AA70338

ID AAP70338 standard; protein; 549 AA.

XX AAP70338;

AC 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 12-MAR-1991 (first entry)

XX Alpha-amylase gene product.

DE Bacillus licheniformis.

XX

XX Geobacillus stearothermophilus.

OS

XX EP208491-A.

PN

XX 14-JAN-1987.

PD

XX 30-JUN-1986; 86EP-00305057.

PF

XX 03-JUL-1985; 85US-00752267.

PR

XX (GENEV) GENENCOR INC.

PA

XX Gray GL;

PI

XX WPI; 1987-009126/02.

DR

XX N-PSDB; AAN70538.

DR

XX

XX Hybrid DNA sequence prodn. - by forming a circular vector from 3 DNA

PT sequences and transforming a rec positive microorganism with the vector.

PT

XX

XX

XX Disclosure; Fig 2; 5app; English.

PS

XX

XX A method is claimed for transforming a host with a recombinant Bacillus

CC alpha-amylase gene, made up of a steaothermophilus N- terminal and a

CC licheniformis C-terminal. The method involves constructing a plasmid with

CC a sequence separating the two terminals containing a unique restriction

CC site which may be cut allowing the plasmid to recombine. See also

CC AAN70539. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-

CC OCT-2003 to standardise OS field)

CC

XX

XX

SQ Sequence 549 AA;

QY

Query Match 98.4%; Score 2801; DB 1; Length 549;

Best Local Similarity 98.6%; Pred. No. 5.4e-241;

Matches 507; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 35 AAFPNQTMQYFWMYLPDDGTLMTKYANBANNNLSIGITALMLPPAYKGTSSDVGYGY 94

QY 1 AAFPNQTMQYFWMYLPDDGTLMTKYANBANNNLSIGITALMLPPAYKGTSSDVGYGY 60

Db 61 DLYDLGEFNQKGTVRTKYGTKAQLAIAIAAAGQYADVDFDHKGADGTEWDAVE 120

QY 95 DLYDLGEFNQKGTVRTKYGTKAQLAIAAAGQYADVDFDHKGADGTEWDAVE 154

Db 121 VNFSDNNOEISGTQIOAWTKFDFNGRGNTYSSFKRWYHFGVDWDESRKLSRIYKFRG 180

QY 155 VNFSDNNOEISGTQIOAWTKFDFNGRGNTYSSFKRWYHFGVDWDESRKLSRIYKFRG 214

Db 181 IGAAMQMEVDTEGNTGNDYLMYADLDNDHPEVVTLEKNWGMVNTNINIGFRLDAVKHIX 240

QY 215 IGAAMQMEVDTEGNTGNDYLMYADLDNDHPEVVTLEKNWGMVNTNINIGFRLDAVKHIX 274

QY 241 FSPFPDWLSYRSQOTKPLFTVGEWWSYDINKLANYITKTDGMSLFDAPLHNKFTASK 300

Db 275 FSPFPDWLSYRSQOTKPLFTVGEWWSYDINKLANYITKTDGMSLFDAPLHNKFTASK 334

QY 301 SGGAFDRLTMTLTKMDQPTLAVFVNDHDEFGQALQSWDPWPKPLAYAFILTRQEG 360

Db 335 SGGAFDRLTMTLTKMDQPTLAVFVNDHDEFGQALQSWDPWPKPLAYAFILTRQEG 394

QY 361 YPCVTFGDIYGIPOQNIIPSLKSKIDPULARDYANGTQHDYIDHSDIIGWTRREGTEPR 420

Db 395 YPCVTFGDIYGIPOQNIIPSLKSKIDPULARDYANGTQHDYIDHSDIIGWTRREGTEPR 454

QY 421 GSGIAALITDGGGSKMAYVGHQKQAKVFDLTGNRSDTWTINSDDMGGEFKVNGSVSW 480

Db 455 GSGIAALITDGGGSKMAYVGHQKQAKVFDLTGNRSDTWTINSDDMGGEFKVNGSVSW 514

QY 481 VPRKTTVSTIARPIITRPWTGFEFVWTEPRLVAM 514

Db 515 VPRKTTVSTIARPIITRPWTGFEFVWTEPRLVAM 548

RESULT 13

AAW12955

ID AAW12955 standard; protein; 514 AA.

XX AAW12955;

AC

XX 16-OCT-2003 (revised)

DT 07-APR-1997 (first entry)

DT

XX

XX Alpha-amylase.

DE

XX

XX Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;

KM calcium ion dependency; alpha-amylolytic activity; washing composition;

KM textile desizing; papermaking; beer-making; ethanol production;

KM sweetener.

XX

XX Geobacillus stearothermophilus.

OS

XX WQ9623873-A1.

PN

XX 08-AUG-1996.

PD

XX 05-FEB-1996; 96KO-DK000056.

PF

XX 03-FEB-1995; 95DK-00000126.

PR 29-MAR-1995; 95DK-00000336.

PR 29-SEP-1995; 95DK-00001097.

PR 06-OCT-1995; 95DK-00001121.

XX

XX (NOVO) NOVO-NORDISK AS.

PA

XX Biegard-Frantzen H, Svendsen A, Borchert T;

PI

XX WPI; 1996-371423/37.

DR

XX

XX Alpha-amylase variants - with improved thermal and oxidation stability

PT and reduced calcium ion dependency.

PT

XX

XX Disclosure; Page 86-88; 11pp; English.

PS

XX

XX AAW12955, AAW12956, AAW18135 and AAW18136 represent the parent alpha-

CC amylases used to create the variants of the invention (such as AAW12098-

CC M1131). This sequence represents the alpha-amylase from Bacillus

CC stearothermophilus. The variants of the invention were created using site

CC directed, or random, mutagenesis of the DNA sequences encoding these

CC parent alpha-amylases. The variants of the invention can have improved

CC thermal stability (such as at temperatures in the range of 40-70 degrees

CC Celsius), and/or oxidation stability, and/or reduced calcium ion

CC dependency. The variants can also have increased alpha-amylolytic

CC activity (especially at pH values in the range of 8.5-10.5), and improved

CC binding of a particular substrate. The variant alpha-amylases also

CC possess improved specificity to a particular substrate, and/or improved

CC specifically with respect to cleavage of substrate. The variants can be
 CC used in detergent and washing compositions, and for textile desizing. The
 CC alpha-amylase variants can also be used in papermaking and beer-making
 CC processes. The variants of the invention can also be used in the
 CC production of sweeteners and ethanol from starch. (Updated on 16-OCT-2003
 CC to standardise OS field)

XX Sequence 514 AA;

Query Match 97.6%; Score 2780; DB 2; Length 514;
 Best Local Similarity 98.1%; Pred. No. 3.7e-239;
 Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAPFNGTMQYFEMYLPPDGLMTKVAEANNLSIGITALLMPPAYKTSRSDYGYGY 60
 DB 1 AAPFNGTMQYFEMYLPPDGLMTKVAEANNLSIGITALLMPPAYKTSRSDYGYGY 60
 QY 61 DLYDLGEFNQKGVTRTKYGTAKYLOAIQAAHAGMAYADVPDHKGADGTEWDAVE 120
 DB 61 DLYDLGEFNQKGVTRTKYGTAKYLOAIQAAHAGMAYADVPDHKGADGTEWDAVE 120
 QY 121 VNPSPDRNOEISGTYOIQAWTKPDPGRGNTYSSFKRWYHFPDGVMDSESKLSRIYKFRG 180
 DB 121 VNPSPDRNOEISGTYOIQAWTKPDPGRGNTYSSFKRWYHFPDGVMDSESKLSRIYKFRG 180
 QY 181 IGRAMDVEVDTENGNYDLYMAYADLMDHPEVTELSKMGKMYNTNIDGFRDAVKHIX 240
 DB 181 IGRAMDVEVDTENGNYDLYMAYADLMDHPEVTELSKMGKMYNTNIDGFRDAVKHIX 240
 QY 241 FSPFPDMLSVRSQSGKPLFTVGEYMSYDINKLHNYITKTGTMSLFPAPLHNFYTSK 300
 DB 241 FSPFPDMLSVRSQSGKPLFTVGEYMSYDINKLHNYITKTGTMSLFPAPLHNFYTSK 300
 QY 301 SGGAPEMRLMTNTLTKMDQPTLAVTFVDNHDTEPGQALQSWDPMFKPLAFAFILTRQEG 360
 DB 301 SGGAPEMRLMTNTLTKMDQPTLAVTFVDNHDTEPGQALQSWDPMFKPLAFAFILTRQEG 360
 QY 361 YPCVFGDYGYGIPOVNIPLSKKIDPLLAARDYAYGTHDYLHSDIIGWREGSTKRP 420
 DB 361 YPCVFGDYGYGIPOVNIPLSKKIDPLLAARDYAYGTHDYLHSDIIGWREGSTKRP 420
 QY 421 GSGLAALITDGPQSGKMYVKGQAHGKVFDLTGNRSDVTYINSDGWGEFKVNGGSVSW 480
 DB 421 GSGLAALITDGPQSGKMYVKGQAHGKVFDLTGNRSDVTYINSDGWGEFKVNGGSVSW 480
 QY 481 VPRKTVSTIARPIITRPWTGEFVRWTEPRLVAM 514
 DB 481 VPRKTVSTIARPIITRPWTGEFVRWTEPRLVAM 514

RESULT 14

AA15417
 ID AA15417 standard; protein; 514 AA.

XX AA15417;

DT 17-OCT-2003 (revised)
 DT 22-JUL-1999 (first entry)

DE Bacillus stearothermophilus alpha-amylase protein.

XX Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
 KW sweetener; ethanol; starch; textile desizing; starch liquefaction;
 XX saccharification process.

OS Geobacillus stearothermophilus.

XX WO9923211-A1.

XX 14-MAY-1999.

XX 30-OCT-1998; 98WO-DK000471.

PR 30-OCT-1997; 97DK-00001240.
 PR 14-JUL-1998; 98DK-00000936.

PA (NOVO) NOVO-NORDISK AS.

PI Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;
 PI Kjaerulf S;

DR WPI; 1999-326987/27.

XX New Termamyl-like alpha-amylase variants.

PS Claim 38; Page 81-82; 115pp; English.

XX The specification describes termamyl-like alpha-amylase variants that
 CC have altered amino acid sequences to improve properties. The variants are
 CC produced by creating one or more of the following mutations in amino acid
 CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,
 CC D144, F145, P146, G147, K148, G149, Q174, R181, G182, D183, K184, K185,
 CC A186, W189, S193, N195, H107, K108, G109, D166, W167, Q169, S170,
 CC K171, Q172, F173, F268, K269, N270, D271, L272, G273, A274, L275,
 CC K311, E346, K385, G456, W457, K458, P459, G460, T461, V462, T463. The
 CC variants can be used for washing and/or dishwashing. They can also be
 CC used in the production of sweeteners and ethanol from starch, and/or for
 CC textile desizing, and in starch liquefaction and/or saccharification
 CC processes. The present amylase can function as the parent sequence in the
 CC production of the variants of the invention. (Updated on 17-OCT-2003 to
 CC standardise OS field)

XX Sequence 514 AA;

Query Match 97.6%; Score 2780; DB 2; Length 514;
 Best Local Similarity 98.1%; Pred. No. 3.7e-239;
 Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAPFNGTMQYFEMYLPPDGLMTKVAEANNLSIGITALLMPPAYKTSRSDYGYGY 60
 DB 1 AAPFNGTMQYFEMYLPPDGLMTKVAEANNLSIGITALLMPPAYKTSRSDYGYGY 60
 QY 61 DLYDLGEFNQKGVTRTKYGTAKYLOAIQAAHAGMAYADVPDHKGADGTEWDAVE 120
 DB 61 DLYDLGEFNQKGVTRTKYGTAKYLOAIQAAHAGMAYADVPDHKGADGTEWDAVE 120
 QY 121 VNPSPDRNOEISGTYOIQAWTKPDPGRGNTYSSFKRWYHFPDGVMDSESKLSRIYKFRG 180
 DB 121 VNPSPDRNOEISGTYOIQAWTKPDPGRGNTYSSFKRWYHFPDGVMDSESKLSRIYKFRG 180
 QY 181 IGRAMDVEVDTENGNYDLYMAYADLMDHPEVTELSKMGKMYNTNIDGFRDAVKHIX 240
 DB 181 IGRAMDVEVDTENGNYDLYMAYADLMDHPEVTELSKMGKMYNTNIDGFRDAVKHIX 240
 QY 241 FSPFPDMLSVRSQSGKPLFTVGEYMSYDINKLHNYITKTGTMSLFPAPLHNFYTSK 300
 DB 241 FSPFPDMLSVRSQSGKPLFTVGEYMSYDINKLHNYITKTGTMSLFPAPLHNFYTSK 300
 QY 301 SGGAPEMRLMTNTLTKMDQPTLAVTFVDNHDTEPGQALQSWDPMFKPLAFAFILTRQEG 360
 DB 301 SGGAPEMRLMTNTLTKMDQPTLAVTFVDNHDTEPGQALQSWDPMFKPLAFAFILTRQEG 360
 QY 361 YPCVFGDYGYGIPOVNIPLSKKIDPLLAARDYAYGTHDYLHSDIIGWREGSTKRP 420
 DB 361 YPCVFGDYGYGIPOVNIPLSKKIDPLLAARDYAYGTHDYLHSDIIGWREGSTKRP 420
 QY 421 GSGLAALITDGPQSGKMYVKGQAHGKVFDLTGNRSDVTYINSDGWGEFKVNGGSVSW 480
 DB 421 GSGLAALITDGPQSGKMYVKGQAHGKVFDLTGNRSDVTYINSDGWGEFKVNGGSVSW 480
 QY 481 VPRKTVSTIARPIITRPWTGEFVRWTEPRLVAM 514
 DB 481 VPRKTVSTIARPIITRPWTGEFVRWTEPRLVAM 514

RESULT 15

AAV07383
 ID AAV07383 standard; protein; 514 AA.
 XX
 AC AAV07383;
 XX
 DT 16-JUL-1999 (first entry)
 XX
 DE Wild type Termamy1(RTM)-like alpha-amylase protein #3.
 XX
 KW Variant; Termamy1; alpha-amylase; mutation; Bacillus; detergent;
 KM dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;
 KM ethanol.
 XX
 OS Bacillus sp.
 XX
 Key Location/Qualifiers
 FH Misc-difference 179..182
 FT /note= "optionally 1, 2, 3 or all residues are deleted"
 FT Misc-difference 193
 FT /note= "optionally altered to any amino acid except an
 Asn residue"
 FT Misc-difference 204
 FT /note= "optionally altered to any amino acid except a Leu
 residue"
 FT Misc-difference 210
 FT /note= "optionally altered to any amino acid except a Glu
 residue"
 FT Misc-difference 214
 FT /note= "optionally altered to any amino acid except a Glu
 residue"
 FT Misc-difference 267
 FT /note= "optionally altered to any amino acid except a Ser
 residue"
 FT
 MO9919467-A1.
 XX
 PD 22-APR-1999.
 XX
 PE 13-OCT-1998; 98WC-DK000444.
 XX
 PR 13-OCT-1997; 97DK-00001172.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Svendsen A, Borchert TV, Bisgard-Prantzen H;
 XX
 DR WPI; 1999-277632/23.
 XX
 PT Variant alpha-amylases - useful as detergents or for textile desizing or
 starch liquefaction.
 XX
 PS Claim 1; Page 65-66; 93pp; English.
 XX
 CC This sequence represents the parent sequence for new variants of a parent
 CC Termamy1-like alpha-amylase with alpha-amylase activity. The variants
 CC comprise mutations in 2-6 regions/positions relative to an alpha-amylase
 CC from either of two Bacillus species in WO9526397, B. stearothermophilus,
 CC B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-
 CC amylase variants are detergent additives for use in detergents for
 CC dishwashing, manual or automatic laundry. The variants can also be used
 CC for textile desizing or starch liquefaction (e.g. for production of
 CC sweeteners or ethanol)
 CC
 SQ Sequence 514 AA;

Query Match 97.6%; Score 2780; DB 2; Length 514;
 Best Local Similarity 98.1%; Pred. No. 3.7e-239;
 Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAPFNGTMMQYFEWYLPDDGTLMTK/VANEANLSSLGITLALMLPPAYKGTSRSDVGYGVY 60
 DB 1 AAPFNGTMMQYFEWYLPDDGTLMTK/VANEANLSSLGITLALMLPPAYKGTSRSDVGYGVY 60

QY 61 DLYDLGEFNQKGVTRTKYKQYLOAIQAAHAGNQVADVVDHKGADGETWYDAVE 120
 DB 61 DLYDLGEFNQKGVTRTKYKQYLOAIQAAHAGNQVADVVDHKGADGETWYDAVE 120
 QY 121 VNPEDRNOEISGTQYIOAMTKFDPFGSGNTYSSFKRMWYHFDGVDMDSEKLSRIYKFRG 180
 DB 121 VNPEDRNOEISGTQYIOAMTKFDPFGSGNTYSSFKRMWYHFDGVDMDSEKLSRIYKFRG 180
 QY 181 IGAAMDWEVDTEGNNDYLYADLDMDHPEVTELKSMGKMYNTNIDGFRLDAYVGHK 240
 DB 181 IGAAMDWEVDTEGNNDYLYADLDMDHPEVTELKSMGKMYNTNIDGFRLDAYVGHK 240
 QY 241 FSPFPDMLSYVRSGTGKPLFTVGEYMSYDINKLHNYITTKTDGTMSLFDAPLHKKFYTASK 300
 DB 241 FSPFPDMLSYVRSGTGKPLFTVGEYMSYDINKLHNYITTKTDGTMSLFDAPLHKKFYTASK 300
 QY 301 SGAFFDMRTMTNTLMKDQPLAVTFYDNHDEPQALQSWVDPMFKPLAYAFILTRQEG 360
 DB 301 SGAFFDMRTMTNTLMKDQPLAVTFYDNHDEPQALQSWVDPMFKPLAYAFILTRQEG 360
 QY 361 YPCVFGYGYGIPQYNIPLSKSKTDPLLIARQYAYGTHQDYLDHSDIIGMTREGTEKP 420
 DB 361 YPCVFGYGYGIPQYNIPLSKSKTDPLLIARQYAYGTHQDYLDHSDIIGMTREGTEKP 420
 QY 421 GSGLAALITDGPGGSKMYVYGVKQHAGVFFYDLTGNRSDTYTINSDGWGEFKVNGGSVSW 480
 DB 421 GSGLAALITDGPGGSKMYVYGVKQHAGVFFYDLTGNRSDTYTINSDGWGEFKVNGGSVSW 480
 QY 481 VPKRTYVSTIARPTITRPWIGEFPRATEPRIVAM 514
 DB 481 VPKRTYVSTIARPTITRPWIGEFPRATEPRIVAM 514

Search completed: May 3, 2004, 20:50:32
 Job time : 54.2004 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: May 3, 2004, 20:34:58 ; Search time 48.7475 Seconds

(without alignments)
2782.151 Million cell updates/sec

Title: US-10-644-187-4

Perfect score: 2624

Sequence: 1 VNGTLMQYFEWYTPNDQHW.....KIGSDGGEFHVNDGSVSIY 480

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
2	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
3	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
4	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
5	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
6	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
7	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
8	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
9	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
10	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
11	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
12	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
13	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
14	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
15	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
16	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
17	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
18	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
19	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
20	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
21	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
22	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
23	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
24	2624	100.0	480	2 AAR78268	Aar78268 Bacillus
25	2624	100.0	480	2 AAR78268	Aar78268 Bacillus

26	2600	99.1	480	3 AAY99771	Aay99771 Bacillus
27	2584	98.5	483	6 ABP60493	Abp60493 Bacillus
28	2555	97.5	485	6 ABP60494	Abp60494 Bacillus
29	2427	92.5	483	6 ABP60492	Abp60492 Bacillus
30	2330	88.8	483	6 ABP60495	Abp60495 Bacillus
31	2279	86.9	481	6 ABP60491	Abp60491 Bacillus
32	2244	85.5	481	6 ABP60490	Abp60490 Bacillus
33	2214	84.4	481	6 ABP60489	Abp60489 Bacillus
34	2202	83.9	483	2 AAW57979	Aaw57979 Bacillus
35	2202	83.9	483	2 AAW57975	Aaw57975 Bacillus
36	2200	83.8	483	2 AAW57976	Aaw57976 Bacillus
37	2200	83.8	483	2 AAW57976	Aaw57976 Bacillus
38	2199	83.8	483	2 AAW57976	Aaw57976 Bacillus
39	2199	83.8	483	2 AAW57976	Aaw57976 Bacillus
40	2199	83.8	483	2 AAW57976	Aaw57976 Bacillus
41	2197	83.7	483	2 AAW57971	Aaw57971 Bacillus
42	2197	83.7	483	2 AAW57971	Aaw57971 Bacillus
43	2197	83.7	483	2 AAW57971	Aaw57971 Bacillus
44	2197	83.7	483	2 AAW57971	Aaw57971 Bacillus
45	2197	83.7	483	2 AAW57971	Aaw57971 Bacillus

ALIGNMENTS

RESULT 1

ID AAR78268 standard; protein; 480 AA.

XX AAR78268;

DT 17-JAN-1996 (first entry)

XX Bacillus amyloliquefaciens alpha amylase (mature protein).

XX Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch;

XX thermolabile; methionine; Bacillus licheniformis;

XX Bacillus amyloliquefaciens; Bacillus stearothermophilus.

XX Bacillus amyloliquefaciens.

XX W05521247-A1.

XX 10-AUG-1995.

XX 05-OCT-1994; 94WO-DK000371.

XX 02-FEB-1994; 94DK-00000141.

XX (NOVO) NOVO-NORDISK AS.

XX Toft AH, Marcher D, Pedersen HH, Nilsson TE;

XX WPI; 1995-283767/37.

XX N-PSDB; AAC95032.

XX Use of an oxidation stable alpha-amylase - for simultaneous desizing and

XX bleaching or scouring of fabrics contg. starch or starch derive.

XX Claim 7, Page 24, 37pp; English.

XX Oxidation stable alpha amylases can be used for the simultaneous desizing

XX and bleaching or scouring of a fabric comprising starch or starch

XX derivatives. They exhibit a better heat stability, especially in the

XX presence of oxidizing agents. They are obtained from a parent alpha

XX amylase by replacing one or more methionine residues with any amino acid

XX different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or

XX Asp. The parent alpha amylase is derived from a Bacillus species. This

XX sequence is the wild type (unmodified) alpha amylase

XX Sequence 480 AA;

XX Query Match 100.0%; Score 2624; DB 2; Length 480;

DR WPI; 1996-371424/37.

XX Alpha-amylase variants and methods of production - have altered
PT properties such as calcium dependency, substrate binding and stability.

XX Disclosure; Page 86; 177pp; English.

XX The present sequence is the mature *Bacillus amyloliquefaciens* alpha-
CC amylase (A). Variants of parent termamyli-like alpha-amylases (and methods
CC of constructing them) are claimed. Examples of variants are featured
CC above. At least one of the amino acids of the parent, which is present in
CC a fragment identified above, is/are deleted or replaced with one or more
CC residues, which is/are present in a fragment corresponding to a fragment
CC of AA14500 (*Aspergillus oryzae* fungamyl alpha-amylase). The variants
CC have altered properties such as calcium dependency, substrate binding and
CC stability. Also one or more proline or cysteine residues in the variant
CC is modified or replaced with a non-proline or non-cysteine residue such as
CC alanine. The variants can be used for (dish)washing, as detergent
CC additives or for fabric desizing or starch liquefaction. They can also be
CC used for the production of sweeteners and ethanol from starch. See also
CC AA14498 and AA14500

XX Sequence 480 AA;

Query Match 100.0%; Score 2624; DB 2; Length 480;

Best Local Similarity 100.0%; Pred. No. 8.1e-218; Indels 0; Gaps 0;

Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VNGTLMOYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPPAVKGLSDNGYGEYDLY 60

1 VNGTLMOYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPPAVKGLSDNGYGEYDLY 60

61 DLGEFOQKGTAVRTKYGTGKSELQDAIGSLHRSRVQYGVVNLNKAAGADATEDVTAVERN 120

61 DLGEFOQKGTAVRTKYGTGKSELQDAIGSLHRSRVQYGVVNLNKAAGADATEDVTAVERN 120

121 ANRNOETSEBYQIKAWTDFRPPRGNTYSDFKMHWYHFDGADWDSRKISRIKFRGEK 180

121 ANRNOETSEBYQIKAWTDFRPPRGNTYSDFKMHWYHFDGADWDSRKISRIKFRGEK 180

181 AMDWVSSENGNDYLYAVDVYDHPDVVAETKKMGWYANELSLDGRFIDAAXIKFSF 240

181 AMDWVSSENGNDYLYAVDVYDHPDVVAETKKMGWYANELSLDGRFIDAAXIKFSF 240

241 LRDWVAVROATGKEMFTVAEYQWNNAGKLENTLNTKTSFNQSVFVPLHFNLOAASOGG 300

241 LRDWVAVROATGKEMFTVAEYQWNNAGKLENTLNTKTSFNQSVFVPLHFNLOAASOGG 300

301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAFAFILTRESGYPO 360

301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAFAFILTRESGYPO 360

361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPDHDIIDHPDVIGWTRGDSAA 420

361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPDHDIIDHPDVIGWTRGDSAA 420

421 KSGIALALITDGPQGSKRYMAGLKNAGETWYDTGNRSYVTKIGSDGGEFHVNDGSVSIY 480

421 KSGIALALITDGPQGSKRYMAGLKNAGETWYDTGNRSYVTKIGSDGGEFHVNDGSVSIY 480

RESULT 3

AA15419 standard; protein; 480 AA.

XX AA15419;

XX 22-JUL-1999 (first entry)

XX *Bacillus amyloliquefaciens* alpha-amylase protein.

XX Termamyli-like; alpha-amylase; variant; washing; dishwashing; production;
KW sweetener; ethanol; starch; textile desizing; starch liquefaction;

KM saccharification process.

OS *Bacillus amyloliquefaciens*.

XX WO923211-A1.

XX 14-MAY-1999.

XX 30-OCT-1998; 98WO-DK000471.

XX 30-OCT-1997; 97DK-00001240.

XX 14-JUL-1998; 98DK-0000936.

XX (NOVO) NOVO-NORDISK AS.

XX Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;

XX Kjaerulf S;

XX WPI; 1999-326987/27.

XX New Termamyli-like alpha-amylase variants.

XX Claim 38; Page 84-86; 115pp; English.

XX The specification describes termamyli-like alpha-amylase variants that

XX have altered amino acid sequences to improve properties. The variants are

XX produced by creating one or more of the following mutations in amino acid

XX sequence of the parent termamyli-like alpha-amylase: T141, K142, F143,

XX D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,

XX A186, W189, S193, N195, H107, K108, G109, D166, M167, D168, Q169, S170,

XX R171, Q172, F173, F267, W268, K269, N270, D271, L272, G272, A274, L275,

XX K311, E346, K385, G456, N457, K458, P459, G460, T461, V462, T463. The

XX variants can be used for washing and/or dishwashing. They can also be

XX used in the production of sweeteners and ethanol from starch, and/or for

XX textile desizing, and in starch liquefaction and/or saccharification

XX processes. The present amylase can function as the parent sequence in the

XX production of the variants of the invention

XX Sequence 480 AA;

Query Match 100.0%; Score 2624; DB 2; Length 480;

Best Local Similarity 100.0%; Pred. No. 8.1e-218; Indels 0; Gaps 0;

Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VNGTLMOYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPPAVKGLSDNGYGEYDLY 60

1 VNGTLMOYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPPAVKGLSDNGYGEYDLY 60

61 DLGEFOQKGTAVRTKYGTGKSELQDAIGSLHRSRVQYGVVNLNKAAGADATEDVTAVERN 120

61 DLGEFOQKGTAVRTKYGTGKSELQDAIGSLHRSRVQYGVVNLNKAAGADATEDVTAVERN 120

121 ANRNOETSEBYQIKAWTDFRPPRGNTYSDFKMHWYHFDGADWDSRKISRIKFRGEK 180

121 ANRNOETSEBYQIKAWTDFRPPRGNTYSDFKMHWYHFDGADWDSRKISRIKFRGEK 180

181 AMDWVSSENGNDYLYAVDVYDHPDVVAETKKMGWYANELSLDGRFIDAAXIKFSF 240

181 AMDWVSSENGNDYLYAVDVYDHPDVVAETKKMGWYANELSLDGRFIDAAXIKFSF 240

241 LRDWVAVROATGKEMFTVAEYQWNNAGKLENTLNTKTSFNQSVFVPLHFNLOAASOGG 300

241 LRDWVAVROATGKEMFTVAEYQWNNAGKLENTLNTKTSFNQSVFVPLHFNLOAASOGG 300

301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAFAFILTRESGYPO 360

301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAFAFILTRESGYPO 360

361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPDHDIIDHPDVIGWTRGDSAA 420

361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPDHDIIDHPDVIGWTRGDSAA 420

421 KSGIALALITDGPQGSKRYMAGLKNAGETWYDTGNRSYVTKIGSDGGEFHVNDGSVSIY 480

421 KSGIALALITDGPQGSKRYMAGLKNAGETWYDTGNRSYVTKIGSDGGEFHVNDGSVSIY 480

Db 421 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

RESULT 4

ID AAY07385 standard; protein; 480 AA.

AA07385;

16-JUN-1999 (first entry)

Wild type Termamyl (RTM)-like alpha-amylase protein #5.

Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent; dishwashing; laundry; textile; desizing; starch liquefaction; sweetener; ethanol.

Bacillus sp.

Key Location/Qualifiers

Misc-difference 176..179 /note= "optionally 1, 2, 3 or all residues are deleted"

Misc-difference 190 /note= "optionally altered to any amino acid except an Asn residue"

Misc-difference 201 /note= "optionally altered to any amino acid except a Val residue"

Misc-difference 207 /note= "optionally altered to any amino acid except an Asp residue"

Misc-difference 211 /note= "optionally altered to any amino acid except a Glu residue"

Misc-difference 264 /note= "optionally altered to any amino acid except a Gln residue"

Misc-difference 264 /note= "optionally altered to any amino acid except a Gln residue"

Misc-difference 264 /note= "optionally altered to any amino acid except a Gln residue"

Misc-difference 264 /note= "optionally altered to any amino acid except a Gln residue"

Misc-difference 264 /note= "optionally altered to any amino acid except a Gln residue"

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Misc-difference 264 /note= "optionally altered to any amino acid except a Gln residue"

Misc-difference 264 /note= "optionally altered to any amino acid except a Gln residue"

Misc-difference 264 /note= "optionally altered to any amino acid except a Gln residue"

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Misc-difference 264 /note= "optionally altered to any amino acid except a Gln residue"

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Misc-difference 264 /note= "optionally altered to any amino acid except a Gln residue"

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Misc-difference 264 /note= "optionally altered to any amino acid except a Gln residue"

Misc-difference 264 /note= "optionally altered to any amino acid except a Gln residue"

Misc-difference 264 /note= "optionally altered to any amino acid except a Gln residue"

Misc-difference 264 /note= "optionally altered to any amino acid except a Gln residue"

Misc-difference 264 /note= "optionally altered to any amino acid except a Gln residue"

Misc-difference 264 /note= "optionally altered to any amino acid except a Gln residue"

QY 1 VNGTLMQYFEWYTNPDGQHWKRLQNDAEHLSDIGITAWMIIPAYKGLSQSDNGYGPYDLY 60

Db 1 VNGTLMQYFEWYTNPDGQHWKRLQNDAEHLSDIGITAWMIIPAYKGLSQSDNGYGPYDLY 60

QY 61 DIGEFQCKGTWRTKTKYTSLEQDAIGSLHSNNQYGVGYVLTNKRQADATEDVAVFNP 120

Db 61 DIGEFQCKGTWRTKTKYTSLEQDAIGSLHSNNQYGVGYVLTNKRQADATEDVAVFNP 120

QY 121 ANRQETSEEVQIKAWTDFRPPGKNTYSDPKWMYHFDGADWDESKISRIFFRREGK 180

Db 121 ANRQETSEEVQIKAWTDFRPPGKNTYSDPKWMYHFDGADWDESKISRIFFRREGK 180

QY 181 AWDWEVSSSENGYDYLWADVDYDHPDVAAETKKWGIYANLSDGFRIDAAGIKFSF 240

Db 181 AWDWEVSSSENGYDYLWADVDYDHPDVAAETKKWGIYANLSDGFRIDAAGIKFSF 240

QY 241 LRDWQAVRQATGKMFVVAEYQWQNAKLENYLNKTSFNQSVFDPVLFHNLQAASSGCG 300

Db 241 LRDWQAVRQATGKMFVVAEYQWQNAKLENYLNKTSFNQSVFDPVLFHNLQAASSGCG 300

QY 301 GYDWERLLDGTIVVSSHPEKAVTFVENHDTQPGQSLSTVQTFWFLPAAFLITRESGYPQ 360

Db 301 GYDWERLLDGTIVVSSHPEKAVTFVENHDTQPGQSLSTVQTFWFLPAAFLITRESGYPQ 360

QY 361 VFGYDWTGKTSPEKIPSLKONIEPILKAREYVGPQHDYIDHPVIGWTRBGSSEA 420

Db 361 VFGYDWTGKTSPEKIPSLKONIEPILKAREYVGPQHDYIDHPVIGWTRBGSSEA 420

QY 421 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

Db 421 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

QY 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

Db 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

QY 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

Db 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

QY 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

Db 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

QY 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

Db 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

QY 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

Db 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

QY 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

Db 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

QY 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

Db 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

QY 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

Db 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

QY 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

Db 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

QY 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

Db 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

QY 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

Db 480 KSGLAALITDPGSGSKMYAGLKNAGETWYDITGNRSDTYKISGDGGEFHVNDGSVSIY 480

CC Isolated from a *Bacillus amyloliquefaciens* genomic DNA library. A variant
CC may contain mutations in one or more solvent exposed amino acid residues
CC to increase the overall hydrophobicity of the enzyme or the overall
CC number of methyl groups in the side chains of exposed residues may be
CC increased. The mutations can be incorporated by site-directed mutagenesis
CC or by random mutagenesis. As a result of their increased stability, the
CC variants are suitable for the industrial processing of starch, i.e.
CC starch liquefaction and saccharification. They may also be useful for
CC washing, dishwashing and textile desizing. Hybrid alpha-amylases
CC comprising partial amino acid sequences derived from two or more alpha-
CC amylases have also been created in order to increase enzyme stability
XX

SQ Sequence 480 AA;

Query Match 100.0%; Score 2624; DB 3; Length 480;
Best Local Similarity 100.0%; Pred. No. 8.1e-218;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAWIPPAVKGLSGSDNGYGPYDLY 60
DB 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAWIPPAVKGLSGSDNGYGPYDLY 60
QY 61 DLGEFOQKGTVRKTKGTSKSELDAIGSLHSRNQVYGVVLAHKAQADATEDVTAVERN 120
DB 61 DLGEFOQKGTVRKTKGTSKSELDAIGSLHSRNQVYGVVLAHKAQADATEDVTAVERN 120
QY 121 ANRNOETSEEEYOIKAWTDFRPGKNTYSDFKMWHYFDGADWDSRKISRIFKRGEGK 180
DB 121 ANRNOETSEEEYOIKAWTDFRPGKNTYSDFKMWHYFDGADWDSRKISRIFKRGEGK 180
QY 181 AMDWEVSSSENGNDYLMYADVDDHPVVAETKKMGITWANEISLDGFRIDAKHIKFSF 240
DB 181 AMDWEVSSSENGNDYLMYADVDDHPVVAETKKMGITWANEISLDGFRIDAKHIKFSF 240
QY 241 LRDWVQAVROATGKEMFTVAEYQNNAGKLENYLNTKTSFNQSVFVPLHFNLOAASSQGG 300
DB 241 LRDWVQAVROATGKEMFTVAEYQNNAGKLENYLNTKTSFNQSVFVPLHFNLOAASSQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTPQGSLSTVQTFKPLAFAFILLRESGYPQ 360
DB 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTPQGSLSTVQTFKPLAFAFILLRESGYPQ 360
QY 361 VFYGDWYGTGTSKPEIPELKNIEPIILKARKEVAYGPQHDYIDHPDIVGWTREGDSSAA 420
DB 361 VFYGDWYGTGTSKPEIPELKNIEPIILKARKEVAYGPQHDYIDHPDIVGWTREGDSSAA 420
QY 421 KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNNSDTYKIGSDGGEFFHNDGSVSIT 480
DB 421 KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNNSDTYKIGSDGGEFFHNDGSVSIT 480

RESULT 6

AAR72448 ID AAR72448 standard; protein; 483 AA.

XX AAR72448;

XX 25-MAR-2003 (revised)

DT 01-DEC-1995 (first entry)

XX *Bacillus amyloliquefaciens* alpha amylase (mature protein).

XX alpha amylase; variant; enzyme; detergent; additive; dishwashing;

XX washing; *Bacillus licheniformis*; *Bacillus amyloliquefaciens*;XX *Bacillus stearothermophilus*; dyeing; bleaching; scouring; textile;

XX thermostable.

XX *Bacillus amyloliquefaciens*.

XX WO9510603-A1.

XX 20-APR-1995.

PF 05-OCT-1994; 94MO-DK000370.
XX
XX 08-OCT-1993; 93DK-00001133.
PR 02-FEB-1994; 94DK-00000140.
XX
XX (NOVO) NOVO-NORDISK AS.
PA
PI Borchert TV, Bisgard-Frantzen H, Svendsen A, Thellersen M;
PI Van Der Zee P;
XX WPI: 1995-161790/21.
DR N-PSDB; AAQ8067.
XX
XX New *Bacillus* derived alpha-amylase variants - having amino acid
PT modifications to improve washing and/or dishwashing performance.
XX
PS Claim 34; Page 11-12; 105pp; English.
XX
XX Variant alpha amylase enzymes which have improved washing and/or as
CC detergent additives. The enzymes have one or more amino acid residues
CC added, deleted or substituted. The variants can also be used for textile
CC desizing, prior to scouring, bleaching and dyeing. The variants have
CC improved thermostability, acid/alkaline stability; low temperature
CC optimum; pH optimum; higher hydrolysis velocity and improved tolerance to
CC other composition constituents, e.g. oxidation agents. (Updated on 25-MAR
CC -2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
XX

SQ Sequence 483 AA;

Query Match 100.0%; Score 2624; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 8.2e-218;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAWIPPAVKGLSGSDNGYGPYDLY 60
DB 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAWIPPAVKGLSGSDNGYGPYDLY 60
QY 61 DLGEFOQKGTVRKTKGTSKSELDAIGSLHSRNQVYGVVLAHKAQADATEDVTAVERN 120
DB 61 DLGEFOQKGTVRKTKGTSKSELDAIGSLHSRNQVYGVVLAHKAQADATEDVTAVERN 120
QY 121 ANRNOETSEEEYOIKAWTDFRPGKNTYSDFKMWHYFDGADWDSRKISRIFKRGEGK 180
DB 121 ANRNOETSEEEYOIKAWTDFRPGKNTYSDFKMWHYFDGADWDSRKISRIFKRGEGK 180
QY 181 AMDWEVSSSENGNDYLMYADVDDHPVVAETKKMGITWANEISLDGFRIDAKHIKFSF 240
DB 181 AMDWEVSSSENGNDYLMYADVDDHPVVAETKKMGITWANEISLDGFRIDAKHIKFSF 240
QY 241 LRDWVQAVROATGKEMFTVAEYQNNAGKLENYLNTKTSFNQSVFVPLHFNLOAASSQGG 300
DB 241 LRDWVQAVROATGKEMFTVAEYQNNAGKLENYLNTKTSFNQSVFVPLHFNLOAASSQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTPQGSLSTVQTFKPLAFAFILLRESGYPQ 360
DB 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTPQGSLSTVQTFKPLAFAFILLRESGYPQ 360
QY 361 VFYGDWYGTGTSKPEIPELKNIEPIILKARKEVAYGPQHDYIDHPDIVGWTREGDSSAA 420
DB 361 VFYGDWYGTGTSKPEIPELKNIEPIILKARKEVAYGPQHDYIDHPDIVGWTREGDSSAA 420
QY 421 KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNNSDTYKIGSDGGEFFHNDGSVSIT 480
DB 421 KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNNSDTYKIGSDGGEFFHNDGSVSIT 480

RESULT 7

AAW31405 ID AAW31405 standard; protein; 483 AA.

XX AAW31405;

XX 11-MAY-1998 (first entry)

XX DE Bacillus amyloliquefaciens Termamyl-like alpha-amylase.
 XX XX Termamyl¹, alpha-amylase; enzyme engineering; protein engineering; starch;
 XX KM liquefaction; saccharification; sweetener; textile desizing;
 XX KW detergent additive; ss.
 XX OS Bacillus amyloliquefaciens.
 XX PN WO9741213-A1.
 XX PD 06-NOV-1997.
 XX PF 30-APR-1997; 97WO-DK000197.
 XX PR 30-APR-1996; 96DX-00000515.
 XX PR 28-JUN-1996; 96DX-00000712.
 XX PR 11-JUL-1996; 96DX-00000775.
 XX PR 08-NOV-1996; 96DX-00001263.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX PI Svendsen A, Borchert TV, Bisgard-Frantzen H;
 XX DR WPI: 1997-549718/50.
 XX DR N-PsDB; AAV02472.
 XX PT Termamyl-like alpha-amylase variants with improved properties - e.g.
 XX PT increased stability at low pH and low calcium, useful as detergent
 XX PT additives and in industrial starch processing e.g. liquefaction.
 XX PS Disclosure; Page 84; 101pp; English.
 CC This protein comprises the Termamyl-like alpha-amylase of Bacillus
 CC amyloliquefaciens. The invention relates to novel variants of Termamyl-
 CC like alpha-amylases that have alpha-amylase activity and exhibit an
 CC alteration in at least one property selected from: substrate specificity;
 CC binding or cleavage pattern; thermal stability; pH/activity or
 CC pH/stability profile; stability towards oxidation; Ca²⁺ dependency and
 CC specific activity. The variant has one or more mutations from those
 CC listed in the specification in relation to Bacillus licheniformis
 CC Termamyl¹ (see AAV31404). Also claimed are constructs comprising DNA
 CC encoding the variant (see AAV02471-73), and recombinant expression
 CC vectors and transformed cells containing the DNA. The Termamyl-like alpha
 CC -amylase variant is useful as a detergent additive and can also be used
 CC in industrial starch processing e.g. liquefaction (claimed) or
 CC saccharification to produce sweeteners, and in textile desizing (claimed)
 CC XX
 XX Sequence 483 AA;
 SQ
 Query Match 100.0%; Score 2624; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 8.2e-218; Mismatches 0; Gaps 0;
 Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GYDMRLDGTGVSRRPEKAVTFVFNHDPQPGQSLESTVQWFKRLAYAFILITRESSGYQ 360
 DB 301 GYDMRLDGTGVSRRPEKAVTFVFNHDPQPGQSLESTVQWFKRLAYAFILITRESSGYQ 360
 QY 361 VFYGDWYGTGKTSPEKIPSLKONIEPIILAKREYVYQHDYIDHPDIYIGWREGSSAA 420
 DB 361 VFYGDWYGTGKTSPEKIPSLKONIEPIILAKREYVYQHDYIDHPDIYIGWREGSSAA 420
 QY 421 KSGLLALITDGPQSGSRMAYAGIKMAGETWYDITGRSDTYKISGKGEFFHNDSSVILY 480
 DB 421 KSGLLALITDGPQSGSRMAYAGIKMAGETWYDITGRSDTYKISGKGEFFHNDSSVILY 480
 421 KSGLLALITDGPQSGSRMAYAGIKMAGETWYDITGRSDTYKISGKGEFFHNDSSVILY 480
 RESULT 8
 ID AAY97546 standard; protein; 483 AA.
 XX AAY97546;
 AC AAY97546;
 XX 12-FEB-2001 (first entry)
 DT 12-FEB-2001 (first entry)
 XX DE B. amyloliquefaciens termamyl-like alpha amylase.
 XX KM Termamyl-like alpha-amylase; variant; starch liquefaction; fuel;
 XX KM detergent composition; laundry cleaning composition; ethanol production;
 XX KM dish washing composition; composition; hard surface cleaning composition;
 XX KM industrial ethanol production; textile desizing.
 XX OS Bacillus amyloliquefaciens.
 XX XX
 XX PN WO200060059-A2.
 XX PD 12-OCT-2000.
 XX PF 28-MAR-2000; 2000WO-DK000148.
 XX PR 30-MAR-1999; 99DX-00000437.
 XX PA (NOVO) NOVO NORDISK AS.
 XX PI Andersen C, Jorgensen CT, Bisgard-Frantzen H, Svendsen A;
 XX PI Kjaerulff S;
 XX WPI: 2001-015656/02.
 XX DR N-PsDB; AAV37850.
 XX PT New variants of parent Termamyl-like alpha-amylase, useful in starch
 XX PT liquefaction, in detergent compositions and in ethanol production,
 XX PT exhibit altered cleavage pattern relative to the parent.
 XX PS Claim 9; Page 64-67; 78pp; English.
 CC This sequence represents a termamyl-like alpha amylase. The invention
 CC relates to a variant (I) of parent Termamyl-like alpha-amylase comprising
 CC alteration at one or more of the positions W13, G48, T49, S50, Q51, A52,
 CC D53, V54, G57, G107, G108, A111, S168 and M197. The alterations in (I)
 CC are independently an insertion of an amino acid downstream of the amino
 CC acid which occupies the position or deletion or substitution of the amino
 CC acid which occupies the position with a different amino acid. The variant
 CC has alpha-amylase activity. (I) or compositions containing it are useful
 CC in starch liquefaction, in detergent compositions such as laundry, dish
 CC washing and hard surface cleaning compositions, ethanol production, desizing
 CC as fuel, drinking and industrial ethanol production, desizing of
 CC textiles, fabrics or garments. (I) exhibits a reduced capability of
 CC cleaving a substrate close to the branching point, and further exhibits
 CC improved substrate specificity and/or improved specific activity relative
 CC to the parent alpha-amylase
 CC XX
 XX Sequence 483 AA;
 SQ
 Query Match 100.0%; Score 2624; DB 4; Length 483;
 Best Local Similarity 100.0%; Pred. No. 8.2e-218;

Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VNGTLQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAKGLSOSDNGYGPYDLY 60
DB 1 VNGTLQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAKGLSOSDNGYGPYDLY 60
QY 61 DLGEFOQKGTVRTKYGKSELODAIGSLHSRNVQYGDVVLNKAAGADATEDVTAVERN 120
DB 61 DLGEFOQKGTVRTKYGKSELODAIGSLHSRNVQYGDVVLNKAAGADATEDVTAVERN 120
QY 121 ANRNOETSEBYQIKAWTDFRPPRGKNTYSPFKMWHFPGADWDESRKISRIFKRGSK 180
DB 121 ANRNOETSEBYQIKAWTDFRPPRGKNTYSPFKMWHFPGADWDESRKISRIFKRGSK 180
QY 181 AMDWEVSSSENGNDYLMYADVDYDHPDVVAETKKGIWYANELSLDGFRIIDAAKHIFSF 240
DB 181 AMDWEVSSSENGNDYLMYADVDYDHPDVVAETKKGIWYANELSLDGFRIIDAAKHIFSF 240
QY 241 LRDWVQAVROATGKEMFTVAEYQWNNAGKLENTLAKTSFVQSVFDPVPLHFNLOAASSQGG 300
DB 241 LRDWVQAVROATGKEMFTVAEYQWNNAGKLENTLAKTSFVQSVFDPVPLHFNLOAASSQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFWFKPLAVAFILTRBSGYPO 360
DB 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFWFKPLAVAFILTRBSGYPO 360
QY 361 VFYGDWYGTGTSPEKLEPSLKDNTEPILKAKKEYAYGQCHYIDHPDVIGMTREDSGSA 420
DB 361 VFYGDWYGTGTSPEKLEPSLKDNTEPILKAKKEYAYGQCHYIDHPDVIGMTREDSGSA 420
QY 421 KSGLAALITDGGSKRYAGLKNAGETWYDITGNRSPTYKIGSDGWGEFFHVNDGSVSIY 480
DB 421 KSGLAALITDGGSKRYAGLKNAGETWYDITGNRSPTYKIGSDGWGEFFHVNDGSVSIY 480

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RESULT 9

ABR06937 standard; protein; 483 AA.

ABR06937;

19-JUN-2002 (first entry)

B. amyloliquefaciens termamyl-like alpha-amylase protein SEQ ID NO:10.

KM Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;

KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;

XX washing; sweetener; ethanol; starch.

OS Bacillus amyloliquefaciens.

XX MO20016712-A2.

PD 13-SEP-2001.

PF 07-MAR-2001; 2001WO-DK000144.

PR 08-MAR-2000; 2000DK-00000376.

PR 15-MAR-2000; 2000US-0189857P.

PR 23-FEB-2001; 2001DK-00000303.

PR 26-FEB-2001; 2001US-0271382P.

FA (NOVO) NOVOZYMES AS.

XX Andersen C, Borchert TV, Nielsen BR;

XX WPI; 2002-239612/29.

XX N-PSDB; ABL50568.

XX Novel variant of parent termamyl-like alpha-amylase useful as a component in washing and dishwashing compositions, for textile desizing, for starch liquefaction, and for producing sweeteners and ethanol from starch.

PS Claim 8; Page 145-146; 153pp; English.

XX The present invention describes a variant of a parent termamyl-like alpha
CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
CC positions of a group of 31 possible amino acid positions. The alteration
CC in (I) may be at Arg28, Arg118, Asn174, Asp182, Asp183, Gly184,
CC Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Asn306,
CC Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
CC Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
CC washing and/or dishwashing, textile desizing, and starch liquefaction.
CC (I) is useful as a component in hard surface cleaning detergent
CC composition, and for producing sweeteners and ethanol from starch. (I)
CC has altered solubility, preferably increased solubility, in particular
CC under washing, dish washing or hard surface cleaning conditions. The
CC present sequence represents a Bacillus amyloliquefaciens termamyl-like
CC alpha-amylase which is used in the exemplification of the present
CC invention

SO Sequence 483 AA;

Query Match 100.0%; Score 2624; DB 5; Length 483;

Best Local Similarity 100.0%; Pred. No. 8.2e-218; Indels 0; Gaps 0;

Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 VNGTLQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAKGLSOSDNGYGPYDLY 60
DB 1 VNGTLQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWMIPPAKGLSOSDNGYGPYDLY 60
QY 61 DLGEFOQKGTVRTKYGKSELODAIGSLHSRNVQYGDVVLNKAAGADATEDVTAVERN 120
DB 61 DLGEFOQKGTVRTKYGKSELODAIGSLHSRNVQYGDVVLNKAAGADATEDVTAVERN 120
QY 121 ANRNOETSEBYQIKAWTDFRPPRGKNTYSPFKMWHFPGADWDESRKISRIFKRGSK 180
DB 121 ANRNOETSEBYQIKAWTDFRPPRGKNTYSPFKMWHFPGADWDESRKISRIFKRGSK 180
QY 181 AMDWEVSSSENGNDYLMYADVDYDHPDVVAETKKGIWYANELSLDGFRIIDAAKHIFSF 240
DB 181 AMDWEVSSSENGNDYLMYADVDYDHPDVVAETKKGIWYANELSLDGFRIIDAAKHIFSF 240
QY 241 LRDWVQAVROATGKEMFTVAEYQWNNAGKLENTLAKTSFVQSVFDPVPLHFNLOAASSQGG 300
DB 241 LRDWVQAVROATGKEMFTVAEYQWNNAGKLENTLAKTSFVQSVFDPVPLHFNLOAASSQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFWFKPLAVAFILTRBSGYPO 360
DB 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPGQSLSTVQTFWFKPLAVAFILTRBSGYPO 360
QY 361 VFYGDWYGTGTSPEKLEPSLKDNTEPILKAKKEYAYGQCHYIDHPDVIGMTREDSGSA 420
DB 361 VFYGDWYGTGTSPEKLEPSLKDNTEPILKAKKEYAYGQCHYIDHPDVIGMTREDSGSA 420
QY 421 KSGLAALITDGGSKRYAGLKNAGETWYDITGNRSPTYKIGSDGWGEFFHVNDGSVSIY 480
DB 421 KSGLAALITDGGSKRYAGLKNAGETWYDITGNRSPTYKIGSDGWGEFFHVNDGSVSIY 480

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RESULT 10

AAU12153 standard; protein; 483 AA.

AAU12153;

09-APR-2002 (first entry)

Bacillus TERMAMYL-like alpha-amylase BAN.

XX TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing;

XX starch liquefaction; ethanol production; hard surface cleaner; sweetener;

XX amylopectin; limit dextrin; NOVAMYL; BAN.

XX Bacillus amyloliquefaciens.

PN WO200188107-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 10-MAY-2001; 2001WO-DK000323.
 XX
 PR 12-MAY-2000; 2000DK-00000779.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Svendsen A, Jorgensen CT, Nielsen BR;
 XX
 DR WPI; 2002-106123/14.
 DR N-PSDB; AAS20026.
 XX
 PT New variant of parent Termamyl-like alpha-amylase for use as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX

Claim 5; Fig 1; 84pp; English.

CC The invention relates to a variant of parent TERMAMYL-like alpha-amylase
 CC comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,
 CC or at position 234, where the variant has alpha-amylase activity and each
 CC position corresponds to a position of a parent Termamyl-like alpha-
 CC amylase sequence having a Bacillus licheniformis alpha-amylase sequence
 CC of 483 amino acids, given in specification. The variant alpha-amylase, a
 CC detergent additive comprising the variant or a detergent composition
 CC comprising the variant, is useful for washing and/or dishwashing or
 CC textile desizing. The alpha-amylase is useful for starch liquefaction or
 CC ethanol production and as a component in a hard surface cleaning
 CC detergent composition, and for producing sweeteners from starch. The
 CC variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage
 CC activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic
 CC branch linkage cleavage activity of amylopectin or a limit dextrin
 CC prepared by TERMAMYL (RTM) or NOVAMYL (RTM). The present sequence is a
 CC natural variant of the TERMAMYL alpha-amylase, BAN
 CC
 XX

Sequence 483 AA;

Query Match 100.0%; Score 2624; DB 5; Length 483;

Best Local Similarity 100.0%; Pred. No. 8, 2e-218; Indels 0; Gaps 0;

Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWYTPNDGQHWKRLONDAEHLSDIGITAVWIPRAYKGLSOSDNGYGPYDLY 60
 DB 1 VNGTLMQYFEMWYTPNDGQHWKRLONDAEHLSDIGITAVWIPRAYKGLSOSDNGYGPYDLY 60
 QY 61 DLGEFOQKGVRTKYGTGKSELQDAIGLSHRNVQVGDVVLNHRKAGADATEDVTAVERN 120
 DB 61 DLGEFOQKGVRTKYGTGKSELQDAIGLSHRNVQVGDVVLNHRKAGADATEDVTAVERN 120
 QY 121 ANRNOETSEBYQIKAWTDFRPPGRGNITSPFKWMWHPGADWDSRKSIRLFEKRGCK 180
 DB 121 ANRNOETSEBYQIKAWTDFRPPGRGNITSPFKWMWHPGADWDSRKSIRLFEKRGCK 180
 QY 181 ARWMEVSSSENGNDYLYADVDYDHPVAVETKKNGIWNANESLDFGFIIDAKXHKKEF 240
 DB 181 ARWMEVSSSENGNDYLYADVDYDHPVAVETKKNGIWNANESLDFGFIIDAKXHKKEF 240
 QY 181 ARWMEVSSSENGNDYLYADVDYDHPVAVETKKNGIWNANESLDFGFIIDAKXHKKEF 240
 DB 181 ARWMEVSSSENGNDYLYADVDYDHPVAVETKKNGIWNANESLDFGFIIDAKXHKKEF 240
 QY 241 LRDMVQAVROATGKEMFTVAEYQONNAGKLENYLNTSFQSVFDPVLFHNLQPAASQGG 300
 DB 241 LRDMVQAVROATGKEMFTVAEYQONNAGKLENYLNTSFQSVFDPVLFHNLQPAASQGG 300
 QY 301 GYDMRLLDGTIVSRHEKAVTEVENHDTOPGOSLESSTVQWTKPLAVAFILTRREGGYQ 360
 DB 301 GYDMRLLDGTIVSRHEKAVTEVENHDTOPGOSLESSTVQWTKPLAVAFILTRREGGYQ 360
 QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEAYVPGHDYIDHPVDIGMTREGDSAA 420
 DB 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEAYVPGHDYIDHPVDIGMTREGDSAA 420
 QY 421 KSGLAALITDGPQGSKMYAGLKNAGETWYDTIGNRSDYTKIGSDGGEFHVNDGSVSY 480

DB 421 KSGLAALITDGPQGSKMYAGLKNAGETWYDTIGNRSDYTKIGSDGGEFHVNDGSVSY 480

RESULT 11
 ID AAB47854 standard; protein; 483 AA.
 XX
 AC AAB47854;
 XX
 DT 02-APR-2002 (first entry)
 XX
 DE Bacillus alpha amylase BAN.
 XX
 KM Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup;
 KM starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;
 KM bakery; cereal bar; ice cream; coffee whitener; salad dressing;
 KM cured meat; fermented meat; spice.
 XX

Bacillus amyloliquefaciens.

XX WO200196537-A2.

XX 20-DEC-2001.

XX 13-JUN-2001; 2001WO-DK000404.

XX 14-JUN-2000; 2000DK-00000917.

XX 20-JUN-2000; 2000US-0212852P.

XX (NOVO) NOVOZYMES AS.

XX Nielsen BR, Welbye M;

XX WPI; 2002-098064/13.

XX N-PSDB; AAI72215.

XX New modified alpha-amylase derived from the genus Bacillus and/or is a
 PT Termamyl-like alpha-amylase, which has been pre-oxidized for producing
 PT maltodextrin or glucose syrup.
 XX

PS Claim 5; Page 39-41; 47pp; English.

CC The sequences given in AAB47850-56 show modified alpha-amylases derived
 CC from the genus Bacillus. These alpha amylases are Termamyl-like alpha-
 CC amylase and they have been pre-oxidized. The alpha amylase is useful for
 CC producing a maltodextrin or glucose syrup, by treating starch with a pre-
 CC oxidized alpha-amylase until a product with a DE between 5-45 has been
 CC provided and/or until a product with a molecular weight of between 5-30
 CC kDa has been provided. The product comprises a maltodextrin with a DE of
 CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kDa. The
 CC alpha amylase is useful for producing a maltodextrin or glucose syrup,
 CC where the glucose syrup is useful as an ingredient in food, feed or
 CC pharmaceuticals. Glucose syrup is useful in confectionery such as
 CC candies, beverages such as isotonic drinks, bakery such as cereal bars,
 CC dairy and ice cream such as coffee whiteners, conventional foods such as
 CC salad dressings, and food ingredients and preparations such as cured
 CC meat, fermented meat, spices and seasoning encapsulated flavours
 XX

Sequence 483 AA;

Query Match 100.0%; Score 2624; DB 5; Length 483;

Best Local Similarity 100.0%; Pred. No. 8, 2e-218; Indels 0; Gaps 0;

Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWYTPNDGQHWKRLONDAEHLSDIGITAVWIPRAYKGLSOSDNGYGPYDLY 60
 DB 1 VNGTLMQYFEMWYTPNDGQHWKRLONDAEHLSDIGITAVWIPRAYKGLSOSDNGYGPYDLY 60
 QY 61 DLGEFOQKGVRTKYGTGKSELQDAIGLSHRNVQVGDVVLNHRKAGADATEDVTAVERN 120
 DB 61 DLGEFOQKGVRTKYGTGKSELQDAIGLSHRNVQVGDVVLNHRKAGADATEDVTAVERN 120

QY 121 ANRNOETSEBYOIKAMTDFRFGNGTYSDFKMWYHFGADWDESRKISRIFKFRGEGK 180
 DB 121 ANRNOETSEBYOIKAMTDFRFGNGTYSDFKMWYHFGADWDESRKISRIFKFRGEGK 180
 QY 181 AMDWEVSSSENGNYDYLMTADVDYDHPDVAETKKGIMWYANLSDGFRIDAARHKKFSF 240
 DB 181 AMDWEVSSSENGNYDYLMTADVDYDHPDVAETKKGIMWYANLSDGFRIDAARHKKFSF 240
 QY 241 LRDWQAVRQATGKEMFTVAEYKONNAGKLENTSFNOSVFPVPLHFNLOAASSOGG 300
 DB 241 LRDWQAVRQATGKEMFTVAEYKONNAGKLENTSFNOSVFPVPLHFNLOAASSOGG 300
 QY 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTOPGQSLSTVQTWFKPLAVAFILTRBSGYPO 360
 DB 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTOPGQSLSTVQTWFKPLAVAFILTRBSGYPO 360
 QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPLTKARKEVAYGPOHDYDHPDVGWTRBSGSA 420
 DB 361 VFYGDWYGTGTSPEKIPSLKDNIEPLTKARKEVAYGPOHDYDHPDVGWTRBSGSA 420
 QY 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSJTVKIGSDGWSGFHVNDGSVSIV 480
 DB 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSJTVKIGSDGWSGFHVNDGSVSIV 480
 RESULT 12
 ABB76590 standard; protein; 483 AA.
 AC ABB76590;
 XX 19-AUG-2002 (first entry)
 DT Termamy1-like-alpha-amyase #5.
 DE Termamy1-like-alpha-amyase #5.
 XX Termamy1, alpha amyase; starch liquefaction; ethanol production;
 KM textile desizing; detergent; enzyme.
 OS Bacillus amyloliquefaciens.
 XX WO200210355-A2.
 PN 07-FEB-2002.
 PD 12-JUL-2001; 2001WO-DK000488.
 PF 01-AUG-2000; 2000DK-00001160.
 PR 12-SEP-2000; 2000DK-00001354.
 PR 10-NOV-2000; 2000DK-00001687.
 PR 26-APR-2001; 2001DK-00000655.
 XX (NOVO) NOVOZYMES AS.
 PA Thisted T, Kjaerulff S, Andersen C, Fuglsang CC;
 PI WPI; 2002-280633/32.
 DR N-PSDB; ABL96211.
 XX Variant of parent Termamy1-like alpha amyase, useful in detergent
 PT composition, for starch liquefaction, ethanol production, washing and/or
 PT dish washing, and textile desizing.
 PS Claim 4; Fig 3; 90pp; English.
 CC This invention relates to variants of a parent Termamy1-like alpha-
 CC amyases. These are used for starch liquefaction, ethanol production,
 CC detergent, and textile desizing. The amyases have altered stability,
 CC particularly at high temperatures from 70-120pH and low pH in the
 CC range from pH 4.0-6.0. The present sequence is a termamy1-like-alpha-
 CC amyase
 SQ Sequence 483 AA;

Query Match 100.0%; Score 2624; DB 5; Length 483;
 Best Local Similarity 100.0%; Pred. No. 8.2e-216; Indels 0; Gaps 0;
 Matches 480; Conservative 0; Mismatches 0;
 QY 1 VNGTLMOYFEMWYTPNGOHKRLQNDAREHLSIDGITAWYIPPAVKGLSQSDNDNGYGPYDLY 60
 DB 1 VNGTLMOYFEMWYTPNGOHKRLQNDAREHLSIDGITAWYIPPAVKGLSQSDNDNGYGPYDLY 60
 QY 61 DLGEFOQKGTATKTKGTSELODAISGLHSRNVQVGTGVYVLAHKAQADATEDVTAENV 120
 DB 61 DLGEFOQKGTATKTKGTSELODAISGLHSRNVQVGTGVYVLAHKAQADATEDVTAENV 120
 QY 121 ANRNOETSEBYOIKAMTDFRFGNGTYSDFKMWYHFGADWDESRKISRIFKFRGEGK 180
 DB 121 ANRNOETSEBYOIKAMTDFRFGNGTYSDFKMWYHFGADWDESRKISRIFKFRGEGK 180
 QY 181 AMDWEVSSSENGNYDYLMTADVDYDHPDVAETKKGIMWYANLSDGFRIDAARHKKFSF 240
 DB 181 AMDWEVSSSENGNYDYLMTADVDYDHPDVAETKKGIMWYANLSDGFRIDAARHKKFSF 240
 QY 241 LRDWQAVRQATGKEMFTVAEYKONNAGKLENTSFNOSVFPVPLHFNLOAASSOGG 300
 DB 241 LRDWQAVRQATGKEMFTVAEYKONNAGKLENTSFNOSVFPVPLHFNLOAASSOGG 300
 QY 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTOPGQSLSTVQTWFKPLAVAFILTRBSGYPO 360
 DB 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTOPGQSLSTVQTWFKPLAVAFILTRBSGYPO 360
 QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPLTKARKEVAYGPOHDYDHPDVGWTRBSGSA 420
 DB 361 VFYGDWYGTGTSPEKIPSLKDNIEPLTKARKEVAYGPOHDYDHPDVGWTRBSGSA 420
 QY 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSJTVKIGSDGWSGFHVNDGSVSIV 480
 DB 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSJTVKIGSDGWSGFHVNDGSVSIV 480
 RESULT 13
 ABB60488 standard; protein; 483 AA.
 AC ABB60488;
 XX 10-MAY-2003 (first entry)
 DT Bacillus amyloliquefaciens alpha-amyase SEQ ID NO 4.
 DE Bacillus amyloliquefaciens alpha-amyase SEQ ID NO 4.
 XX Bacillus amyloliquefaciens; alpha-amyase; washing; cleaning; textile;
 KM dishwashing machine; starch-based capsule; EC 3.2.1.1; enzyme.
 OS Bacillus amyloliquefaciens.
 XX WO2003014358-A2.
 PN 20-FEB-2003.
 PD 27-JUL-2002; 2002WO-EP008391.
 PF 07-AUG-2001; 2001DE-01038753.
 PR (HENK) HENKEL KGAA.
 PA Kotwicz B, Breves R, Maurer K;
 PI WPI; 2003-278480/27.
 DR N-PSDB; ABE59264.
 XX Washing and cleaning composition, useful for laundry and hard surface
 PT cleaning, contains hybrid amyase derived from two Bacillus enzymes.
 PS Claim 4; Fig 2; 118pp; German.
 CC The invention relates to a washing and cleaning composition (A)

CC containing an amylolytic hybrid protein (I) containing sequences from the
 CC alpha-amylases (EC 3.2.1.1) of *Bacillus amyloliquefaciens* and B.
 CC licheniformis. (A) are used for cleaning textiles (by hand or machine) or
 CC hard surfaces (metal, glass, plastic etc.), especially in dishwashing
 CC machines. (I) can also be used to release other components of the
 CC compositions from starch-based capsules. The present sequence is that of
 CC the *Bacillus amyloliquefaciens* alpha-amylase of the invention
 XX

SO Sequence 483 AA;

Query Match 100.0%; Score 2624; DB 6; Length 483;
 Best Local Similarity 100.0%; Pred. No. 8.2e-218;
 Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAVWIPPAKGLSDSDNGYGPYDLY 60
DB 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAVWIPPAKGLSDSDNGYGPYDLY 60
QY 61 DLGEFOQKGTVRTKYGKSELQDAIGSLHSRNQYGVVLAHKAQADATEDVTAVEVNP 120
DB 61 DLGEFOQKGTVRTKYGKSELQDAIGSLHSRNQYGVVLAHKAQADATEDVTAVEVNP 120
QY 121 ANRNETSEBYOIKAWTDFRPGRGNTYSDPKMHWHPGADWDSRKISRIFFKRGEGK 180
DB 121 ANRNETSEBYOIKAWTDFRPGRGNTYSDPKMHWHPGADWDSRKISRIFFKRGEGK 180
QY 181 AMDWEVSSENGNDYLMYADVDDHPDVAETKKGIMYANELSLDGFRIIDAKHIXFSF 240
DB 181 AMDWEVSSENGNDYLMYADVDDHPDVAETKKGIMYANELSLDGFRIIDAKHIXFSF 240
QY 241 LRDVQAVROATGKEMFTVAEYQNNAGKLENYLNTKTSFNQSVFDPVLFHNLQAASSQGG 300
DB 241 LRDVQAVROATGKEMFTVAEYQNNAGKLENYLNTKTSFNQSVFDPVLFHNLQAASSQGG 300
QY 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGSLSTVQTFWFKPLAVAFILTRBSGYPQ 360
DB 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGSLSTVQTFWFKPLAVAFILTRBSGYPQ 360
QY 361 VFYGDWYGTGKTSPEKIPSLKDNIEPLTKARKEAYAGPQHDYIDHPDVIQWTRBSSAA 420
DB 361 VFYGDWYGTGKTSPEKIPSLKDNIEPLTKARKEAYAGPQHDYIDHPDVIQWTRBSSAA 420
QY 421 KSGIALLITDGPQGSKRMVAGLKNAGETWYDITGNRSDTYKISDGMGEFHNVDGSVSIY 480
DB 421 KSGIALLITDGPQGSKRMVAGLKNAGETWYDITGNRSDTYKISDGMGEFHNVDGSVSIY 480

```

RESULT 14
 AAY29853
 ID AAY29853 standard; protein; 514 AA.

XX AAY29853;

DT 18-NOV-1999 (first entry)

XX *Bacillus amyloliquefaciens* Termamyl-1-like alpha-amylase.

XX Alpha-amylase; Termamyl-1-like alpha-amylase; glucose syrup; starch.

XX *Bacillus amyloliquefaciens*.

XX Key Location/Qualifiers

FT Peptide 1..31

FT Protein /label= signal

XX W09946399-A1.

XX 16-SEP-1999.

XX 08-MAR-1999; 99W0-DK000114.

PR 09-MAR-1998; 98DK-00000321.

XX (NOVO) NOVO-NORDISK AS.

XX Norman BE, Hendriksen HV;

XX WPI; 1999-551422/46.

DR N-PSDB; AA221079.

PT Preparation of a glucose syrup, using a Termamyl-1-like alpha-amylase.

XX Disclosure; Page 32-34; 36pp; English.

CC A method has been developed for the preparation of a glucose syrup using
 CC a Termamyl-1-like alpha-amylase containing a substitution at Val(54). The
 CC glucose syrup obtained by the process is useful as an ingredient in food
 CC products. The Termamyl-1-like alpha-amylase facilitates the preparation of
 CC glucose syrups suitable for the food industry, previously only possible
 CC using acid hydrolysis. The present sequence represents *Bacillus*
 CC *amyloliquefaciens* Termamyl-1-like alpha-amylase
 XX

SO Sequence 514 AA;

Query Match 100.0%; Score 2624; DB 2; Length 514;
 Best Local Similarity 100.0%; Pred. No. 9e-218;
 Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAVWIPPAKGLSDSDNGYGPYDLY 60
DB 32 VNGTLMQYFEMWTPNDGQHKRLQNDAEHLSDIGITAVWIPPAKGLSDSDNGYGPYDLY 91
QY 61 DLGEFOQKGTVRTKYGKSELQDAIGSLHSRNQYGVVLAHKAQADATEDVTAVEVNP 120
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DB 121 ANRNETSEBYOIKAWTDFRPGRGNTYSDPKMHWHPGADWDSRKISRIFFKRGEGK 180
QY 152 ANRNETSEBYOIKAWTDFRPGRGNTYSDPKMHWHPGADWDSRKISRIFFKRGEGK 211
DB 181 AMDWEVSSENGNDYLMYADVDDHPDVAETKKGIMYANELSLDGFRIIDAKHIXFSF 240
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DB 212 AMDWEVSSENGNDYLMYADVDDHPDVAETKKGIMYANELSLDGFRIIDAKHIXFSF 271
QY 241 LRDVQAVROATGKEMFTVAEYQNNAGKLENYLNTKTSFNQSVFDPVLFHNLQAASSQGG 300
DB 272 LRDVQAVROATGKEMFTVAEYQNNAGKLENYLNTKTSFNQSVFDPVLFHNLQAASSQGG 331
QY 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGSLSTVQTFWFKPLAVAFILTRBSGYPQ 360
DB 332 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGSLSTVQTFWFKPLAVAFILTRBSGYPQ 391
QY 361 VFYGDWYGTGKTSPEKIPSLKDNIEPLTKARKEAYAGPQHDYIDHPDVIQWTRBSSAA 420
DB 392 VFYGDWYGTGKTSPEKIPSLKDNIEPLTKARKEAYAGPQHDYIDHPDVIQWTRBSSAA 451
QY 421 KSGIALLITDGPQGSKRMVAGLKNAGETWYDITGNRSDTYKISDGMGEFHNVDGSVSIY 480
DB 452 KSGIALLITDGPQGSKRMVAGLKNAGETWYDITGNRSDTYKISDGMGEFHNVDGSVSIY 511

```

RESULT 15

ABAB12433
 ID ABAB12433 standard; protein; 514 AA.

XX ABAB12433;

DT 19-OCT-2000 (first entry)

XX *Bacillus amyloliquefaciens* amylose protein SEQ ID NO:9.

XX *Bacillus amyloliquefaciens*; alpha-amylase; thermostable; bread.

XX *Bacillus amyloliquefaciens*.

Job time : 49.7475 secs

XX JP2000135093-A.

XX 16-MAY-2000.

XX 20-AUG-1999; 99JP-00234813.

XX 24-AUG-1998; 98JP-00237839.

XX (DAIW) DAIWA KASEI KK.

XX WPI; 2000-403584/35.

PT Novel thermostable alpha-amylase, useful for improving the preparation of
PT bread, comprises alpha-amylase activity with less than 80% activity after
PT treatment at 65degrec for 30 min.

PS Claim 1; Page 18-19; 22pp; Japanese.

CC The present invention describes a thermostable alpha-amylase (I)
CC comprising the sequence given in AAB12433 (A) or deletions, replacements
CC or insertions of one or more amino acid(s) in the sequence and alpha-
CC amylase activity with less than 80% activity after treatment at 65 plus
CC degrees Celsius for 30 minutes. Also described are: (1) DNAs encoding (I)
CC ; (2) DNAs containing one of 4 nucleotide sequences comprising 1545 base
CC pairs (see AAA60576 to AAA60579); (3) expression vectors containing the
CC above mentioned DNAs; (4) host cells containing the above mentioned
CC expression vectors; (5) preparation of a polypeptide having alpha-amylase
CC activity by culture of the recombinant host cells; and (6) preparation of
CC bread including a process to add (I) to the dough. (I) is useful in the
CC preparation of bread. (I) improves the soft volume of the bread and
CC prevents it aging

SQ Sequence 514 AA:

Query Match 100.0%; Score 2624; DB 3; Length 514;

Best Local Similarity 100.0%; Pred. No. 9e-218; Mismatches 0; Indels 0; Gaps 0;

Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 DLGEPOQKGTIVRTKTKYKSELDQAIQSLHSRNVQYGDVLTNKAQADATEDVTAENVP 120
DB 92 DLGEPOQKGTIVRTKTKYKSELDQAIQSLHSRNVQYGDVLTNKAQADATEDVTAENVP 151
QY 121 ANRQETSEFYQIKAWTDFRFGKNTYSDPKWMYHFDGADWDESKISRIFFKRGEGK 180
DB 152 ANRQETSEFYQIKAWTDFRFGKNTYSDPKWMYHFDGADWDESKISRIFFKRGEGK 211
QY 181 AMDWEVSSENGYDYLMTADVVDYHPDVVATKKGITWYANELSLDGFRIIDAKHIFS 240
DB 212 AMDWEVSSENGYDYLMTADVVDYHPDVVATKKGITWYANELSLDGFRIIDAKHIFS 271
QY 241 LRDWVOAAROATGKEMFTVAEYQNNAGKLENYLNTKTSFNQSVFDPVPLHFNLOAASSQGG 300
DB 272 LRDWVOAAROATGKEMFTVAEYQNNAGKLENYLNTKTSFNQSVFDPVPLHFNLOAASSQGG 331
QY 301 GYDMRLLDGTIVSSHPEKAVTFVENHDTQPGQSLESTVQTFKPLAYAFILITRESGYPQ 360
DB 332 GYDMRLLDGTIVSSHPEKAVTFVENHDTQPGQSLESTVQTFKPLAYAFILITRESGYPQ 391
QY 361 VFGMYGKGTSPKEIPSLKNIETPILKARKEYAYGPHDIHPDYIGWTRREGSSAA 420
DB 392 VFGMYGKGTSPKEIPSLKNIETPILKARKEYAYGPHDIHPDYIGWTRREGSSAA 451
QY 421 KSGLAALITDGPQGSKRYAGLKNAGETWYDITGNRSDTVKIGSDGMBFHYNDGSVSIY 480
DB 452 KSGLAALITDGPQGSKRYAGLKNAGETWYDITGNRSDTVKIGSDGMBFHYNDGSVSIY 511
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Tue May 4 14:34:46 2004

US-10-644-187-4.rat

Page 1

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OM protein - protein search, using sw model

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(without alignments)
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Title: US-10-644-187-4

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Total number of hits satisfying chosen parameters: 389414

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/prodata/2/iaa/backfillset1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2624	100.0	480	3	US-09-170-670-5
3	2624	100.0	480	3	US-09-193-068-5
4	2624	100.0	480	3	US-09-183-412-5
5	2624	100.0	480	3	US-09-290-734-5
6	2624	100.0	480	4	US-09-672-459-4
7	2624	100.0	480	4	US-09-545-586-5
8	2624	100.0	480	4	US-10-186-042-4
9	2624	100.0	480	4	US-09-769-864-5
10	2624	100.0	483	4	US-09-291-023A-16
11	2624	100.0	483	4	US-09-537-168-6
12	2624	100.0	483	4	US-09-381-687-6
13	2624	100.0	483	4	US-09-540-715A-16
14	2624	100.0	514	1	US-08-720-899-4
15	2624	100.0	514	1	US-08-459-610-4
16	2624	100.0	514	2	US-08-343-804-4
17	2624	100.0	514	2	US-08-607-399-4
18	2624	100.0	514	2	US-08-600-908A-4
19	2624	100.0	514	2	US-08-683-838A-4
20	2624	100.0	514	3	US-09-264-097-4
21	2624	100.0	514	3	US-09-636-252A-4
22	2624	100.0	520	1	US-08-468-700-36
23	2624	100.0	520	1	US-08-645-971-4
24	2624	100.0	520	2	US-08-468-220-34
25	2624	100.0	520	2	US-08-468-698-34
26	2624	100.0	520	2	US-08-704-706A-36
27	2624	100.0	520	3	US-08-890-383-5

28	2624	100.0	520	3	US-08-914-679A-5
29	2624	100.0	520	3	US-08-985-659-37
30	2624	100.0	520	3	US-08-194-664A-34
31	2624	100.0	520	5	PCT-US94-01553A-34
32	2624	100.0	520	5	PCT-US95-10426-34
33	2475	94.3	483	2	US-08-600-908A-13
34	2475	94.3	483	2	US-08-683-838A-13
35	2475	94.3	483	4	US-09-636-252A-13
36	2190	83.5	481	4	US-09-537-168-2
37	2176	82.9	483	1	US-08-468-700-34
38	2176	82.9	483	1	US-08-645-971-2
39	2176	82.9	483	2	US-08-468-220-32
40	2176	82.9	483	2	US-08-468-698-32
41	2176	82.9	483	2	US-08-704-706A-34
42	2176	82.9	483	3	US-08-890-383-3
43	2176	82.9	483	3	US-08-914-679A-3
44	2176	82.9	483	3	US-08-985-659-35
45	2176	82.9	483	3	US-08-194-664A-32

ALIGNMENTS

RESULT 1					
US-09-182-859-4					
Sequence 4, Application US/09182859					
Patent No. 6143708					
GENERAL INFORMATION:					
APPLICANT: Svendsen, Allan					
APPLICANT: Borchert, Torben					
APPLICANT: Bisgaard-Frantzen, Henrik					
TITLE OF INVENTION: Alpha-Amylase Mutants					
FILE REFERENCE: 4796.204-US					
CURRENT APPLICATION NUMBER: US/09/182,859					
CURRENT FILING DATE: 1998-10-29					
EARLIER APPLICATION NUMBER: 0515/96					
EARLIER FILING DATE: 1996-04-30					
EARLIER APPLICATION NUMBER: 0712/96					
EARLIER FILING DATE: 1996-06-28					
EARLIER APPLICATION NUMBER: 0775/96					
EARLIER FILING DATE: 1996-07-11					
EARLIER APPLICATION NUMBER: 1263/96					
EARLIER FILING DATE: 1996-11-08					
NUMBER OF SEQ ID NOS: 37					
SOFTWARE: FASTSEQ for Windows Version 3.0					
SEQ ID NO 4					
LENGTH: 480					
TYPE: PRT					
ORGANISM: Bacillus amyloliquefaciens					
US-09-182-859-4					
Query Match					
Best Local Similarity 100.0%; Pred. No. 3.8e-230; Indels 0; Gaps 0;					
Matches 480; Conservative					
QY	1	VNGTLMQYFETTPDQGMWRLQNDALHSLDIGTAWIPPAKGLSOSDNGYGPYDLY	60		Sequence 5, Appl1
DB	1	VNGTLMQYFETTPDQGMWRLQNDALHSLDIGTAWIPPAKGLSOSDNGYGPYDLY	60		Sequence 37, Appl
QY	61	DIGEEQOQGVTRTKTGTSELODAIGSHSNVOYGVVNLHKAADATDVAVEVNP	120		Sequence 34, Appl
DB	61	DIGEEQOQGVTRTKTGTSELODAIGSHSNVOYGVVNLHKAADATDVAVEVNP	120		Sequence 34, Appl
QY	121	ANRNETSEYQIKAMTDFRFGKNTYSDPKMWHYFDGADWDSRKISIFKRGSGK	180		Sequence 13, Appl
DB	121	ANRNETSEYQIKAMTDFRFGKNTYSDPKMWHYFDGADWDSRKISIFKRGSGK	180		Sequence 13, Appl
QY	181	ANDWEVSSNGYDYLTADVDYDHPDYVAETKKKGIYANELSIDGERIDAAKIKRSF	240		Sequence 2, Appl
DB	181	ANDWEVSSNGYDYLTADVDYDHPDYVAETKKKGIYANELSIDGERIDAAKIKRSF	240		Sequence 2, Appl
QY	241	LADWVOAVQATGKEMFTVAEYWNNAKGLSNYLNKTSFNOSVDPVPLHFNLOAASOGG	300		Sequence 32, Appl
DB	241	LADWVOAVQATGKEMFTVAEYWNNAKGLSNYLNKTSFNOSVDPVPLHFNLOAASOGG	300		Sequence 32, Appl

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us-10-644-187-4.ra1

Page 2

Db 241 LBDWQAVRQATGKEMFTVAEYQNNAGKLENTKTSFNOSGVPDPLHFNLOAASSQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTEVENHDTPQGSLESTVQTFKPLAFAFILTRBSGYPO 360
Db 301 GYDMRRLDGTIVSRHPEKAVTEVENHDTPQGSLESTVQTFKPLAFAFILTRBSGYPO 360
QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPOHDYIDHPDYIGWTRBDSGSA 420
Db 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPOHDYIDHPDYIGWTRBDSGSA 420
QY 421 KSGLAALITDGPBGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGGEFHVNDGSVSII 480
Db 421 KSGLAALITDGPBGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGGEFHVNDGSVSII 480

RESULT 2
US-09-170-670-5
Sequence 5, Application US/09170670
Patent No. 6187576
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 5276-200-US
CURRENT APPLICATION NUMBER: US/09/170,670
CURRENT FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 1172/97
EARLIER FILING DATE: 1997-10-13
EARLIER APPLICATION NUMBER: 60/063,306
EARLIER FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 480
TYPE: PRT
ORGANISM: B. amyloliquefaciens
US-09-170-670-5

Query Match 100.0%; Score 2624; DB 3; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.8e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLNQYFEMWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKLSQSDNGYGPYDLY 60
Db 1 VNGTLNQYFEMWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKLSQSDNGYGPYDLY 60
QY 61 DLGEFOOKGTIVRTKYGTGKSELQDAIGLSHRNVOYGVAVLNHKKAGADTEVTAVERNVP 120
Db 61 DLGEFOOKGTIVRTKYGTGKSELQDAIGLSHRNVOYGVAVLNHKKAGADTEVTAVERNVP 120
QY 121 ANRNOETSEBYQIKAWTDFRFPGRGNTYSDFKMHWYHPGADWDESRKISRIFKRGGEK 180
Db 121 ANRNOETSEBYQIKAWTDFRFPGRGNTYSDFKMHWYHPGADWDESRKISRIFKRGGEK 180
QY 121 ANRNOETSEBYQIKAWTDFRFPGRGNTYSDFKMHWYHPGADWDESRKISRIFKRGGEK 180
Db 121 ANRNOETSEBYQIKAWTDFRFPGRGNTYSDFKMHWYHPGADWDESRKISRIFKRGGEK 180
QY 181 AMDEWSSSENGNDYLYADVDYDHPVVAETKMGWYANELSLDGFIDAKIKRSEF 240
Db 181 AMDEWSSSENGNDYLYADVDYDHPVVAETKMGWYANELSLDGFIDAKIKRSEF 240
QY 241 LBDWQAVRQATGKEMFTVAEYQNNAGKLENTKTSFNOSGVPDPLHFNLOAASSQGG 300
Db 241 LBDWQAVRQATGKEMFTVAEYQNNAGKLENTKTSFNOSGVPDPLHFNLOAASSQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTEVENHDTPQGSLESTVQTFKPLAFAFILTRBSGYPO 360
Db 301 GYDMRRLDGTIVSRHPEKAVTEVENHDTPQGSLESTVQTFKPLAFAFILTRBSGYPO 360
QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPOHDYIDHPDYIGWTRBDSGSA 420
Db 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPOHDYIDHPDYIGWTRBDSGSA 420
QY 421 KSGLAALITDGPBGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGGEFHVNDGSVSII 480
Db 421 KSGLAALITDGPBGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGGEFHVNDGSVSII 480

Db 421 KSGLAALITDGPBGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGGEFHVNDGSVSII 480
RESULT 3
US-09-193-068-5
Sequence 5, Application US/09193068
Patent No. 6197565
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Kjullif, Soren
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Andersen, Carsten
TITLE OF INVENTION: -Amylase Variants
FILE REFERENCE: 5709,000-US
CURRENT APPLICATION NUMBER: US/09/193,068
CURRENT FILING DATE: 1998-11-16
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 480
TYPE: PRT
ORGANISM: B. amyloliquefaciens
US-09-193-068-5

Query Match 100.0%; Score 2624; DB 3; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.8e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLNQYFEMWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKLSQSDNGYGPYDLY 60
Db 1 VNGTLNQYFEMWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKLSQSDNGYGPYDLY 60
QY 61 DLGEFOOKGTIVRTKYGTGKSELQDAIGLSHRNVOYGVAVLNHKKAGADTEVTAVERNVP 120
Db 61 DLGEFOOKGTIVRTKYGTGKSELQDAIGLSHRNVOYGVAVLNHKKAGADTEVTAVERNVP 120
QY 121 ANRNOETSEBYQIKAWTDFRFPGRGNTYSDFKMHWYHPGADWDESRKISRIFKRGGEK 180
Db 121 ANRNOETSEBYQIKAWTDFRFPGRGNTYSDFKMHWYHPGADWDESRKISRIFKRGGEK 180
QY 121 ANRNOETSEBYQIKAWTDFRFPGRGNTYSDFKMHWYHPGADWDESRKISRIFKRGGEK 180
Db 121 ANRNOETSEBYQIKAWTDFRFPGRGNTYSDFKMHWYHPGADWDESRKISRIFKRGGEK 180
QY 181 AMDEWSSSENGNDYLYADVDYDHPVVAETKMGWYANELSLDGFIDAKIKRSEF 240
Db 181 AMDEWSSSENGNDYLYADVDYDHPVVAETKMGWYANELSLDGFIDAKIKRSEF 240
QY 241 LBDWQAVRQATGKEMFTVAEYQNNAGKLENTKTSFNOSGVPDPLHFNLOAASSQGG 300
Db 241 LBDWQAVRQATGKEMFTVAEYQNNAGKLENTKTSFNOSGVPDPLHFNLOAASSQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTEVENHDTPQGSLESTVQTFKPLAFAFILTRBSGYPO 360
Db 301 GYDMRRLDGTIVSRHPEKAVTEVENHDTPQGSLESTVQTFKPLAFAFILTRBSGYPO 360
QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPOHDYIDHPDYIGWTRBDSGSA 420
Db 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPOHDYIDHPDYIGWTRBDSGSA 420
QY 421 KSGLAALITDGPBGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGGEFHVNDGSVSII 480
Db 421 KSGLAALITDGPBGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGGEFHVNDGSVSII 480

RESULT 4
US-09-183-412-5
Sequence 5, Application US/09183412
Patent No. 6204232
GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Kjullif, Soren
TITLE OF INVENTION: Alpha-Amylase Mutants

FILE REFERENCE: 5368.200-US
CURRENT APPLICATION NUMBER: US/09/183,412
CURRENT FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: 60/064,662
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 60/093,234
EARLIER FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 1240/97
EARLIER FILING DATE: 1997-10-30
EARLIER APPLICATION NUMBER: PA 1998 00936
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 480
TYPE: PRT
ORGANISM: Bacillus amyloliquefaciens
US-09-183-412-5

Query Match 100.0%; Score 2624; DB 3; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.8e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKLSQSDNGYGPYDLY 60
DB 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKLSQSDNGYGPYDLY 60
QY 61 DLGFEQOKGTVRTKYGTSKSLQDAISLSRNQYGVVNLNKAQADATEVTAVERN 120
DB 61 DLGFEQOKGTVRTKYGTSKSLQDAISLSRNQYGVVNLNKAQADATEVTAVERN 120
QY 121 ANRNOETSEBYOIKAMTDFRFPGRGNTYSDFKWMWHFPGADWDESRKISRIFKFGEGK 180
DB 121 ANRNOETSEBYOIKAMTDFRFPGRGNTYSDFKWMWHFPGADWDESRKISRIFKFGEGK 180
QY 181 AMWWEVSENGNDYLMYADVDDYDHPDVAETKKMGITWANELSLDGFRIIDAKHIKFSF 240
DB 181 AMWWEVSENGNDYLMYADVDDYDHPDVAETKKMGITWANELSLDGFRIIDAKHIKFSF 240
QY 241 LRDWVAVRQATGKEMFTVAEYQNNAGKLENTLNTSFNOSVFDPVPLHFNLOAASSQGG 300
DB 241 LRDWVAVRQATGKEMFTVAEYQNNAGKLENTLNTSFNOSVFDPVPLHFNLOAASSQGG 300
QY 301 GYDMRRLLDGTIVSRHEKAVTVEENHDTPQGSLESTVQTWKPLAYAFILTRREGYPO 360
DB 301 GYDMRRLLDGTIVSRHEKAVTVEENHDTPQGSLESTVQTWKPLAYAFILTRREGYPO 360
QY 361 VFYGDWYGTGTSKPEIPLSKDNIETPLKARKEAYGPOHDYIDHPDIVIGMTREGSSAA 420
DB 361 VFYGDWYGTGTSKPEIPLSKDNIETPLKARKEAYGPOHDYIDHPDIVIGMTREGSSAA 420
QY 421 KSGLAALITDGPQGSKRYAGLKNAGETWYDITGNRSYTYKISDGGGEHFVNDGSYSIY 480
DB 421 KSGLAALITDGPQGSKRYAGLKNAGETWYDITGNRSYTYKISDGGGEHFVNDGSYSIY 480

RESULT 5
US-09-290-734-5
Sequence 5, Application US/09290734
Patent No. 6361989
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
APPLICANT: Bisgaard-Frantzen Henrik
APPLICANT: Oultup, Helle
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Hoeck, Lisbeth Hedegaard
TITLE OF INVENTION: No. 6361989e1 -Amylase And -Amylase Mutants
FILE REFERENCE: 5276.400-US
CURRENT APPLICATION NUMBER: US/09/290,734
CURRENT FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 480
TYPE: PRT
ORGANISM: B. amyloliquefaciens
US-09-290-734-5

Query Match 100.0%; Score 2624; DB 4; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.8e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKLSQSDNGYGPYDLY 60
DB 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKLSQSDNGYGPYDLY 60
QY 61 DLGFEQOKGTVRTKYGTSKSLQDAISLSRNQYGVVNLNKAQADATEVTAVERN 120
DB 61 DLGFEQOKGTVRTKYGTSKSLQDAISLSRNQYGVVNLNKAQADATEVTAVERN 120
QY 121 ANRNOETSEBYOIKAMTDFRFPGRGNTYSDFKWMWHFPGADWDESRKISRIFKFGEGK 180
DB 121 ANRNOETSEBYOIKAMTDFRFPGRGNTYSDFKWMWHFPGADWDESRKISRIFKFGEGK 180
QY 181 AMWWEVSENGNDYLMYADVDDYDHPDVAETKKMGITWANELSLDGFRIIDAKHIKFSF 240
DB 181 AMWWEVSENGNDYLMYADVDDYDHPDVAETKKMGITWANELSLDGFRIIDAKHIKFSF 240
QY 241 LRDWVAVRQATGKEMFTVAEYQNNAGKLENTLNTSFNOSVFDPVPLHFNLOAASSQGG 300
DB 241 LRDWVAVRQATGKEMFTVAEYQNNAGKLENTLNTSFNOSVFDPVPLHFNLOAASSQGG 300
QY 301 GYDMRRLLDGTIVSRHEKAVTVEENHDTPQGSLESTVQTWKPLAYAFILTRREGYPO 360
DB 301 GYDMRRLLDGTIVSRHEKAVTVEENHDTPQGSLESTVQTWKPLAYAFILTRREGYPO 360
QY 361 VFYGDWYGTGTSKPEIPLSKDNIETPLKARKEAYGPOHDYIDHPDIVIGMTREGSSAA 420
DB 361 VFYGDWYGTGTSKPEIPLSKDNIETPLKARKEAYGPOHDYIDHPDIVIGMTREGSSAA 420
QY 421 KSGLAALITDGPQGSKRYAGLKNAGETWYDITGNRSYTYKISDGGGEHFVNDGSYSIY 480
DB 421 KSGLAALITDGPQGSKRYAGLKNAGETWYDITGNRSYTYKISDGGGEHFVNDGSYSIY 480

RESULT 5
US-09-672-459-4
Sequence 4, Application US/09672459
Patent No. 6436888
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/672,459
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 480
TYPE: PRT
ORGANISM: Bacillus amyloliquefaciens
US-09-672-459-4

Query Match 100.0%; Score 2624; DB 4; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.8e-230; Indels 0; Gaps 0;
Matches 480; Conservative 0; Mismatches 0;

QY 1 VNGTLMQYFEMWTPNDQGMKRLQNDABHLSDIGITAWIPPAVKGLSGSDNGYGYDLY 60
DB 1 VNGTLMQYFEMWTPNDQGMKRLQNDABHLSDIGITAWIPPAVKGLSGSDNGYGYDLY 60

QY 61 DLGEFOQKGVTRTKYKTSKSELQDAIGLSHRNVQYGVVLNHKAQADATEDVTAVERN 120
DB 61 DLGEFOQKGVTRTKYKTSKSELQDAIGLSHRNVQYGVVLNHKAQADATEDVTAVERN 120

QY 121 ANRNOETSEEVQIKAMTDFRFGNGNTYSDFKMWHYHDGADWDESKRISIRIFKRGEGK 180
DB 121 ANRNOETSEEVQIKAMTDFRFGNGNTYSDFKMWHYHDGADWDESKRISIRIFKRGEGK 180

QY 181 AMDWEVSSSENGNYDYLMTADVDYDHPDVAAETKKGIIWYANELSLDGRFRIIDAAHIXFSF 240
DB 181 AMDWEVSSSENGNYDYLMTADVDYDHPDVAAETKKGIIWYANELSLDGRFRIIDAAHIXFSF 240

QY 241 LRDWVOAARQATGKEMFTVAEYWNNAKLENYLNKTSFNOSVDPVLFHNLQAASSQGG 300
DB 241 LRDWVOAARQATGKEMFTVAEYWNNAKLENYLNKTSFNOSVDPVLFHNLQAASSQGG 300

QY 301 GYDMRRLDGTIVSSHPEKAVTFVENHDTQPGQSLESTVQTFKPLAVALITRESGYPQ 360
DB 301 GYDMRRLDGTIVSSHPEKAVTFVENHDTQPGQSLESTVQTFKPLAVALITRESGYPQ 360

QY 361 VFYGMWYGTGKTSPEIKSLKDNIEPIIKAREYAYGQOHYIDHPDVIQWTRREGSSAA 420
DB 361 VFYGMWYGTGKTSPEIKSLKDNIEPIIKAREYAYGQOHYIDHPDVIQWTRREGSSAA 420

QY 421 KSGLAALITDGPQSGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGWEFFHNDGVSIIY 480
DB 421 KSGLAALITDGPQSGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGWEFFHNDGVSIIY 480

RESULT 7
US-09-545-586-5
Sequence 5; Application US/09545586
Patent No. 6528298
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
APPLICANT: Bisgaard-Frantzen Henrik
APPLICANT: Cuistrup, Heile
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Hoeck, Lisbeth Hedegaard
TITLE OF INVENTION: No. 6528298-1 -Amylase And -Amylase Mutants
FILE REFERENCE: 5276.400-US
CURRENT APPLICATION NUMBER: US/09/545,586
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: US/09/290,734
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 480
TYPE: PRT
ORGANISM: B. amyloliquefaciens
US-09-545-586-5

Query Match 100.0%; Score 2624; DB 4; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.8e-230; Indels 0; Gaps 0;
Matches 480; Conservative 0; Mismatches 0;

QY 1 VNGTLMQYFEMWTPNDQGMKRLQNDABHLSDIGITAWIPPAVKGLSGSDNGYGYDLY 60
DB 1 VNGTLMQYFEMWTPNDQGMKRLQNDABHLSDIGITAWIPPAVKGLSGSDNGYGYDLY 60

QY 61 DLGEFOQKGVTRTKYKTSKSELQDAIGLSHRNVQYGVVLNHKAQADATEDVTAVERN 120
DB 61 DLGEFOQKGVTRTKYKTSKSELQDAIGLSHRNVQYGVVLNHKAQADATEDVTAVERN 120

QY 61 DLGEFOQKGVTRTKYKTSKSELQDAIGLSHRNVQYGVVLNHKAQADATEDVTAVERN 120
DB 61 DLGEFOQKGVTRTKYKTSKSELQDAIGLSHRNVQYGVVLNHKAQADATEDVTAVERN 120

QY 121 ANRNOETSEEVQIKAMTDFRFGNGNTYSDFKMWHYHDGADWDESKRISIRIFKRGEGK 180
DB 121 ANRNOETSEEVQIKAMTDFRFGNGNTYSDFKMWHYHDGADWDESKRISIRIFKRGEGK 180

QY 181 AMDWEVSSSENGNYDYLMTADVDYDHPDVAAETKKGIIWYANELSLDGRFRIIDAAHIXFSF 240
DB 181 AMDWEVSSSENGNYDYLMTADVDYDHPDVAAETKKGIIWYANELSLDGRFRIIDAAHIXFSF 240

QY 241 LRDWVOAARQATGKEMFTVAEYWNNAKLENYLNKTSFNOSVDPVLFHNLQAASSQGG 300
DB 241 LRDWVOAARQATGKEMFTVAEYWNNAKLENYLNKTSFNOSVDPVLFHNLQAASSQGG 300

QY 301 GYDMRRLDGTIVSSHPEKAVTFVENHDTQPGQSLESTVQTFKPLAVALITRESGYPQ 360
DB 301 GYDMRRLDGTIVSSHPEKAVTFVENHDTQPGQSLESTVQTFKPLAVALITRESGYPQ 360

QY 361 VFYGMWYGTGKTSPEIKSLKDNIEPIIKAREYAYGQOHYIDHPDVIQWTRREGSSAA 420
DB 361 VFYGMWYGTGKTSPEIKSLKDNIEPIIKAREYAYGQOHYIDHPDVIQWTRREGSSAA 420

QY 421 KSGLAALITDGPQSGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGWEFFHNDGVSIIY 480
DB 421 KSGLAALITDGPQSGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGWEFFHNDGVSIIY 480

RESULT 8
US-10-186-042-4
Sequence 4; Application US/10186042
Patent No. 6642044
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/186,042
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 480
TYPE: PRT
ORGANISM: Bacillus amyloliquefaciens
US-10-186-042-4

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Best Local Similarity 100.0%; Pred. No. 3.8e-230; Indels 0; Gaps 0;
Matches 480; Conservative 0; Mismatches 0;

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RESULT 9
US-09-769-864-5
; Sequence 5, Application US/09769864
; Patent No. 6673589
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-amylase Mutants
; FILE REFERENCE: 5368-200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Bacillus amyloliquifaciens
US-09-769-864-5

Query Match 100.0%; Score 2624; DB 4; Length 480;
Best Local Similarity 100.0%; Pred. No. 3,8e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKGLSQSDNGYGPYDLY 60
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Db 361 VFYGDWYGTGKTSPEKIPSLKONIEPIILKARKEVAYGPOHDYIDHPDYIGMTREGDSAA 420
Qy 421 KSGLAALITDGPQGSKRYAGLKNAGETWYDITGNRSDTVKIGSDGWSGFHVNDGSVSIY 480
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; Sequence 16, Application US/09291023A
; Patent No. 6303871
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
; FILE REFERENCE: 5821-010-US
; CURRENT APPLICATION NUMBER: US/09/291,023A
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: DK 1999 00438
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentn version 3.0
; SEQ ID NO 16
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus
US-09-291-023A-16

Query Match 100.0%; Score 2624; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 3,8e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 DLGEFOOKGTIVRTKYGTSKSELQDAIGLSHRNVQYGVVNLHKGADATEDEVTAVERNVP 120
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Db 181 AMDWEVSSSENGNYDYLMYADVDYDHPDYVAETKKGIVANELSLDGRIDAAKIKFSF 240
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Db 241 LRDWVAOAVQATGKEMFTVAEYVONNAGKLENTLNTKTSFNQSVFDPVLFHNLQAASSQGG 300
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Db 301 GYDMERLLDGTIVSSRHPKAVTFVENHDTOPGQSLSTVQWTFKPLAYAFILITRESGYPO 360
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RESULT 11
US-09-537-168-6
; Sequence 6, Application US/09537168
; Patent No. 6410295
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/09/537,168
; EARLIER FILING DATE: 2000-03-29
; EARLIER APPLICATION NUMBER: PA 1999 00437
; EARLIER FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: 60/127,427
; EARLIER FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 483
; TYPE: PRF
; ORGANISM: Bacillus amyloliquefaciens
US-09-537-168-6

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Best Local Similarity 100.0%; Pred. No. 3.8e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; APPLICANT: IGARASHI, Kazuaki
; APPLICANT: HAYASHI, Hiroshi
; APPLICANT: HAYASHI, Yasunori
; APPLICANT: ARAKI, Hiroyuki
; APPLICANT: OZAKI, Katsuya
; TITLE OF INVENTION: MUTANT ALPHA-AMYLASES
; FILE REFERENCE: 2173-0115P
; CURRENT APPLICATION NUMBER: US/09/381,687
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 483
; TYPE: PRF
; ORGANISM: B. amyloliquefaciens
US-09-381-687-6

Query Match      100.0%; Score 2624; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.8e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
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; Sequence 16, Application US/09540715A
; Patent No. 6623948
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Videke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic Ac
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/540,715A
; EARLIER FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: 09/291,023
; EARLIER FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0

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Page 7

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,610
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowrey Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-610-4

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Best Local Similarity 100.0%; Pred. No. 4.2e-230;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Job time: 17.2492 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:33:58 ; Search time 37.3731 Seconds

(without alignments)
3560.078 Million cell updates/sec

Title: US-10-644-187-4

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Gapop 10.0, Gapext 0.5

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Total number of hits satisfying chosen parameters: 1136120

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Published Applications AA:
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2: /cgn2_6/prodata/2/pubppa/PCR_NEW_PUB.pep:*
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SUMMARIES

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2	2624	100.0	480	12 US-10-665-667-5	Sequence 5, Appl1
3	2624	100.0	480	12 US-10-644-187-4	Sequence 4, Appl1
4	2624	100.0	480	12 US-10-327-837-5	Sequence 5, Appl1
5	2624	100.0	480	14 US-10-186-042-4	Sequence 4, Appl1
6	2624	100.0	483	9 US-09-854-346-10	Sequence 10, Appl1
7	2624	100.0	483	9 US-09-918-543-10	Sequence 10, Appl1
8	2624	100.0	483	10 US-09-925-576C-10	Sequence 10, Appl1
9	2624	100.0	483	14 US-10-146-327-6	Sequence 6, Appl1
10	2624	100.0	514	14 US-10-184-771-4	Sequence 4, Appl1
11	2475	94.3	483	14 US-10-184-771-13	Sequence 13, Appl1
12	2190	83.5	481	14 US-10-146-327-2	Sequence 2, Appl1
13	2182	83.2	512	14 US-10-081-872-114	Sequence 114, App
14	2182	83.2	512	14 US-10-105-733-8	Sequence 8, Appl1
15	2182	83.2	512	14 US-10-081-739A-8	Sequence 8, Appl1

16	2182	83.2	512	15 US-10-385-305-114	Sequence 114, App
17	2176	82.9	512	14 US-10-199-922-2	Sequence 2, Appl1
18	2173	82.8	483	9 US-09-769-864-4	Sequence 4, Appl1
19	2173	82.8	483	9 US-09-854-346-8	Sequence 8, Appl1
20	2173	82.8	483	9 US-09-918-543-8	Sequence 8, Appl1
21	2173	82.8	483	9 US-09-918-543-30	Sequence 30, Appl1
22	2173	82.8	483	10 US-09-925-576C-8	Sequence 8, Appl1
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27	2173	82.8	483	14 US-10-186-042-2	Sequence 2, Appl1
28	2173	82.8	512	14 US-10-184-771-2	Sequence 2, Appl1
29	1921	73.2	513	14 US-10-081-872-146	Sequence 146, App
30	1921	73.2	513	15 US-10-385-305-146	Sequence 146, App
31	1919	73.1	513	14 US-10-081-872-70	Sequence 70, App
32	1919	73.1	513	15 US-10-385-305-70	Sequence 70, App
33	1911	72.8	478	14 US-10-081-872-166	Sequence 166, App
34	1911	72.8	478	15 US-10-385-305-166	Sequence 166, App
35	1863	71.0	485	9 US-09-769-864-2	Sequence 2, Appl1
36	1863	71.0	485	9 US-09-769-864-8	Sequence 8, Appl1
37	1863	71.0	485	9 US-09-854-346-4	Sequence 4, Appl1
38	1863	71.0	485	9 US-09-902-188A-2	Sequence 2, Appl1
39	1863	71.0	485	9 US-09-918-543-4	Sequence 4, Appl1
40	1863	71.0	485	9 US-09-795-211-2	Sequence 2, Appl1
41	1863	71.0	485	10 US-09-925-576C-4	Sequence 4, Appl1
42	1863	71.0	485	12 US-10-665-667-2	Sequence 2, Appl1
43	1863	71.0	485	12 US-10-665-667-8	Sequence 8, Appl1
44	1863	71.0	485	12 US-10-025-648-2	Sequence 2, Appl1
45	1863	71.0	485	12 US-10-327-837-2	Sequence 2, Appl1

ALIGNMENTS

```
RESULT 1
US-09-769-864-5
; Sequence 5, Application US/09769864
; Patent No. US20010039253A1
GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjørne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Søren
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5368.200-US
CURRENT APPLICATION NUMBER: US/09/769,864
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 480
TYPE: PRT
ORGANISM: Bacillus amyloliquifaciens
US-09-769-864-5

Query Match
Best Local Similarity 100.0%; Pred. No. 3.6e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMTNDGQHWRLONDAHLSDITLAWIIPAYKGISQSDNGYGPYDLY 60
DB 1 VNGTLMQYFEMTNDGQHWRLONDAHLSDITLAWIIPAYKGISQSDNGYGPYDLY 60
QY 61 DLGEQOQKGTATYKGTGSELODAIGSLHSRNVOGVVTLNKAQADATEDYAVEVNP 120
DB 61 DLGEQOQKGTATYKGTGSELODAIGSLHSRNVOGVVTLNKAQADATEDYAVEVNP 120
QY 121 ANRQETISEYQIAWTDFFPPGRGNTYSDPKWYHFDGADWDSEKISRIIFRBEQK 180
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Db 121 ANRNOETSEBYQIKAWTDFFRPGKNTYSDFKMWHYFDGADWDESRKISRIFKRGSG 180
Qy 181 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKKGIMWANELSLDGRIDAAGKIKFSF 240
Db 181 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKKGIMWANELSLDGRIDAAGKIKFSF 240
Qy 241 LRDWQAVRQATGKEMFTVAEYQONNAGKLENYLNTKTSFNOSVDFVPLHFNLOAASSOGG 300
Db 241 LRDWQAVRQATGKEMFTVAEYQONNAGKLENYLNTKTSFNOSVDFVPLHFNLOAASSOGG 300
Qy 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPQGSLESTVQTMFKPLAVAFILTRBSGYPO 360
Db 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPQGSLESTVQTMFKPLAVAFILTRBSGYPO 360
Qy 361 VFYGDWYGTGKTSPEIKSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRREGSSAA 420
Db 361 VFYGDWYGTGKTSPEIKSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRREGSSAA 420
Qy 421 KSGLAALITDGPQSGSKRMVAGIKNAGETWYDITGNRSPTVKIGSDGWGEFHVNDGSVSIY 480
Db 421 KSGLAALITDGPQSGSKRMVAGIKNAGETWYDITGNRSPTVKIGSDGWGEFHVNDGSVSIY 480
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RESULT 2

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US-10-665-667-5
; Sequence 5, Application US/10665667
; Publication No. US20040038368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5368-200-US
; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 480
; TYPE: PRF
; ORGANISM: Bacillus amyloliquefaciens
US-10-665-667-5
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Query Match 100.0%; Score 2624; DB 12; Length 480;

Best Local Similarity 100.0%; Pred. No. 3.6e-237; Indels 0; Gaps 0;

Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 VNGTLNQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAVWIPRAYKGLSGSDNGYGPYDLY 60
Db 1 VNGTLNQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAVWIPRAYKGLSGSDNGYGPYDLY 60
Qy 61 DLGEFOQKGVTRKTKYGTSELDQATGSLSRNVQYGVVNLHKKAGADTEDTVAEYVNP 120
Db 61 DLGEFOQKGVTRKTKYGTSELDQATGSLSRNVQYGVVNLHKKAGADTEDTVAEYVNP 120
Qy 121 ANRNOETSEBYQIKAWTDFFRPGKNTYSDFKMWHYFDGADWDESRKISRIFKRGSGK 180
Db 121 ANRNOETSEBYQIKAWTDFFRPGKNTYSDFKMWHYFDGADWDESRKISRIFKRGSGK 180
Qy 181 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKKGIMWANELSLDGRIDAAGKIKFSF 240
Db 181 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKKGIMWANELSLDGRIDAAGKIKFSF 240
Qy 241 LRDWQAVRQATGKEMFTVAEYQONNAGKLENYLNTKTSFNOSVDFVPLHFNLOAASSOGG 300
Db 241 LRDWQAVRQATGKEMFTVAEYQONNAGKLENYLNTKTSFNOSVDFVPLHFNLOAASSOGG 300
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Db 241 LRDWQAVRQATGKEMFTVAEYQONNAGKLENYLNTKTSFNOSVDFVPLHFNLOAASSOGG 300
Qy 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPQGSLESTVQTMFKPLAVAFILTRBSGYPO 360
Db 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPQGSLESTVQTMFKPLAVAFILTRBSGYPO 360
Qy 361 VFYGDWYGTGKTSPEIKSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRREGSSAA 420
Db 361 VFYGDWYGTGKTSPEIKSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRREGSSAA 420
Qy 421 KSGLAALITDGPQSGSKRMVAGIKNAGETWYDITGNRSPTVKIGSDGWGEFHVNDGSVSIY 480
Db 421 KSGLAALITDGPQSGSKRMVAGIKNAGETWYDITGNRSPTVKIGSDGWGEFHVNDGSVSIY 480
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RESULT 3

```
US-10-644-187-4
; Sequence 4, Application US/10644187
; Publication No. US20040048351A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796-204-US
; CURRENT APPLICATION NUMBER: US/10/644,187
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 480
; TYPE: PRF
; ORGANISM: Bacillus amyloliquefaciens
US-10-644-187-4
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Query Match 100.0%; Score 2624; DB 12; Length 480;

Best Local Similarity 100.0%; Pred. No. 3.6e-237; Indels 0; Gaps 0;

Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 VNGTLNQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAVWIPRAYKGLSGSDNGYGPYDLY 60
Db 1 VNGTLNQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAVWIPRAYKGLSGSDNGYGPYDLY 60
Qy 61 DLGEFOQKGVTRKTKYGTSELDQATGSLSRNVQYGVVNLHKKAGADTEDTVAEYVNP 120
Db 61 DLGEFOQKGVTRKTKYGTSELDQATGSLSRNVQYGVVNLHKKAGADTEDTVAEYVNP 120
Qy 121 ANRNOETSEBYQIKAWTDFFRPGKNTYSDFKMWHYFDGADWDESRKISRIFKRGSGK 180
Db 121 ANRNOETSEBYQIKAWTDFFRPGKNTYSDFKMWHYFDGADWDESRKISRIFKRGSGK 180
Qy 181 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKKGIMWANELSLDGRIDAAGKIKFSF 240
Db 181 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKKGIMWANELSLDGRIDAAGKIKFSF 240
Qy 241 LRDWQAVRQATGKEMFTVAEYQONNAGKLENYLNTKTSFNOSVDFVPLHFNLOAASSOGG 300
Db 241 LRDWQAVRQATGKEMFTVAEYQONNAGKLENYLNTKTSFNOSVDFVPLHFNLOAASSOGG 300
Qy 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPQGSLESTVQTMFKPLAVAFILTRBSGYPO 360
Db 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPQGSLESTVQTMFKPLAVAFILTRBSGYPO 360
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QY 361 VFYGMVGTGKTSPEIKSLKNDIPEILKARKEAYGPOHDIYDHPVIGTWTREGSSAA 420
DB 361 VFYGMVGTGKTSPEIKSLKNDIPEILKARKEAYGPOHDIYDHPVIGTWTREGSSAA 420
QY 421 KSGLAALITDGPSSKRYAGLKNAGETWYDITGNRSPTVYKIGSDGGEFFHVNDGSVSIY 480
DB 421 KSGLAALITDGPSSKRYAGLKNAGETWYDITGNRSPTVYKIGSDGGEFFHVNDGSVSIY 480

RESULT 4

US-10-327-837-5
; Sequence 5, Application US/10327837
; Publication No. US20030211958A1
GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgaard-Frantzen Henrik
; APPLICANT: Cuettrup, Heile
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
FILE REFERENCE: 5276.400-US
CURRENT APPLICATION NUMBER: US/10/327,837
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US/09/290,734
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 480
TYPE: PRT
ORGANISM: B. amylioliquefaciens
US-10-327-837-5

Query Match 100.0%; Score 2624; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.6e-237; Indels 0; Gaps 0;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMTYPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKGLSGSDNGYGPYDLY 60
DB 1 VNGTLMQYFEMTYPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKGLSGSDNGYGPYDLY 60
QY 61 DLGEFOQKGTVRKTYGKTSKSELQDAIGSLHSRNVQYGVVYLNHKAQADATEDVTAVEVNP 120
DB 61 DLGEFOQKGTVRKTYGKTSKSELQDAIGSLHSRNVQYGVVYLNHKAQADATEDVTAVEVNP 120
QY 121 ANRNOETSEERYQIKAMTDRFPGRGNTYSDPKMHWHPFGADMDSEKTSRIIFKFRGEK 180
DB 121 ANRNOETSEERYQIKAMTDRFPGRGNTYSDPKMHWHPFGADMDSEKTSRIIFKFRGEK 180
QY 181 AMDWEVSSSENGNDYLMYADVDDHPDVAETKMGIWYANELSLDGFRIIDAKHIKFSF 240
DB 181 AMDWEVSSSENGNDYLMYADVDDHPDVAETKMGIWYANELSLDGFRIIDAKHIKFSF 240
QY 241 LRDVQAVRQATGKEMFTVAEYQNNAGKLENTYLNKTSFNQSVFDPVPLHNLQAASSQGG 300
DB 241 LRDVQAVRQATGKEMFTVAEYQNNAGKLENTYLNKTSFNQSVFDPVPLHNLQAASSQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGQSLSESTVQWTWFKPLAFAFILLRESGYPQ 360
DB 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGQSLSESTVQWTWFKPLAFAFILLRESGYPQ 360
QY 361 VFYGMVGTGKTSPEIKSLKNDIPEILKARKEAYGPOHDIYDHPVIGTWTREGSSAA 420
DB 361 VFYGMVGTGKTSPEIKSLKNDIPEILKARKEAYGPOHDIYDHPVIGTWTREGSSAA 420
QY 421 KSGLAALITDGPSSKRYAGLKNAGETWYDITGNRSPTVYKIGSDGGEFFHVNDGSVSIY 480
DB 421 KSGLAALITDGPSSKRYAGLKNAGETWYDITGNRSPTVYKIGSDGGEFFHVNDGSVSIY 480

RESULT 5

US-10-186-042-4
; Sequence 4, Application US/10186042
; Publication No. US20030171236A1
GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/186,042
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 480
TYPE: PRT
ORGANISM: Bacillus amylioliquefaciens
US-10-186-042-4

Query Match 100.0%; Score 2624; DB 14; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.6e-237; Indels 0; Gaps 0;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMTYPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKGLSGSDNGYGPYDLY 60
DB 1 VNGTLMQYFEMTYPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKGLSGSDNGYGPYDLY 60
QY 61 DLGEFOQKGTVRKTYGKTSKSELQDAIGSLHSRNVQYGVVYLNHKAQADATEDVTAVEVNP 120
DB 61 DLGEFOQKGTVRKTYGKTSKSELQDAIGSLHSRNVQYGVVYLNHKAQADATEDVTAVEVNP 120
QY 121 ANRNOETSEERYQIKAMTDRFPGRGNTYSDPKMHWHPFGADMDSEKTSRIIFKFRGEK 180
DB 121 ANRNOETSEERYQIKAMTDRFPGRGNTYSDPKMHWHPFGADMDSEKTSRIIFKFRGEK 180
QY 181 AMDWEVSSSENGNDYLMYADVDDHPDVAETKMGIWYANELSLDGFRIIDAKHIKFSF 240
DB 181 AMDWEVSSSENGNDYLMYADVDDHPDVAETKMGIWYANELSLDGFRIIDAKHIKFSF 240
QY 241 LRDVQAVRQATGKEMFTVAEYQNNAGKLENTYLNKTSFNQSVFDPVPLHNLQAASSQGG 300
DB 241 LRDVQAVRQATGKEMFTVAEYQNNAGKLENTYLNKTSFNQSVFDPVPLHNLQAASSQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGQSLSESTVQWTWFKPLAFAFILLRESGYPQ 360
DB 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGQSLSESTVQWTWFKPLAFAFILLRESGYPQ 360
QY 361 VFYGMVGTGKTSPEIKSLKNDIPEILKARKEAYGPOHDIYDHPVIGTWTREGSSAA 420
DB 361 VFYGMVGTGKTSPEIKSLKNDIPEILKARKEAYGPOHDIYDHPVIGTWTREGSSAA 420
QY 421 KSGLAALITDGPSSKRYAGLKNAGETWYDITGNRSPTVYKIGSDGGEFFHVNDGSVSIY 480
DB 421 KSGLAALITDGPSSKRYAGLKNAGETWYDITGNRSPTVYKIGSDGGEFFHVNDGSVSIY 480

RESULT 6
US-09-854-346-10
; Sequence 10, Application US/09854346
; Patent No. US20020068352A1
GENERAL INFORMATION:

APPLICANT: No. US20020068352A1ozymes A/S
APPLICANT: Svendsen, Allan
APPLICANT: Jorgensen, Christel Thea
APPLICANT: Nielsen, Bjarne Ronfeldt
TITLE OF INVENTION: Alpha-amylose variants with altered 1,6 activity
FILE REFERENCE: 6140-200-US
CURRENT APPLICATION NUMBER: US/09/854,346
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus amyloliquefaciens
US-09-854-346-10

Query Match 100.0%; Score 2624; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No.: 3.6e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPPAKGLSGSDNGYGYDLY 60
DB 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPPAKGLSGSDNGYGYDLY 60
QY 61 DLGEFOQKGTIVRTKYGKSELQDAIGSLHSRNVOYGVVNLHKAADATEDVTAVERN 120
DB 61 DLGEFOQKGTIVRTKYGKSELQDAIGSLHSRNVOYGVVNLHKAADATEDVTAVERN 120
QY 121 ANRQETSEEEYQIKAWMDFFRPGRGNTYSDPKMWHYFDGADWDESKRISIRIFRGECK 180
DB 121 ANRQETSEEEYQIKAWMDFFRPGRGNTYSDPKMWHYFDGADWDESKRISIRIFRGECK 180
QY 181 AMDWEVSENGNYDLYMADVDYDHPDVVAETKKGIMYANELSLDGFRIIDAKHIFSF 240
DB 181 AMDWEVSENGNYDLYMADVDYDHPDVVAETKKGIMYANELSLDGFRIIDAKHIFSF 240
QY 241 LRDWQAVROATGKEMFTVAEYQWQNAKLENYLNKTSFNOSVDPVPLHFNLOAASSQGG 300
DB 241 LRDWQAVROATGKEMFTVAEYQWQNAKLENYLNKTSFNOSVDPVPLHFNLOAASSQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGQSLESTVQTFWFLAYAFILTRSGYPQ 360
DB 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGQSLESTVQTFWFLAYAFILTRSGYPQ 360
QY 361 VFYGMVGTGKTSPEIPLSKDNIEPIIKARKEVAYGQHDYIDHPVIGWTRGDSAA 420
DB 361 VFYGMVGTGKTSPEIPLSKDNIEPIIKARKEVAYGQHDYIDHPVIGWTRGDSAA 420
QY 421 KSGLAALITDGPQSKRYAGLKNAGETWYDITGNRSPTVKIGSDGWEFFVNDGSYIY 480
DB 421 KSGLAALITDGPQSKRYAGLKNAGETWYDITGNRSPTVKIGSDGWEFFVNDGSYIY 480

RESULT 7
US-09-918-543-10
Sequence 10, Application US/09918543
Patent No. US20020155574A1
GENERAL INFORMATION:
APPLICANT: No. US20020155574A1ozymes A/S
APPLICANT: Thisted, Thomas
APPLICANT: Kjaerulf, Soren
APPLICANT: Andersen, Carsten
APPLICANT: Fuglsang, Claus Crone
TITLE OF INVENTION: Alpha-amylose mutants with altered properties
FILE REFERENCE: 10062-200-US
CURRENT APPLICATION NUMBER: US/09/918,543
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus amyloliquefaciens

US-09-918-543-10

Query Match 100.0%; Score 2624; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No.: 3.6e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPPAKGLSGSDNGYGYDLY 60
DB 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPPAKGLSGSDNGYGYDLY 60
QY 61 DLGEFOQKGTIVRTKYGKSELQDAIGSLHSRNVOYGVVNLHKAADATEDVTAVERN 120
DB 61 DLGEFOQKGTIVRTKYGKSELQDAIGSLHSRNVOYGVVNLHKAADATEDVTAVERN 120
QY 121 ANRQETSEEEYQIKAWMDFFRPGRGNTYSDPKMWHYFDGADWDESKRISIRIFRGECK 180
DB 121 ANRQETSEEEYQIKAWMDFFRPGRGNTYSDPKMWHYFDGADWDESKRISIRIFRGECK 180
QY 181 AMDWEVSENGNYDLYMADVDYDHPDVVAETKKGIMYANELSLDGFRIIDAKHIFSF 240
DB 181 AMDWEVSENGNYDLYMADVDYDHPDVVAETKKGIMYANELSLDGFRIIDAKHIFSF 240
QY 241 LRDWQAVROATGKEMFTVAEYQWQNAKLENYLNKTSFNOSVDPVPLHFNLOAASSQGG 300
DB 241 LRDWQAVROATGKEMFTVAEYQWQNAKLENYLNKTSFNOSVDPVPLHFNLOAASSQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGQSLESTVQTFWFLAYAFILTRSGYPQ 360
DB 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGQSLESTVQTFWFLAYAFILTRSGYPQ 360
QY 361 VFYGMVGTGKTSPEIPLSKDNIEPIIKARKEVAYGQHDYIDHPVIGWTRGDSAA 420
DB 361 VFYGMVGTGKTSPEIPLSKDNIEPIIKARKEVAYGQHDYIDHPVIGWTRGDSAA 420
QY 421 KSGLAALITDGPQSKRYAGLKNAGETWYDITGNRSPTVKIGSDGWEFFVNDGSYIY 480
DB 421 KSGLAALITDGPQSKRYAGLKNAGETWYDITGNRSPTVKIGSDGWEFFVNDGSYIY 480

RESULT 8
US-09-925-576C-10
Sequence 10, Application US/09925576C
Publication No. US20030129718A1
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Borchert, Torben Vedel
APPLICANT: Nielsen, Bjarne Ronfeldt
TITLE OF INVENTION: Amylase Variants
FILE REFERENCE: 10004-204-US
CURRENT APPLICATION NUMBER: US/09/925,576C
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus amyloliquefaciens
US-09-925-576C-10

Query Match 100.0%; Score 2624; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No.: 3.6e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPPAKGLSGSDNGYGYDLY 60
DB 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPPAKGLSGSDNGYGYDLY 60
QY 61 DLGEFOQKGTIVRTKYGKSELQDAIGSLHSRNVOYGVVNLHKAADATEDVTAVERN 120
DB 61 DLGEFOQKGTIVRTKYGKSELQDAIGSLHSRNVOYGVVNLHKAADATEDVTAVERN 120
QY 121 ANRQETSEEEYQIKAWMDFFRPGRGNTYSDPKMWHYFDGADWDESKRISIRIFRGECK 180
DB 121 ANRQETSEEEYQIKAWMDFFRPGRGNTYSDPKMWHYFDGADWDESKRISIRIFRGECK 180

Db 121 ANRQETSEBYQIKAWTDFFPPGRGNTYSDFKMHWHFDGADWDESRKISIFKFEGBK 180
Qy 181 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKMGIMYANELSLDGRIDAAGHIFSF 240
Db 181 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKMGIMYANELSLDGRIDAAGHIFSF 240
Qy 241 LRDWQAVROATGKEMFTVAEYQWONNAGKLENTLNTKTSFNOSVDFVPLHFNLOAASSOGG 300
Db 241 LRDWQAVROATGKEMFTVAEYQWONNAGKLENTLNTKTSFNOSVDFVPLHFNLOAASSOGG 300
Qy 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGOSLESTVQWTFKPLAFAFLITRESGPQ 360
Db 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGOSLESTVQWTFKPLAFAFLITRESGPQ 360
Qy 361 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRBGSSAA 420
Db 361 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRBGSSAA 420
Qy 421 KSGLAALITDGGGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGGEFFHNDGSVSIY 480
Db 421 KSGLAALITDGGGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGGEFFHNDGSVSIY 480

RESULT 9

US-10-146-327-6
Sequence 6, Application US/10146327
Publication No. US20030044954A1
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Jorgensen, Christel T.
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Kjaerulff, Soren
TITLE OF INVENTION: Alpha-Amylase Variants
FILE REFERENCE: 5886.280-US
CURRENT APPLICATION NUMBER: US/10/146,327
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: US/09/537,168
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: PA 1999 00437
PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: 60/127,427
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus amyloliquefaciens
US-10-146-327-6

Query Match 100.0%; Score 2624; DB 14; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.6e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKGLSOSDNGYGYDLY 60
Db 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKGLSOSDNGYGYDLY 60
Qy 61 DLGEFOOKGTVRTKYGKSELQDAIGLSHRNVQYGVVYLNHKAAGADATEDVTAVERN 120
Db 61 DLGEFOOKGTVRTKYGKSELQDAIGLSHRNVQYGVVYLNHKAAGADATEDVTAVERN 120
Qy 121 ANRQETSEBYQIKAWTDFFPPGRGNTYSDFKMHWHFDGADWDESRKISIFKFEGBK 180
Db 121 ANRQETSEBYQIKAWTDFFPPGRGNTYSDFKMHWHFDGADWDESRKISIFKFEGBK 180
Qy 181 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKMGIMYANELSLDGRIDAAGHIFSF 240
Db 181 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKMGIMYANELSLDGRIDAAGHIFSF 240
Qy 241 LRDWQAVROATGKEMFTVAEYQWONNAGKLENTLNTKTSFNOSVDFVPLHFNLOAASSOGG 300
Db 241 LRDWQAVROATGKEMFTVAEYQWONNAGKLENTLNTKTSFNOSVDFVPLHFNLOAASSOGG 300

Db 241 LRDWQAVROATGKEMFTVAEYQWONNAGKLENTLNTKTSFNOSVDFVPLHFNLOAASSOGG 300
Qy 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGOSLESTVQWTFKPLAFAFLITRESGPQ 360
Db 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGOSLESTVQWTFKPLAFAFLITRESGPQ 360
Qy 361 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRBGSSAA 420
Db 361 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRBGSSAA 420
Qy 421 KSGLAALITDGGGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGGEFFHNDGSVSIY 480
Db 421 KSGLAALITDGGGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGGEFFHNDGSVSIY 480

RESULT 10

US-10-184-771-4
Sequence 4, Application US/10184771
Publication No. US20030170769A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/10/184,771
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 514
TYPE: PRT
ORGANISM: B. amyloliquefaciens
US-10-184-771-4

Query Match 100.0%; Score 2624; DB 14; Length 514;
Best Local Similarity 100.0%; Pred. No. 4e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKGLSOSDNGYGYDLY 60
Db 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIIPRAYKGLSOSDNGYGYDLY 60
Qy 61 DLGEFOOKGTVRTKYGKSELQDAIGLSHRNVQYGVVYLNHKAAGADATEDVTAVERN 120
Db 61 DLGEFOOKGTVRTKYGKSELQDAIGLSHRNVQYGVVYLNHKAAGADATEDVTAVERN 120
Qy 92 DLGEFOOKGTVRTKYGKSELQDAIGLSHRNVQYGVVYLNHKAAGADATEDVTAVERN 151
Db 92 DLGEFOOKGTVRTKYGKSELQDAIGLSHRNVQYGVVYLNHKAAGADATEDVTAVERN 151
Qy 121 ANRQETSEBYQIKAWTDFFPPGRGNTYSDFKMHWHFDGADWDESRKISIFKFEGBK 180
Db 121 ANRQETSEBYQIKAWTDFFPPGRGNTYSDFKMHWHFDGADWDESRKISIFKFEGBK 180
Qy 181 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKMGIMYANELSLDGRIDAAGHIFSF 240
Db 181 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKMGIMYANELSLDGRIDAAGHIFSF 240
Qy 212 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKMGIMYANELSLDGRIDAAGHIFSF 271
Db 212 AMDWEVSSENGNDYLMYADVDYDHPDVVAETKMGIMYANELSLDGRIDAAGHIFSF 271
Qy 241 LRDWQAVROATGKEMFTVAEYQWONNAGKLENTLNTKTSFNOSVDFVPLHFNLOAASSOGG 300
Db 241 LRDWQAVROATGKEMFTVAEYQWONNAGKLENTLNTKTSFNOSVDFVPLHFNLOAASSOGG 300
Qy 272 LRDWQAVROATGKEMFTVAEYQWONNAGKLENTLNTKTSFNOSVDFVPLHFNLOAASSOGG 331
Db 272 LRDWQAVROATGKEMFTVAEYQWONNAGKLENTLNTKTSFNOSVDFVPLHFNLOAASSOGG 331
Qy 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGOSLESTVQWTFKPLAFAFLITRESGPQ 360
Db 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGOSLESTVQWTFKPLAFAFLITRESGPQ 360
Qy 332 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGOSLESTVQWTFKPLAFAFLITRESGPQ 391
Db 332 GYDMRRLDGTIVSRHPEKAVTFVENHDTOPGOSLESTVQWTFKPLAFAFLITRESGPQ 391
Qy 361 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRBGSSAA 420
Db 361 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRBGSSAA 420
Qy 392 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRBGSSAA 451
Db 392 VFYGDWYGTGKTSPEKIPSLKDNIEPILKARKEVAYGQHDYIDHPDVIQWTRBGSSAA 451
Qy 421 KSGLAALITDGGGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGGEFFHNDGSVSIY 480
Db 421 KSGLAALITDGGGSKRYAGLKNAGETWYDITGNRSPTVKIGSDGGEFFHNDGSVSIY 480

Page 7

Query Match	83.2%;	Score 2182;	DB 14;	Length 512;
Best Local Similarity	80.8%;	Pred. No. 1.2e-195;		
Matches 388;	Conservative 42;	Mismatches 48;	Indels 2;	Gaps 1

```

PRIORITY APPLICATION NUMBER: 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/291,122
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 512
TYPE: PR1
ORGANISM: Environmental
US-10-105-733-8

Query Match      83.2%; Score 2182; DB 14; Length 512;
Best Local Similarity 80.8%; Pred. No. 1,2e-195;
Matches 388; Conservative 42; Mismatches 48; Indels 2; Gaps 1

QY 1 VNGTLMQYEWMTPTPDGQHMTRCLNDCEHLSDIGITAWTIPRAYKLSGSDNGYGPDY 60
DB 32 LNTTLMQYEWMTPTPDGQHMTRCLNDCEHLSDIGITAWTIPRAYKLSGSDNGYGPDY 91
QY 61 DLGEFOOKGTAVTKYGTGSELDQAIIGSLHSNVAQYGVVLLNKAQADATEDVTAVERN 120
DB 92 DLGEFHQGTAVTKYGTGSELDQAIIGSLHSNVAQYGVVLLNKAQADATEDVTAVERN 151
QY 121 ANRNOTSEBYQIKAWTDFRPPGNGNTYSDPKMWTMFPDQADMBDESRKLSRIKPKGEQK 180
DB 152 ADNRRYISEBHIKAWTHFHPFGKSTYSDPKMWTMFPDQADMBDESRKLSRIKPK- 209
QY 181 AMDMVESSENGVADYLMADVDYDHPDVVAETKMGIMVANELSLDGFRIIDAKHIKESF 240
DB 210 AMDMVESSENGVADYLMADVDYDHPDVVAETKMGIMVANELSLDGFRIIDAVGHIKESF 269
QY 241 LRDWVAQVFAQTGKEMFTVAEYWNNAKLENTYLNKTSFPOSYFVDVLEHNLQAASSQGG 300
DB 270 LRDWVAHVAEKTGKEMFTVAEYWNQNDLGALENYLNKTNFHSVFDVPLHQFHAASTQGG 329
QY 301 GYMERLLDGTAVVSRPEKAVTFVENHDTQPGQSLSESTVQTFWFKPLAFAILTRBSGYPO 360
DB 330 GYMERLLDGTAVVSRPEKAVTFVENHDTQPGQSLSESTVQTFWFKPLAFAILTRBSGYPO 389
QY 361 VFYGDWMTGKTGSPKEIPSLKDNIEPIIKAREYAYGQCHDYIDHPVYIGMTRBSGSSAA 420
DB 390 VFYGDWMTGKTGSDREIIPALPKHIIPIILAKQYAYGQCHDYIDHPVYIGMTRBSGSSAA 449
QY 421 KSGLAALITDPPGSGSRMAYGKNNGETMYDITGSRSPYVIGSGDWGEFHWVDSVSIY 480
DB 450 NSGLAALITDPPGSGSRMAYGKNNGETMYDITGSRSEPVYINSGGEFHWVDSVSIY 509

RESULT 15
US-10-081-739A-8
Sequence 8, Application US/10081739A
Publicatlon No. US20030170634A1
GENERAL INFORMATION:
APPLICANT: Callen, Walter
APPLICANT: Richardson, Toby
APPLICANT: Frey, Gerhard
APPLICANT: Miller, Carl
APPLICANT: Kazaoka, Martin
APPLICANT: Short, Uay
APPLICANT: Machut, Eric
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
TITLE OF INVENTION: AND METHODS OF USE THEREOF
FILE REFERENCE: 09010-107001
CURRENT APPLICATION NUMBER: US/10/081,739A
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/270,495
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/291,122
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 69

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SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 512
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Obtained from an environmental sample
US-10-081-739A-8

Query Match 83.2%; Score 2182; DB 14; Length 512;

Beet Local Similarity 80.8%; Pred. No. 1.2e-195;
Matches 388; Conservative 42; Mismatches 46; Indels 2; Gaps 1;

```
QY 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGTAVWIPPAYKGLSQSDNGYGYDLY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 32 LNTGLMQYFEMWTPNDGQHWKRLQNDASAYLAHGITAVWIPPAYKGLSQADVGAYDLY 91
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 DLGEFQKGTVRTKXTGTSLELDAIGSIHSRNVOYGGVVLNKKAGADATEDVTAVEVP 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 92 DLGEFHQKGTVRTKXTGTSLELQSAIKLSHRDINVGVDVNLNKKAGADATEDVTAVEVP 151
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 ANRNOETSEEOIKAMTDFRFPGRGNTYSDFKWHYHFDGADWDESRKISRIFKRGEGK 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 152 ADRNRVIGSEHRIKAMTHHFPGRGSTYSDFKWHYHFDGTDWDESRKLNRIYKF--QK 209
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 181 AMDMEVSSRNQNDYLTADVDYDHPDYVAETKKGITWANELSLDGSPRIDAAKHKESF 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 210 AMDMEVSSRNQNDYLTADVDYDHPDYVAETKKGITWANELSLDGSPRIDAAKHKESF 269
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 241 LEDWQAVQATGKEMFTVAEYQNNAGKLENYLNKTSFNOSVFPDPLHFNLOAASQGG 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 270 LEDWQAVQATGKEMFTVAEYQNNAGKLENYLNKTSFNOSVFPDPLHFNLOAASQGG 329
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLESTVQTFKPLAYAFILITRESGYPQ 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 330 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLESTVQTFKPLAYAFILITRESGYPQ 389
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPOHDYIDHPDVLGWTREGSSAA 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 390 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEVAYGPOHDYIDHPDVLGWTREGSSAA 449
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 421 KSGLAALLITDGPQSGKRMATAGLKNAGETWYDITGNRSDTVKIGSDMGSEFHNDSVSIY 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 450 KSGLAALLITDGPQSGKRMATAGLKNAGETWYDITGNRSDTVKIGSDMGSEFHNDSVSIY 509
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

Search completed: May 3, 2004, 20:47:46
JOB time : 38.3731 sec

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:29:27 ; Search time 16.3507 Seconds
(without alignments)
1525.031 Million cell updates/sec

Title: US-10-644-187-2
Perfect score: 2666
Sequence: 1 ANLNGTLMQYFWMYPMNDGQ.....SEGWGEFHNQGSVSIYVR 483
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCCTS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2666	100.0	483	3	US-09-182-859-2
2	2666	100.0	483	3	US-09-170-670-4
3	2666	100.0	483	3	US-09-193-068-4
4	2666	100.0	483	3	US-09-183-413-4
5	2666	100.0	483	3	US-09-264-097-2
6	2666	100.0	483	3	US-09-291-023A-21
7	2666	100.0	483	4	US-09-290-734-4
8	2666	100.0	483	4	US-09-537-168-4
9	2666	100.0	483	4	US-09-672-459-2
10	2666	100.0	483	4	US-09-545-586-4
11	2666	100.0	483	4	US-09-540-715A-21
12	2666	100.0	483	4	US-10-186-042-2
13	2666	100.0	483	4	US-09-769-864-4
14	2666	100.0	512	1	US-08-720-899-2
15	2666	100.0	512	1	US-08-459-610-2
16	2666	100.0	512	2	US-08-343-804-2
17	2666	100.0	512	2	US-08-687-399-2
18	2666	100.0	512	2	US-08-600-908A-2
19	2666	100.0	512	2	US-08-683-838A-2
20	2666	100.0	512	4	US-09-636-252A-2
21	2666	100.0	631	3	US-08-814-052-8
22	2666	100.0	631	3	US-08-812-829-8
23	2663	99.9	483	1	US-08-468-700-34
24	2663	99.9	483	2	US-08-468-220-32
25	2663	99.9	483	2	US-08-468-698-32
26	2663	99.9	483	2	US-08-704-706A-34
27	2663	99.9	483	3	US-08-890-383-3

28	2663	99.9	483	3	US-08-914-679A-3	Sequence 3, Appli
29	2663	99.9	483	3	US-08-985-659-35	Sequence 35, Appl
30	2663	99.9	483	3	US-08-194-664A-32	Sequence 32, Appl
31	2663	99.9	483	5	PCT-US94-01553A-32	Sequence 32, Appl
32	2663	99.9	483	5	PCT-US95-10426-32	Sequence 32, Appl
33	2663	99.9	487	2	US-08-468-220-37	Sequence 37, Appl
34	2663	99.9	487	2	US-08-468-698-37	Sequence 37, Appl
35	2663	99.9	487	2	US-08-194-664A-37	Sequence 37, Appl
36	2663	99.9	487	5	PCT-US94-01553A-37	Sequence 37, Appl
37	2663	99.9	487	5	PCT-US95-10426-37	Sequence 37, Appl
38	2663	99.9	512	1	US-07-623-953-3	Sequence 3, Appli
39	2663	99.9	512	1	US-07-623-953-3	Sequence 5, Appli
40	2663	99.9	512	3	US-08-985-659-34	Sequence 34, Appl
41	2657	99.7	483	2	US-08-468-220-36	Sequence 36, Appl
42	2657	99.7	483	2	US-08-468-698-36	Sequence 36, Appl
43	2657	99.7	483	3	US-08-194-664A-36	Sequence 36, Appl
44	2657	99.7	483	5	PCT-US94-01553A-36	Sequence 36, Appl
45	2657	99.7	483	5	PCT-US95-10426-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-09-182-859-2
Sequence 2, Application US/09182859
Patent No. 6143708
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borcherdt, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Rmylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT FILING DATE: 1998-10-29
EARLIER FILING DATE: 1998-10-29
EARLIER FILING DATE: 1996-04-30
EARLIER FILING DATE: 1996-06-28/96
EARLIER FILING DATE: 1996-07-11/96
EARLIER FILING DATE: 1996-07-11/96
EARLIER FILING DATE: 1996-07-11/96
EARLIER FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-09-182-859-2
Query Match 100.0%; Score 2666; DB 3; Length 483;
Best Local Similarity 100.0%; Pred NO. 2.9e-240; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0

1 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
2 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
3 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
4 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
5 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
6 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
7 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
8 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
9 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
10 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
11 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
12 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
13 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
14 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
15 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
16 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
17 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
18 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
19 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
20 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
21 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
22 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
23 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
24 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
25 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
26 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60
27 ANLNGTLMQYFWMYPMNDGQMRRLONDSAYLAHSGITAWIIPAYKGSQADVGYAYD 60

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Db 241 LRDVNVHREKIGKEMFTVAEYQNDLGALENYLNKTNFNSVFDVPLHYGFHAASTOGG 300
Qy 301 GYDMRKLLNGTVVSKPKLSVTVDNDHDTOPGOSLESTVQTFKPLAFAFILTRESGYPO 360
Db 301 GYDMRKLLNGTVVSKPKLSVTVDNDHDTOPGOSLESTVQTFKPLAFAFILTRESGYPO 360
Qy 361 VFYGDWYGTGKDSQREIPALKKIEPILKARKQYAGACHDYFDHDIWGMTREGDSVA 420
Db 361 VFYGDWYGTGKDSQREIPALKKIEPILKARKQYAGACHDYFDHDIWGMTREGDSVA 420
Qy 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSKGMEFHVNGGSVSIY 480
Db 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSKGMEFHVNGGSVSIY 480
Qy 481 VOR 483
Db 481 VOR 483
Qy 481 VOR 483
Db 481 VOR 483

RESULT 2
US-09-170-670-4
; Sequence 4, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276,200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; EARLIER FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRN
; ORGANISM: B. licheniformis
US-09-170-670-4

Query Match 100.0%; Score 2666; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 2,9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 361 VFYGDWYGTGKDSQREIPALKKIEPILKARKQYAGACHDYFDHDIWGMTREGDSVA 420
Qy 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSKGMEFHVNGGSVSIY 480
Db 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSKGMEFHVNGGSVSIY 480
Qy 481 VOR 483
Db 481 VOR 483

RESULT 3
US-09-193-068-4
; Sequence 4, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjulf, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709,000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRN
; ORGANISM: B. licheniformis
US-09-193-068-4

Query Match 100.0%; Score 2666; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 2,9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
US-09-183-412-4
/ Sequence 4, Application US/09183412
/ Patent No. 6204232
/ GENERAL INFORMATION:
/ APPLICANT: Borchert, Torben V.
/ APPLICANT: Svendsen, Allan
/ APPLICANT: Andersen, Carsten
/ APPLICANT: Nielsen, Bjarne
/ APPLICANT: Madsen, Torben L.
/ APPLICANT: Kjærulff, Søren
/ TITLE OF INVENTION: Alpha-Amulase Mutants
/ FILE REFERENCE: 5368.200-US
/ CURRENT APPLICATION NUMBER: US/09/183,412
/ EARLIER FILING DATE: 1998-10-30
/ EARLIER APPLICATION NUMBER: 60/064,662
/ EARLIER FILING DATE: 1997-11-06
/ EARLIER APPLICATION NUMBER: 60/093,234
/ EARLIER FILING DATE: 1998-07-17
/ EARLIER APPLICATION NUMBER: 1240/97
/ EARLIER FILING DATE: 1997-10-30
/ EARLIER APPLICATION NUMBER: PA 1998 00936
/ EARLIER FILING DATE: 1998-07-14
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 483
/ TYPE: PRT
/ ORGANISM: Bacillus licheniformis
US-09-183-412-4
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Query Match 100.0%; Score 2666; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0;
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DB 1 ANINGTLMQYFEMWYMPNDGQHWRLQNDASAYLAHSGITAVWIPAYKGTSGADVGAYD 60
QY 61 LYDLGEFHQKGTATKTKGTGELQSAIKSLHSRDINVGVDVNNHKGADATEDVTAVEY 120
DB 61 LYDLGEFHQKGTATKTKGTGELQSAIKSLHSRDINVGVDVNNHKGADATEDVTAVEY 120
QY 121 DPADRNVIISGEHLIKATWTFHFPGRGSTYSDFKMWYHFDGTDWDSRLNRIYKFGK 180
DB 121 DPADRNVIISGEHLIKATWTFHFPGRGSTYSDFKMWYHFDGTDWDSRLNRIYKFGK 180
QY 181 AMDWEVSNEGNNDYDLYMADIDYDHPVAAEIKRWGTWYANELODGFRLDAYKHKEF 240
DB 181 AMDWEVSNEGNNDYDLYMADIDYDHPVAAEIKRWGTWYANELODGFRLDAYKHKEF 240
QY 241 LRDVNVNHYREKTKGEMFTVAEYWNQDGLALENYLNTKTFNHSVFDVPLHYQFHAAS 300
DB 241 LRDVNVNHYREKTKGEMFTVAEYWNQDGLALENYLNTKTFNHSVFDVPLHYQFHAAS 300
QY 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPGQSLSTVQTFKPLAFAFLITRESGPQ 360
DB 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPGQSLSTVQTFKPLAFAFLITRESGPQ 360
QY 361 VFYGDWYTKGDSOREIPALKHKEFLIKAKQYAYGAQHDYFPHHDIVGMTREGDSSVA 420
DB 361 VFYGDWYTKGDSOREIPALKHKEFLIKAKQYAYGAQHDYFPHHDIVGMTREGDSSVA 420
QY 421 NSGLAALITDGPFGAKRYVGRQNAGETWHDITGNRSEPVVINSGEWGFHVNGGSVSIY 480
DB 421 NSGLAALITDGPFGAKRYVGRQNAGETWHDITGNRSEPVVINSGEWGFHVNGGSVSIY 480
QY 481 VOR 483
DB 481 VOR 483
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US-09-264-097-2
/ Sequence 2, Application US/09264097
/ Patent No. 6287826
/ GENERAL INFORMATION:
/ APPLICANT: No. 6287826man, Barrie Edmund
/ APPLICANT: Hendriksen, Hanne Vang
/ TITLE OF INVENTION: Enzymatic Preparation of Glucose Syrup
/ FILE REFERENCE: 5276.200-US
/ CURRENT APPLICATION NUMBER: US/09/264,097
/ EARLIER FILING DATE: 1999-03-08
/ EARLIER APPLICATION NUMBER: PA 0321/98
/ EARLIER FILING DATE: 1998-03-09
/ EARLIER APPLICATION NUMBER: 60/079,209
/ EARLIER FILING DATE: 1998-03-24
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 2
/ LENGTH: 483
/ TYPE: PRT
/ ORGANISM: Bacillus licheniformis
US-09-264-097-2
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Query Match 100.0%; Score 2666; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0;
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DB 1 ANINGTLMQYFEMWYMPNDGQHWRLQNDASAYLAHSGITAVWIPAYKGTSGADVGAYD 60
QY 61 LYDLGEFHQKGTATKTKGTGELQSAIKSLHSRDINVGVDVNNHKGADATEDVTAVEY 120
DB 61 LYDLGEFHQKGTATKTKGTGELQSAIKSLHSRDINVGVDVNNHKGADATEDVTAVEY 120
QY 121 DPADRNVIISGEHLIKATWTFHFPGRGSTYSDFKMWYHFDGTDWDSRLNRIYKFGK 180
DB 121 DPADRNVIISGEHLIKATWTFHFPGRGSTYSDFKMWYHFDGTDWDSRLNRIYKFGK 180
QY 181 AMDWEVSNEGNNDYDLYMADIDYDHPVAAEIKRWGTWYANELODGFRLDAYKHKEF 240
DB 181 AMDWEVSNEGNNDYDLYMADIDYDHPVAAEIKRWGTWYANELODGFRLDAYKHKEF 240
QY 241 LRDVNVNHYREKTKGEMFTVAEYWNQDGLALENYLNTKTFNHSVFDVPLHYQFHAAS 300
DB 241 LRDVNVNHYREKTKGEMFTVAEYWNQDGLALENYLNTKTFNHSVFDVPLHYQFHAAS 300
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DB 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPGQSLSTVQTFKPLAFAFLITRESGPQ 360
QY 361 VFYGDWYTKGDSOREIPALKHKEFLIKAKQYAYGAQHDYFPHHDIVGMTREGDSSVA 420
DB 361 VFYGDWYTKGDSOREIPALKHKEFLIKAKQYAYGAQHDYFPHHDIVGMTREGDSSVA 420
QY 421 NSGLAALITDGPFGAKRYVGRQNAGETWHDITGNRSEPVVINSGEWGFHVNGGSVSIY 480
DB 421 NSGLAALITDGPFGAKRYVGRQNAGETWHDITGNRSEPVVINSGEWGFHVNGGSVSIY 480
QY 481 VOR 483
DB 481 VOR 483
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RESULT 6
US-09-291-023A-21
/ Sequence 21, Application US/09291023A
/ Patent No. 6309871
/ GENERAL INFORMATION:
/ APPLICANT: Cuttrup, Helle
/ APPLICANT: Borchert, Torben
/ APPLICANT: Nielsen, Bjarne
/ APPLICANT: Viabeke
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RESULT 5

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; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/291.023A
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: DK 1999 00438
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus
US-09-291-023A-21

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Query Match      100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2,9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANLNGTLNQYFEMWPNPDGQHRRLQNDSAVLAHGIITAWIPRAYKTSQADVGAYD 60
DB 1 ANLNGTLNQYFEMWPNPDGQHRRLQNDSAVLAHGIITAWIPRAYKTSQADVGAYD 60
QY 61 LYDLGEFHQKGTVRTKYGKELQSAIKLSHRDINVGDVVNHKGADATEDVTAVEV 120
DB 61 LYDLGEFHQKGTVRTKYGKELQSAIKLSHRDINVGDVVNHKGADATEDVTAVEV 120
QY 121 DPADNRVYISGHLIKAWTHFFPGRGSTYSDFKMWHFPGDTWDSRKLRIYKQK 180
DB 121 DPADNRVYISGHLIKAWTHFFPGRGSTYSDFKMWHFPGDTWDSRKLRIYKQK 180
QY 181 AMDWVSNGNNGYDLYMTADIDYHPVAAEIKRWGTAYANELQDGFRLDAVHIFSF 240
DB 181 AMDWVSNGNNGYDLYMTADIDYHPVAAEIKRWGTAYANELQDGFRLDAVHIFSF 240
QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNSVDFVPLHYQFHAASQGG 300
DB 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNSVDFVPLHYQFHAASQGG 300
QY 301 GYDMKRLNGTVVSKPLKSVTFVNDHDTQPGQSLESTVQTFKPLAFAFLITRESGYPQ 360
DB 301 GYDMKRLNGTVVSKPLKSVTFVNDHDTQPGQSLESTVQTFKPLAFAFLITRESGYPQ 360
QY 361 VFYGDWYGTGKDSQREIPALKKIEPIILKARQVYAGQHDYFDHHDVGMTREDDSSVA 420
DB 361 VFYGDWYGTGKDSQREIPALKKIEPIILKARQVYAGQHDYFDHHDVGMTREDDSSVA 420
QY 421 NSGLAALLITDGPAGAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
DB 421 NSGLAALLITDGPAGAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483

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RESULT 7
US-09-290-734-4
; Sequence 4, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borcherdt, Torben Vedel
; APPLICANT: Bisgaard-Frantzen Henrik
; APPLICANT: Oultup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989e1 -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13

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; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: B. licheniformis
US-09-290-734-4

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Query Match      100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2,9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANLNGTLNQYFEMWPNPDGQHRRLQNDSAVLAHGIITAWIPRAYKTSQADVGAYD 60
DB 1 ANLNGTLNQYFEMWPNPDGQHRRLQNDSAVLAHGIITAWIPRAYKTSQADVGAYD 60
QY 61 LYDLGEFHQKGTVRTKYGKELQSAIKLSHRDINVGDVVNHKGADATEDVTAVEV 120
DB 61 LYDLGEFHQKGTVRTKYGKELQSAIKLSHRDINVGDVVNHKGADATEDVTAVEV 120
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DB 121 DPADNRVYISGHLIKAWTHFFPGRGSTYSDFKMWHFPGDTWDSRKLRIYKQK 180
QY 181 AMDWVSNGNNGYDLYMTADIDYHPVAAEIKRWGTAYANELQDGFRLDAVHIFSF 240
DB 181 AMDWVSNGNNGYDLYMTADIDYHPVAAEIKRWGTAYANELQDGFRLDAVHIFSF 240
QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNSVDFVPLHYQFHAASQGG 300
DB 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNSVDFVPLHYQFHAASQGG 300
QY 301 GYDMKRLNGTVVSKPLKSVTFVNDHDTQPGQSLESTVQTFKPLAFAFLITRESGYPQ 360
DB 301 GYDMKRLNGTVVSKPLKSVTFVNDHDTQPGQSLESTVQTFKPLAFAFLITRESGYPQ 360
QY 361 VFYGDWYGTGKDSQREIPALKKIEPIILKARQVYAGQHDYFDHHDVGMTREDDSSVA 420
DB 361 VFYGDWYGTGKDSQREIPALKKIEPIILKARQVYAGQHDYFDHHDVGMTREDDSSVA 420
QY 421 NSGLAALLITDGPAGAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
DB 421 NSGLAALLITDGPAGAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483

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RESULT 8
US-09-537-168-4
; Sequence 4, Application US/09537168
; Patent No. 6410295
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/09/537,168
; PRIOR FILING DATE: 2000-03-29
; EARLIER APPLICATION NUMBER: PA 1999 00437
; EARLIER FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: 60/127,427
; EARLIER FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis

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US-09-537-168-4

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0;

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DB 1 ANINGTLMQYFEMWMPNDGQHWRLQNDASVLAHEGITAWEIPPAKGTSGADVGAYD 60
QY 61 LYDGEFHQKGTVRTKGTGKELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEY 120
DB 61 LYDGEFHQKGTVRTKGTGKELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEY 120
QY 121 DPADNRNVIAGEHLIKAMTHFHPGRGSTYSDPKMWHFDDGTDMDESKLRNIYKFOGK 180
DB 121 DPADNRNVIAGEHLIKAMTHFHPGRGSTYSDPKMWHFDDGTDMDESKLRNIYKFOGK 180
QY 181 AMDMEVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWANELQDGFRLDAVKHKKFSF 240
DB 181 AMDMEVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWANELQDGFRLDAVKHKKFSF 240
QY 241 LRDMVNVHREKTEKEMFTVAEYQNDLGALENTLNKTNFHSVFDVPLHYQFHAASSTGG 300
DB 241 LRDMVNVHREKTEKEMFTVAEYQNDLGALENTLNKTNFHSVFDVPLHYQFHAASSTGG 300
QY 301 GYDMRKLLNGTVSKHPLKSVTFVDNHDTPQGSLSTVQTFWKPLAVAFILTRBSGYQ 360
DB 301 GYDMRKLLNGTVSKHPLKSVTFVDNHDTPQGSLSTVQTFWKPLAVAFILTRBSGYQ 360
QY 361 VFYGDYMTGKGDSDREIPALKHKEIPILKARKOYAGAQHDYDHDIDYGMTREGSSVA 420
DB 361 VFYGDYMTGKGDSDREIPALKHKEIPILKARKOYAGAQHDYDHDIDYGMTREGSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGGEFHVNGSVSY 480
DB 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGGEFHVNGSVSY 480
QY 481 VQR 483
DB 481 VQR 483
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RESULT 9

US-09-672-459-2
Sequence 2, Application US/09672459

GENERAL INFORMATION:
PATIENT: Patient No. 643688
APPLICANT: Svendsen, Allan
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/672,459
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-09-672-459-2

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0;

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DB 1 ANINGTLMQYFEMWMPNDGQHWRLQNDASVLAHEGITAWEIPPAKGTSGADVGAYD 60
QY 61 LYDGEFHQKGTVRTKGTGKELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEY 120
DB 61 LYDGEFHQKGTVRTKGTGKELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEY 120
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DB 121 DPADNRNVIAGEHLIKAMTHFHPGRGSTYSDPKMWHFDDGTDMDESKLRNIYKFOGK 180
QY 181 AMDMEVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWANELQDGFRLDAVKHKKFSF 240
DB 181 AMDMEVSNENGNVDYLMYADIDYDHPVAAEIKRWGTWANELQDGFRLDAVKHKKFSF 240
QY 241 LRDMVNVHREKTEKEMFTVAEYQNDLGALENTLNKTNFHSVFDVPLHYQFHAASSTGG 300
DB 241 LRDMVNVHREKTEKEMFTVAEYQNDLGALENTLNKTNFHSVFDVPLHYQFHAASSTGG 300
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DB 301 GYDMRKLLNGTVSKHPLKSVTFVDNHDTPQGSLSTVQTFWKPLAVAFILTRBSGYQ 360
QY 361 VFYGDYMTGKGDSDREIPALKHKEIPILKARKOYAGAQHDYDHDIDYGMTREGSSVA 420
DB 361 VFYGDYMTGKGDSDREIPALKHKEIPILKARKOYAGAQHDYDHDIDYGMTREGSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGGEFHVNGSVSY 480
DB 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGGEFHVNGSVSY 480
QY 481 VQR 483
DB 481 VQR 483
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RESULT 10

US-09-545-586-4
Sequence 4, Application US/09545586

GENERAL INFORMATION:
PATIENT: Patient No. 6528298
APPLICANT: Svendsen, Allan
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Oulstrup, Helle
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Vibeke Skovgaard
TITLE OF INVENTION: No. 6528298-1 -Amylase And -Amylase Mutants
FILE REFERENCE: 5276.400-US
CURRENT APPLICATION NUMBER: US/09/545,586
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: US/09/290,734
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 483
TYPE: PRT
ORGANISM: B. licheniformis
US-09-545-586-4

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0;

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DB 1 ANINGTLMQYFEMWMPNDGQHWRLQNDASVLAHEGITAWEIPPAKGTSGADVGAYD 60
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Db 1 ANINGTLMQYFEWYMPNDGQWRLQNDASAYLAHEGITAIVMPAYKGTSGQADVGYAYD 60
QY 61 LYDGEFHQGTVATKTKGTGELQSAIKSLHSRDINVGVDVINHGADATEDVTAVEV 120
Db 61 LYDGEFHQGTVATKTKGTGELQSAIKSLHSRDINVGVDVINHGADATEDVTAVEV 120
QY 121 DPADRNRVISGEHLIKAMTHFHPGRGSTYSDFKMWYHFDGTDWDESRKLNRIYFQOK 180
Db 121 DPADRNRVISGEHLIKAMTHFHPGRGSTYSDFKMWYHFDGTDWDESRKLNRIYFQOK 180
QY 181 AMDWVSNNENNYLYLWADIDYDHPVAALIKRWGTWYANLQDGFRLDAYKHIFSF 240
Db 181 AMDWVSNNENNYLYLWADIDYDHPVAALIKRWGTWYANLQDGFRLDAYKHIFSF 240
QY 241 LRDWNVHREKTKGEMFTVAEYWNQDGALENTLNKTNFHSYFVDPVLAHYQFHAASTQGG 300
Db 241 LRDWNVHREKTKGEMFTVAEYWNQDGALENTLNKTNFHSYFVDPVLAHYQFHAASTQGG 300
QY 301 GYDMRKLTNGTVSKHPLKSTYTFVNDNDTPQGSLESTVQTFWPKPLAYAFILITRESGYPQ 360
Db 301 GYDMRKLTNGTVSKHPLKSTYTFVNDNDTPQGSLESTVQTFWPKPLAYAFILITRESGYPQ 360
QY 361 VFYGDWYGTGKDSOREIPALKHKEIPIIKAKQYAYGAQHDYFDHDIIVGTREGDSSVA 420
Db 361 VFYGDWYGTGKDSOREIPALKHKEIPIIKAKQYAYGAQHDYFDHDIIVGTREGDSSVA 420
QY 421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSEGMGEFFHNGGSYSIY 480
Db 421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSEGMGEFFHNGGSYSIY 480
QY 481 VQR 483
Db 481 VQR 483

RESULT 11
US-09-540-715A-21
Sequence 21, Application US/09540715A

Patent No. 6623948
GENERAL INFORMATION:
APPLICANT: Borchert, Torben
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Bjarne
APPLICANT: Hoeck, Lisbeth
TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
FILE REFERENCE: 5821-010-US
CURRENT APPLICATION NUMBER: US/09/540,715A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/291,023
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
SEQ ID NO 21
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus
US-09-540-715A-21

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2,9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANINGTLMQYFEWYMPNDGQWRLQNDASAYLAHEGITAIVMPAYKGTSGQADVGYAYD 60
Db 1 ANINGTLMQYFEWYMPNDGQWRLQNDASAYLAHEGITAIVMPAYKGTSGQADVGYAYD 60
QY 61 LYDGEFHQGTVATKTKGTGELQSAIKSLHSRDINVGVDVINHGADATEDVTAVEV 120
Db 61 LYDGEFHQGTVATKTKGTGELQSAIKSLHSRDINVGVDVINHGADATEDVTAVEV 120
QY 121 DPADRNRVISGEHLIKAMTHFHPGRGSTYSDFKMWYHFDGTDWDESRKLNRIYFQOK 180

Db 121 DPADRNRVISGEHLIKAMTHFHPGRGSTYSDFKMWYHFDGTDWDESRKLNRIYFQOK 180
QY 181 AMDWVSNNENNYLYLWADIDYDHPVAALIKRWGTWYANLQDGFRLDAYKHIFSF 240
Db 181 AMDWVSNNENNYLYLWADIDYDHPVAALIKRWGTWYANLQDGFRLDAYKHIFSF 240
QY 241 LRDWNVHREKTKGEMFTVAEYWNQDGALENTLNKTNFHSYFVDPVLAHYQFHAASTQGG 300
Db 241 LRDWNVHREKTKGEMFTVAEYWNQDGALENTLNKTNFHSYFVDPVLAHYQFHAASTQGG 300
QY 301 GYDMRKLTNGTVSKHPLKSTYTFVNDNDTPQGSLESTVQTFWPKPLAYAFILITRESGYPQ 360
Db 301 GYDMRKLTNGTVSKHPLKSTYTFVNDNDTPQGSLESTVQTFWPKPLAYAFILITRESGYPQ 360
QY 361 VFYGDWYGTGKDSOREIPALKHKEIPIIKAKQYAYGAQHDYFDHDIIVGTREGDSSVA 420
Db 361 VFYGDWYGTGKDSOREIPALKHKEIPIIKAKQYAYGAQHDYFDHDIIVGTREGDSSVA 420
QY 421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSEGMGEFFHNGGSYSIY 480
Db 421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSEGMGEFFHNGGSYSIY 480
QY 481 VQR 483
Db 481 VQR 483

RESULT 12
US-10-186-042-2
Sequence 2, Application US/10186042

Patent No. 6642044
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796-204-US
CURRENT APPLICATION NUMBER: US/10/186,042
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-186-042-2

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2,9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANINGTLMQYFEWYMPNDGQWRLQNDASAYLAHEGITAIVMPAYKGTSGQADVGYAYD 60
Db 1 ANINGTLMQYFEWYMPNDGQWRLQNDASAYLAHEGITAIVMPAYKGTSGQADVGYAYD 60
QY 61 LYDGEFHQGTVATKTKGTGELQSAIKSLHSRDINVGVDVINHGADATEDVTAVEV 120
Db 61 LYDGEFHQGTVATKTKGTGELQSAIKSLHSRDINVGVDVINHGADATEDVTAVEV 120
QY 121 DPADRNRVISGEHLIKAMTHFHPGRGSTYSDFKMWYHFDGTDWDESRKLNRIYFQOK 180

Db 121 DPADNRRTISGEHLIKATHTPHFPGRGSTYSDFKMHVHPFGCTMDSRKLRNLYXQCK 180
 Qy 181 AMDWEVSNENGVYDLYMADIDYDHPDVAAEIKMGWYANELDGFRLDAVGHKFSF 240
 Db 181 AMDWEVSNENGVYDLYMADIDYDHPDVAAEIKMGWYANELDGFRLDAVGHKFSF 240
 Qy 241 LRDWVNHREKTKGEMFTVAEYMONDLGALENYLNKTNFNHSEVDPVPHYOFHAASQGG 300
 Db 241 LRDWVNHREKTKGEMFTVAEYMONDLGALENYLNKTNFNHSEVDPVPHYOFHAASQGG 300
 Qy 301 GYDMKRLNGTVSGKPLKSVTFVNDHDTQPGQSLESTVQTMFKPLAFAFLLTRESGYPO 360
 Db 301 GYDMKRLNGTVSGKPLKSVTFVNDHDTQPGQSLESTVQTMFKPLAFAFLLTRESGYPO 360
 Qy 361 VFYGMVGTGKDSOREIPALKEIPILKARKQYVGAQHDFDHHDIVGWTREGDSSVA 420
 Db 361 VFYGMVGTGKDSOREIPALKEIPILKARKQYVGAQHDFDHHDIVGWTREGDSSVA 420
 Qy 421 NSGLAALITDGPAGAKRMVYGRQNGETWHDITGNRSEPVYINSEGMGEFFHNGGSVSIY 480
 Db 421 NSGLAALITDGPAGAKRMVYGRQNGETWHDITGNRSEPVYINSEGMGEFFHNGGSVSIY 480
 Qy 481 VQR 483
 Db 481 VQR 483

RESULT 13
 US-09-769-864-4
 / Sequence 4, Application US/09769864
 / Patent No. 6673589

GENERAL INFORMATION:
 APPLICANT: Borchert, Torben V.
 APPLICANT: Svendsen, Allan
 APPLICANT: Andersen, Carsten
 APPLICANT: Nielsen, Bjarne
 APPLICANT: Nielsen, Torben L.
 APPLICANT: Kjaerulff, Soren
 TITLE OF INVENTION: Alpha-Amulase Mutants
 FILE REFERENCE: 5368.200-US
 CURRENT APPLICATION NUMBER: US/09/769,864
 CURRENT FILING DATE: 2001-01-25
 PRIOR APPLICATION NUMBER: 09/183,412
 PRIOR FILING DATE: 1998-10-30
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 4
 LENGTH: 483
 TYPE: PR
 ORGANISM: Bacillus licheniformis
 US-09-769-864-4

Query Match 100.0%; Score 2666; DB 4; Length 483;
 Best Local Similarity 100.0%; Pred. No. 2,9e-240;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANNGTLMQFEYEMWMDGHRRLONDSAYLAHEGTTAVWIPRAYKTSQADVGAYD 60
 Db 1 ANNGTLMQFEYEMWMDGHRRLONDSAYLAHEGTTAVWIPRAYKTSQADVGAYD 60
 Qy 61 LVDLGEFHQKGVTRTKGTGKELQSAIKSLHSEIDINVYDVYINHGKADATEDVTAVEV 120
 Db 61 LVDLGEFHQKGVTRTKGTGKELQSAIKSLHSEIDINVYDVYINHGKADATEDVTAVEV 120
 Qy 121 DPADNRRTISGEHLIKATHTPHFPGRGSTYSDFKMHVHPFGCTMDSRKLRNLYXQCK 180
 Db 121 DPADNRRTISGEHLIKATHTPHFPGRGSTYSDFKMHVHPFGCTMDSRKLRNLYXQCK 180
 Qy 181 AMDWEVSNENGVYDLYMADIDYDHPDVAAEIKMGWYANELDGFRLDAVGHKFSF 240
 Db 181 AMDWEVSNENGVYDLYMADIDYDHPDVAAEIKMGWYANELDGFRLDAVGHKFSF 240

Qy 241 LRDWVNHREKTKGEMFTVAEYMONDLGALENYLNKTNFNHSEVDPVPHYOFHAASQGG 300
 Db 241 LRDWVNHREKTKGEMFTVAEYMONDLGALENYLNKTNFNHSEVDPVPHYOFHAASQGG 300
 Qy 301 GYDMKRLNGTVSGKPLKSVTFVNDHDTQPGQSLESTVQTMFKPLAFAFLLTRESGYPO 360
 Db 301 GYDMKRLNGTVSGKPLKSVTFVNDHDTQPGQSLESTVQTMFKPLAFAFLLTRESGYPO 360
 Qy 361 VFYGMVGTGKDSOREIPALKEIPILKARKQYVGAQHDFDHHDIVGWTREGDSSVA 420
 Db 361 VFYGMVGTGKDSOREIPALKEIPILKARKQYVGAQHDFDHHDIVGWTREGDSSVA 420
 Qy 421 NSGLAALITDGPAGAKRMVYGRQNGETWHDITGNRSEPVYINSEGMGEFFHNGGSVSIY 480
 Db 421 NSGLAALITDGPAGAKRMVYGRQNGETWHDITGNRSEPVYINSEGMGEFFHNGGSVSIY 480
 Qy 481 VQR 483
 Db 481 VQR 483

RESULT 14
 US-08-720-899-2
 / Sequence 2, Application US/08720899
 / Patent No. 5753460

GENERAL INFORMATION:
 APPLICANT: Bisgaard-Frantzen, Henrik
 APPLICANT: Borchert, Torben Vedel
 APPLICANT: Svendsen, Allan
 APPLICANT: Thellersen, Marianne
 APPLICANT: Van der Zee, Pia
 TITLE OF INVENTION: AMYLASE VARIANTS
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 57534600 No. 5753460disk of No. 5753460ch America, Inc.
 STREET: 405 Lexington Avenue, 64th Floor
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/720,899
 FILING DATE: 10-OCT-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/343,804
 FILING DATE: 22-NOV-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Lowrey Dr., Karen A.
 REGISTRATION NUMBER: 31,274
 REFERENCE/DOCKET NUMBER: 4054,214-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 512 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-720-899-2

Query Match 100.0%; Score 2666; DB 1; Length 512;
 Best Local Similarity 100.0%; Pred. No. 3,2e-240;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANNGTLMQFEYEMWMDGHRRLONDSAYLAHEGTTAVWIPRAYKTSQADVGAYD 60

Tue May 4 14:34:43 2004

us-10-644-187-2.rai

Page 8

Db 30 ANINGTLMQYFEMWPNNDGQHRRLQNDASAYLAHGTITAWIIPAYKGTQADVGYAYD 89
QY 61 LYDLGEFHOKGTVRTKTKGTGKELQSAIKSLHSRDINVGDVYINHGADATEDVTAVEV 120
Db 90 LYDLGEFHOKGTVRTKTKGTGKELQSAIKSLHSRDINVGDVYINHGADATEDVTAVEV 149
QY 121 DPADRRRVISGSHLTKAMTHFHPFGSGTSDPKMWHFPGDIDWDSRKLNRITYKQK 180
Db 150 DPADRRRVISGSHLTKAMTHFHPFGSGTSDPKMWHFPGDIDWDSRKLNRITYKQK 209
QY 181 AMDWEVSNENGVNDYLTADIDYDHPDVAEIKRMGTWYANELQDGFRLDAVKIKFSF 240
Db 210 AMDWEVSNENGVNDYLTADIDYDHPDVAEIKRMGTWYANELQDGFRLDAVKIKFSF 269
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QY 301 GYDMRKLNGTIVSKHPLKSVTFVDNHDTPQGSLSTVQTFKPLAVAFILTRSGYPQ 360
Db 330 GYDMRKLNGTIVSKHPLKSVTFVDNHDTPQGSLSTVQTFKPLAVAFILTRSGYPQ 389
QY 361 VFYGDWYGTGKDSOREIPALKHKEIPILKARKOYAGAOHDFDHDIVGTRGDSVA 420
Db 390 VFYGDWYGTGKDSOREIPALKHKEIPILKARKOYAGAOHDFDHDIVGTRGDSVA 449
QY 421 NSGLAALITDGPQAKRMVYGRONAGETWHDITGNRSEPVVINSBGGEFHVNGSVISY 480
Db 450 NSGLAALITDGPQAKRMVYGRONAGETWHDITGNRSEPVVINSBGGEFHVNGSVISY 509
QY 481 VQR 483
Db 510 VQR 512

RESULT 15
US-08-459-610-2
Sequence 2, Application US/08459610
Patent No. 5801043
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5801043 of No. 5801043 of No. 5801043 of America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,610
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowmey Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-610-2
Query Match 100.0%; Score 2666; DB 1; Length 512;
Best Local Similarity 100.0%; Pred. No. 3.2e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 30 ANINGTLMQYFEMWPNNDGQHRRLQNDASAYLAHGTITAWIIPAYKGTQADVGYAYD 89
QY 61 LYDLGEFHOKGTVRTKTKGTGKELQSAIKSLHSRDINVGDVYINHGADATEDVTAVEV 120
Db 90 LYDLGEFHOKGTVRTKTKGTGKELQSAIKSLHSRDINVGDVYINHGADATEDVTAVEV 149
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Db 150 DPADRRRVISGSHLTKAMTHFHPFGSGTSDPKMWHFPGDIDWDSRKLNRITYKQK 209
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Db 210 AMDWEVSNENGVNDYLTADIDYDHPDVAEIKRMGTWYANELQDGFRLDAVKIKFSF 269
QY 241 LRDMVNVHREKTKGEMFTVAEYQNDLGALNTNPNHNSVFDVPLHYQFHAASSTQG 300
Db 270 LRDMVNVHREKTKGEMFTVAEYQNDLGALNTNPNHNSVFDVPLHYQFHAASSTQG 329
QY 301 GYDMRKLNGTIVSKHPLKSVTFVDNHDTPQGSLSTVQTFKPLAVAFILTRSGYPQ 360
Db 330 GYDMRKLNGTIVSKHPLKSVTFVDNHDTPQGSLSTVQTFKPLAVAFILTRSGYPQ 389
QY 361 VFYGDWYGTGKDSOREIPALKHKEIPILKARKOYAGAOHDFDHDIVGTRGDSVA 420
Db 390 VFYGDWYGTGKDSOREIPALKHKEIPILKARKOYAGAOHDFDHDIVGTRGDSVA 449
QY 421 NSGLAALITDGPQAKRMVYGRONAGETWHDITGNRSEPVVINSBGGEFHVNGSVISY 480
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QY 481 VQR 483
Db 510 VQR 512

Search completed: May 3, 2004, 20:35:55
Job time: 18.3507 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:33:58 ; Search time 37.6066 Seconds

(without alignments)
3560.078 Million cell updates/sec

Title: US-10-644-187-2

Perfect score: 2666

Sequence: 1 ANLNGTLMQYFEMWPNDCQ.....SEGWGEFHWGSGVSIVYQR 483

Scoring table: BLOSUM62

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Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2666	100.0	483	US-09-854-346-8	Sequence 8, Appl1
3	2666	100.0	483	US-09-918-543-8	Sequence 8, Appl1
4	2666	100.0	483	US-09-918-543-10	Sequence 10, Appl1
5	2666	100.0	483	US-09-925-576C-8	Sequence 8, Appl1
6	2666	100.0	483	US-10-665-667-4	Sequence 4, Appl1
7	2666	100.0	483	US-10-644-187-2	Sequence 2, Appl1
8	2666	100.0	483	US-10-327-837-4	Sequence 2, Appl1
9	2666	100.0	483	US-10-146-327-4	Sequence 2, Appl1
10	2666	100.0	483	US-10-186-042-2	Sequence 2, Appl1
11	2666	100.0	512	US-10-184-771-2	Sequence 2, Appl1
12	2663	99.9	512	US-10-189-822-2	Sequence 2, Appl1
13	2654	99.5	512	US-10-081-872-114	Sequence 114, Appl1
14	2654	99.5	512	US-10-105-733-8	Sequence 8, Appl1
15	2654	99.5	512	US-10-081-739A-8	Sequence 8, Appl1

16	2654	99.5	512	US-10-385-305-114	Sequence 114, Appl1
17	2582	96.8	481	US-10-146-327-2	Sequence 2, Appl1
18	2338	87.7	483	US-10-184-771-13	Sequence 13, Appl1
19	2184	81.9	483	US-09-854-346-10	Sequence 10, Appl1
20	2184	81.9	483	US-09-918-543-10	Sequence 10, Appl1
21	2184	81.9	483	US-09-925-576C-10	Sequence 6, Appl1
22	2184	81.9	483	US-10-146-327-6	Sequence 4, Appl1
23	2184	81.9	514	US-10-184-771-4	Sequence 5, Appl1
24	2173	81.5	480	US-09-769-864-5	Sequence 5, Appl1
25	2173	81.5	480	US-10-665-667-5	Sequence 4, Appl1
26	2173	81.5	480	US-10-644-187-4	Sequence 4, Appl1
27	2173	81.5	480	US-10-327-837-5	Sequence 4, Appl1
28	2173	81.5	480	US-10-186-042-4	Sequence 4, Appl1
29	1999	75.0	513	US-10-081-872-70	Sequence 70, Appl1
30	1999	75.0	513	US-10-081-872-146	Sequence 146, Appl1
31	1979	74.2	513	US-10-385-305-146	Sequence 146, Appl1
32	1979	74.2	513	US-10-081-872-166	Sequence 166, Appl1
33	1961	73.6	478	US-10-081-872-166	Sequence 166, Appl1
34	1961	73.6	478	US-10-385-305-166	Sequence 166, Appl1
35	1950	73.1	485	US-09-769-864-2	Sequence 2, Appl1
36	1950	73.1	485	US-09-769-864-8	Sequence 2, Appl1
37	1950	73.1	485	US-09-854-346-4	Sequence 4, Appl1
38	1950	73.1	485	US-09-902-188A-2	Sequence 2, Appl1
39	1950	73.1	485	US-09-918-543-4	Sequence 4, Appl1
40	1950	73.1	485	US-09-925-576C-4	Sequence 4, Appl1
41	1950	73.1	485	US-09-925-576C-4	Sequence 4, Appl1
42	1950	73.1	485	US-10-665-667-2	Sequence 2, Appl1
43	1950	73.1	485	US-10-665-667-8	Sequence 2, Appl1
44	1950	73.1	485	US-10-025-648-2	Sequence 2, Appl1
45	1950	73.1	485	US-10-327-837-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-769-864-4 ; Sequence 4, Application US/09769864
; Patent No. US20010039253A1
GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjørne
APPLICANT: Nissen, Torben L.
APPLICANT: Kjærulff, Søren
TITLE OF INVENTION: Alpha-Amulase Mutants
FILE REFERENCE: 5368.200-US
CURRENT APPLICATION NUMBER: US/09/769,864
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-09-769-864-4
Query Match 100.0%; Score 2666; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 6.9e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANLNGTLMQYFEMWPNDCQHRRLQNSAYAEHGITAATVTPPAYKGTSGQADVGAYD 60
DB 1 ANLNGTLMQYFEMWPNDCQHRRLQNSAYAEHGITAATVTPPAYKGTSGQADVGAYD 60
QY 61 IVDLGFHQKGVTRKYGKGLQSAIKLSRDLNVYGVYVINKGADATEDVTAVEV 120
DB 61 IVDLGFHQKGVTRKYGKGLQSAIKLSRDLNVYGVYVINKGADATEDVTAVEV 120
QY 121 DPADRNRVLSGHLIKAMTHFHPGSGTYSDFKMHWHFPGTDWDSRKLRIYKFGQX 180

```
Db 121 DPADNRKVISGEHLIKAMTHFFHPGRGSTYSDFKMWHFPGDTMDESKLRIRYKFGSK 180
Qy 181 AMDWEVSNGNNDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKIKFSF 240
Db 181 AMDWEVSNGNNDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKIKFSF 240
Qy 241 LRDWVNHREKTKGKMFVAEYQWONDGALSNYLNKTNFNHNSVDFVPLHYOFHAASQGG 300
Db 241 LRDWVNHREKTKGKMFVAEYQWONDGALSNYLNKTNFNHNSVDFVPLHYOFHAASQGG 300
Qy 301 GYDMKRLNGTVVSKPLKSVTFVNDHDTQPGQSLESTVQTFKPLAVALITRESGYPO 360
Db 301 GYDMKRLNGTVVSKPLKSVTFVNDHDTQPGQSLESTVQTFKPLAVALITRESGYPO 360
Qy 361 VFYGDWYGTGDSOREIPALKKHIEPILKARQVYGAQHDFPDHDIWGMTREBDSVA 420
Db 361 VFYGDWYGTGDSOREIPALKKHIEPILKARQVYGAQHDFPDHDIWGMTREBDSVA 420
Qy 421 NSGLAALITDGPQAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGFHNGGSVSIY 480
Db 421 NSGLAALITDGPQAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGFHNGGSVSIY 480
Qy 481 VQR 483
Db 481 VQR 483
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RESULT 2

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US-09-854-346-8
; Sequence 8, Application US/09854346
; Patent No. US20020068352A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020068352A1ozymes A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Jorgensen, Christel Thea
; APPLICANT: Nielsen, Bjarne Ronfelde
; TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
; FILE REFERENCE: 6140.200-US
; CURRENT APPLICATION NUMBER: US/09/854,346
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
; US-09-854-346-8
```

```
Query Match 100.0%; Score 2666; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 6,9e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 ANLNGTLMQYFEWYMPNDGQWRLQNDASAYLAEGITVAVIIPYKGTSGQADVGYAYD 60
Db 1 ANLNGTLMQYFEWYMPNDGQWRLQNDASAYLAEGITVAVIIPYKGTSGQADVGYAYD 60
Qy 61 LVDLGEFHOKGTVRTKYGKELQSAIKSLHSRDINVGDVYINHGADATEVDTAVEV 120
Db 61 LVDLGEFHOKGTVRTKYGKELQSAIKSLHSRDINVGDVYINHGADATEVDTAVEV 120
Qy 121 DPADNRKVISGEHLIKAMTHFFHPGRGSTYSDFKMWHFPGDTMDESKLRIRYKFGSK 180
Db 121 DPADNRKVISGEHLIKAMTHFFHPGRGSTYSDFKMWHFPGDTMDESKLRIRYKFGSK 180
Qy 181 AMDWEVSNGNNDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKIKFSF 240
Db 181 AMDWEVSNGNNDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKIKFSF 240
Qy 241 LRDWVNHREKTKGKMFVAEYQWONDGALSNYLNKTNFNHNSVDFVPLHYOFHAASQGG 300
Db 241 LRDWVNHREKTKGKMFVAEYQWONDGALSNYLNKTNFNHNSVDFVPLHYOFHAASQGG 300
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```
Qy 301 GYDMKRLNGTVVSKPLKSVTFVNDHDTQPGQSLESTVQTFKPLAVALITRESGYPO 360
Db 301 GYDMKRLNGTVVSKPLKSVTFVNDHDTQPGQSLESTVQTFKPLAVALITRESGYPO 360
Qy 361 VFYGDWYGTGDSOREIPALKKHIEPILKARQVYGAQHDFPDHDIWGMTREBDSVA 420
Db 361 VFYGDWYGTGDSOREIPALKKHIEPILKARQVYGAQHDFPDHDIWGMTREBDSVA 420
Qy 421 NSGLAALITDGPQAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGFHNGGSVSIY 480
Db 421 NSGLAALITDGPQAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGFHNGGSVSIY 480
Qy 481 VQR 483
Db 481 VQR 483
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RESULT 3

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US-09-918-543-8
; Sequence 8, Application US/09918543
; Patent No. US20020155574A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020155574A1ozymes A/S
; APPLICANT: Thisted, Thomas
; APPLICANT: Kjaerulff, Soren
; APPLICANT: Andersen, Carsten
; APPLICANT: Fuglsang, Claus Crone
; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
; FILE REFERENCE: 10062.200-US
; CURRENT APPLICATION NUMBER: US/09/918,543
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
; US-09-918-543-8
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```
Query Match 100.0%; Score 2666; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 6,9e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 ANLNGTLMQYFEWYMPNDGQWRLQNDASAYLAEGITVAVIIPYKGTSGQADVGYAYD 60
Db 1 ANLNGTLMQYFEWYMPNDGQWRLQNDASAYLAEGITVAVIIPYKGTSGQADVGYAYD 60
Qy 61 LVDLGEFHOKGTVRTKYGKELQSAIKSLHSRDINVGDVYINHGADATEVDTAVEV 120
Db 61 LVDLGEFHOKGTVRTKYGKELQSAIKSLHSRDINVGDVYINHGADATEVDTAVEV 120
Qy 121 DPADNRKVISGEHLIKAMTHFFHPGRGSTYSDFKMWHFPGDTMDESKLRIRYKFGSK 180
Db 121 DPADNRKVISGEHLIKAMTHFFHPGRGSTYSDFKMWHFPGDTMDESKLRIRYKFGSK 180
Qy 181 AMDWEVSNGNNDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKIKFSF 240
Db 181 AMDWEVSNGNNDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKIKFSF 240
Qy 241 LRDWVNHREKTKGKMFVAEYQWONDGALSNYLNKTNFNHNSVDFVPLHYOFHAASQGG 300
Db 241 LRDWVNHREKTKGKMFVAEYQWONDGALSNYLNKTNFNHNSVDFVPLHYOFHAASQGG 300
Qy 301 GYDMKRLNGTVVSKPLKSVTFVNDHDTQPGQSLESTVQTFKPLAVALITRESGYPO 360
Db 301 GYDMKRLNGTVVSKPLKSVTFVNDHDTQPGQSLESTVQTFKPLAVALITRESGYPO 360
Qy 361 VFYGDWYGTGDSOREIPALKKHIEPILKARQVYGAQHDFPDHDIWGMTREBDSVA 420
Db 361 VFYGDWYGTGDSOREIPALKKHIEPILKARQVYGAQHDFPDHDIWGMTREBDSVA 420
Qy 421 NSGLAALITDGPQAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGFHNGGSVSIY 480
Db 421 NSGLAALITDGPQAKRMVYGRQNGETWHDITGNRSEPVVINSBGWGFHNGGSVSIY 480
```

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DB 421 NSGLAALITDGPAGKRMVYGRONAGETWHDITGNRSEPVVINSSEGGEFHVNGGSVSIY 480
QY 481 VOR 483
DB 481 VOR 483

RESULT 4
US-09-918-543-30
Sequence 30, Application US/09918543
Patent No. US20020155574A1
GENERAL INFORMATION:
APPLICANT: Thisted, Thomas
APPLICANT: Kjærulff, Søren
APPLICANT: Andersen, Carsten
APPLICANT: Fugleang, Claus-Crone
TITLE OF INVENTION: Alpha-amylase mutants with altered properties
FILE REFERENCE: 10062.200-US
CURRENT APPLICATION NUMBER: US/09/918,543
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 30
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-09-918-543-30

Query Match 100.0%; Score 2666; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 6,9e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSAVLAEGITVWIPPAKGTSGADVGYGAYD 60
DB 1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSAVLAEGITVWIPPAKGTSGADVGYGAYD 60
QY 61 LVDLGEFHQKGTVRTKGTGELQSAIKSLHSRDINVGDVYNHKGADATEDVTAVEV 120
DB 61 LVDLGEFHQKGTVRTKGTGELQSAIKSLHSRDINVGDVYNHKGADATEDVTAVEV 120
QY 121 DPADRNRVISEGHLIKAMTHFHPGGRGTYSDPKMWHYFDGTDWDESKLRNIYKFOGK 180
DB 121 DPADRNRVISEGHLIKAMTHFHPGGRGTYSDPKMWHYFDGTDWDESKLRNIYKFOGK 180
QY 181 AMDWENENGNVDYLMVADIDYDHPDVAEIKRWGTWYANLQDGFRLDAVKIKFSF 240
DB 181 AMDWENENGNVDYLMVADIDYDHPDVAEIKRWGTWYANLQDGFRLDAVKIKFSF 240
QY 241 LRDVNVHREKTKEMFTVAEYQNDLGALENYLNKTNFNSVFDVPLHYQFHAASGOG 300
DB 241 LRDVNVHREKTKEMFTVAEYQNDLGALENYLNKTNFNSVFDVPLHYQFHAASGOG 300
QY 301 GYDRKRLNLTGTVSKPELKSVTVDNHDTPQGSLSTVQTWKPLAFAFILTRBSGYQ 360
DB 301 GYDRKRLNLTGTVSKPELKSVTVDNHDTPQGSLSTVQTWKPLAFAFILTRBSGYQ 360
QY 361 VFYGDWYGTGDSQREIPLAKHIEPIILKARKQYAGAOHDYFDHDIIVGWTREGDSSVA 420
DB 361 VFYGDWYGTGDSQREIPLAKHIEPIILKARKQYAGAOHDYFDHDIIVGWTREGDSSVA 420
QY 421 NSGLAALITDGPAGKRMVYGRONAGETWHDITGNRSEPVVINSSEGGEFHVNGGSVSIY 480
DB 421 NSGLAALITDGPAGKRMVYGRONAGETWHDITGNRSEPVVINSSEGGEFHVNGGSVSIY 480
QY 481 VOR 483
DB 481 VOR 483

RESULT 5
US-09-925-576C-8
Sequence 8, Application US/09925576C

Publication No. US20030129718A1
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Borchert, Torben Vedel
APPLICANT: Nielsen, Bjarne Ronfeldt
TITLE OF INVENTION: Amylase Variants
FILE REFERENCE: 10004.204-US
CURRENT APPLICATION NUMBER: US/09/925,576C
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-09-925-576C-8

Query Match 100.0%; Score 2666; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 6,9e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSAVLAEGITVWIPPAKGTSGADVGYGAYD 60
DB 1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSAVLAEGITVWIPPAKGTSGADVGYGAYD 60
QY 61 LVDLGEFHQKGTVRTKGTGELQSAIKSLHSRDINVGDVYNHKGADATEDVTAVEV 120
DB 61 LVDLGEFHQKGTVRTKGTGELQSAIKSLHSRDINVGDVYNHKGADATEDVTAVEV 120
QY 121 DPADRNRVISEGHLIKAMTHFHPGGRGTYSDPKMWHYFDGTDWDESKLRNIYKFOGK 180
DB 121 DPADRNRVISEGHLIKAMTHFHPGGRGTYSDPKMWHYFDGTDWDESKLRNIYKFOGK 180
QY 181 AMDWENENGNVDYLMVADIDYDHPDVAEIKRWGTWYANLQDGFRLDAVKIKFSF 240
DB 181 AMDWENENGNVDYLMVADIDYDHPDVAEIKRWGTWYANLQDGFRLDAVKIKFSF 240
QY 241 LRDVNVHREKTKEMFTVAEYQNDLGALENYLNKTNFNSVFDVPLHYQFHAASGOG 300
DB 241 LRDVNVHREKTKEMFTVAEYQNDLGALENYLNKTNFNSVFDVPLHYQFHAASGOG 300
QY 301 GYDRKRLNLTGTVSKPELKSVTVDNHDTPQGSLSTVQTWKPLAFAFILTRBSGYQ 360
DB 301 GYDRKRLNLTGTVSKPELKSVTVDNHDTPQGSLSTVQTWKPLAFAFILTRBSGYQ 360
QY 361 VFYGDWYGTGDSQREIPLAKHIEPIILKARKQYAGAOHDYFDHDIIVGWTREGDSSVA 420
DB 361 VFYGDWYGTGDSQREIPLAKHIEPIILKARKQYAGAOHDYFDHDIIVGWTREGDSSVA 420
QY 421 NSGLAALITDGPAGKRMVYGRONAGETWHDITGNRSEPVVINSSEGGEFHVNGGSVSIY 480
DB 421 NSGLAALITDGPAGKRMVYGRONAGETWHDITGNRSEPVVINSSEGGEFHVNGGSVSIY 480
QY 481 VOR 483
DB 481 VOR 483

RESULT 6
US-10-665-667-4
Sequence 4, Application US/1065667
Publication No. US20040038368A1
GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Torben L.
APPLICANT: Kjærulff, Søren
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 5368.200-US
CURRENT APPLICATION NUMBER: US/10/665,667
CURRENT FILING DATE: 2003-09-19

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PRIOR APPLICATION NUMBER: US/09/769,864
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-665-667-4

Query Match 100.0%; Score 2666; DB 12; Length 483;
Best Local Similarity 100.0%; Pred. No. 6.9e-239; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0;

QY 1 ANLNGTLMQFEMWPNNDGQHRRLQNDASAYLAHEGITAAMIIPPAKGTSGADVGAYD 60
DB 1 ANLNGTLMQFEMWPNNDGQHRRLQNDASAYLAHEGITAAMIIPPAKGTSGADVGAYD 60
QY 61 LYDLGEFHQKGTVRITKYGKGLQSAIKSLHSRDINVGDVVINKGGADATEDYTAVEV 120
DB 61 LYDLGEFHQKGTVRITKYGKGLQSAIKSLHSRDINVGDVVINKGGADATEDYTAVEV 120
QY 121 DPADRRRVISGHLIKAWTHFHPGRGSTYSDFKMWHYFDGTDWDESRKLNRIYKFGOK 180
DB 121 DPADRRRVISGHLIKAWTHFHPGRGSTYSDFKMWHYFDGTDWDESRKLNRIYKFGOK 180
QY 181 AMDWEVSNNENGVNDYLMVADIDYDHPDVAALIKRGWYANELQJDFRLDAVKIKFSF 240
DB 181 AMDWEVSNNENGVNDYLMVADIDYDHPDVAALIKRGWYANELQJDFRLDAVKIKFSF 240
QY 241 LEDWNVHAREKTKEMFTYAEYQNDLQALENYLNKTNPNHSVFPVPLHYQFHAASIQG 300
DB 241 LEDWNVHAREKTKEMFTYAEYQNDLQALENYLNKTNPNHSVFPVPLHYQFHAASIQG 300
QY 301 GYDMRKILNGTVSSKRPKLSVTFVNDHDTQPGQSLESTVQTFKPLAFAFILLRESGYPQ 360
DB 301 GYDMRKILNGTVSSKRPKLSVTFVNDHDTQPGQSLESTVQTFKPLAFAFILLRESGYPQ 360
QY 361 VFYGMWYGTGDSOREIPALKEIKRQYAYGAOHDFDHDIVGTRREGSSVA 420
DB 361 VFYGMWYGTGDSOREIPALKEIKRQYAYGAOHDFDHDIVGTRREGSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGWGFHVGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGWGFHVGGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483

RESULT 7
US-10-644-187-2
Sequence 2, Application US/10644187
Publication No. US20040048351A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796,204-US
CURRENT APPLICATION NUMBER: US/10/644,187
CURRENT FILING DATE: 2003-08-20
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11

PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-644-187-2

Query Match 100.0%; Score 2666; DB 12; Length 483;
Best Local Similarity 100.0%; Pred. No. 6.9e-239; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0;

QY 1 ANLNGTLMQFEMWPNNDGQHRRLQNDASAYLAHEGITAAMIIPPAKGTSGADVGAYD 60
DB 1 ANLNGTLMQFEMWPNNDGQHRRLQNDASAYLAHEGITAAMIIPPAKGTSGADVGAYD 60
QY 61 LYDLGEFHQKGTVRITKYGKGLQSAIKSLHSRDINVGDVVINKGGADATEDYTAVEV 120
DB 61 LYDLGEFHQKGTVRITKYGKGLQSAIKSLHSRDINVGDVVINKGGADATEDYTAVEV 120
QY 121 DPADRRRVISGHLIKAWTHFHPGRGSTYSDFKMWHYFDGTDWDESRKLNRIYKFGOK 180
DB 121 DPADRRRVISGHLIKAWTHFHPGRGSTYSDFKMWHYFDGTDWDESRKLNRIYKFGOK 180
QY 181 AMDWEVSNNENGVNDYLMVADIDYDHPDVAALIKRGWYANELQJDFRLDAVKIKFSF 240
DB 181 AMDWEVSNNENGVNDYLMVADIDYDHPDVAALIKRGWYANELQJDFRLDAVKIKFSF 240
QY 241 LEDWNVHAREKTKEMFTYAEYQNDLQALENYLNKTNPNHSVFPVPLHYQFHAASIQG 300
DB 241 LEDWNVHAREKTKEMFTYAEYQNDLQALENYLNKTNPNHSVFPVPLHYQFHAASIQG 300
QY 301 GYDMRKILNGTVSSKRPKLSVTFVNDHDTQPGQSLESTVQTFKPLAFAFILLRESGYPQ 360
DB 301 GYDMRKILNGTVSSKRPKLSVTFVNDHDTQPGQSLESTVQTFKPLAFAFILLRESGYPQ 360
QY 361 VFYGMWYGTGDSOREIPALKEIKRQYAYGAOHDFDHDIVGTRREGSSVA 420
DB 361 VFYGMWYGTGDSOREIPALKEIKRQYAYGAOHDFDHDIVGTRREGSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGWGFHVGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGWGFHVGGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483

RESULT 8
US-10-327-837-4
Sequence 4, Application US/10327837
Publication No. US20030211958A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
APPLICANT: Bisgard-Frantzen Henrik
APPLICANT: Outtrup, Helle
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Vibeke Skovgaard
APPLICANT: Hoeck, Lisbeth Hedegaard
TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
FILE REFERENCE: 5276,400-US
CURRENT APPLICATION NUMBER: US/10/327,837
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US/09/290,734
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 483

TYPE: PRT
ORGANISM: B. licheniformis
US-10-327-837-4

Query Match 100.0%; Score 2666; DB 12; Length 483;
Best Local Similarity 100.0%; Pred. No. 6.9e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANNGTLMQYFEWYMPNDGQWRLQNDSAIYLAHGTTAWIPPAKYGTSQADVYGAYD 60
DB 1 ANNGTLMQYFEWYMPNDGQWRLQNDSAIYLAHGTTAWIPPAKYGTSQADVYGAYD 60
QY 61 LYDGEFHQKGTATKTKGTGELQSAIKSLHSRDINVGDVVINKGADATEDVTAVEV 120
DB 61 LYDGEFHQKGTATKTKGTGELQSAIKSLHSRDINVGDVVINKGADATEDVTAVEV 120
QY 121 DPADNRNVIISGEHLIKAMTHFHPGSGTYSDFKMWYHFDGTDWDSRKLNRITYEQGK 180
DB 121 DPADNRNVIISGEHLIKAMTHFHPGSGTYSDFKMWYHFDGTDWDSRKLNRITYEQGK 180
QY 181 AMDWEVSNEGNNDYLMYADIDYDHPVAAEIKRWGTWYANLQDGFRLDAYKHIFSF 240
DB 181 AMDWEVSNEGNNDYLMYADIDYDHPVAAEIKRWGTWYANLQDGFRLDAYKHIFSF 240
QY 241 LRDWVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFHSVFDVPLHYQFHAASTQG 300
DB 241 LRDWVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFHSVFDVPLHYQFHAASTQG 300
QY 301 GYDWRKLLNGTVVSKHPLKSVTFVNDHNDTPQGSLSTVQWTFKPLAYAFILTRREGSYQ 360
DB 301 GYDWRKLLNGTVVSKHPLKSVTFVNDHNDTPQGSLSTVQWTFKPLAYAFILTRREGSYQ 360
QY 361 VFYGDMYGTKDGSOREIPALKHKIEPILKARKQYAGACHDYPDHDIVGWTREGDSSVA 420
DB 361 VFYGDMYGTKDGSOREIPALKHKIEPILKARKQYAGACHDYPDHDIVGWTREGDSSVA 420
QY 421 NSGLAALITDPPGAKMYVGRQNAGETWHDITGNRSEPVVINSSEGGEFHVNGGSVSIV 480
DB 421 NSGLAALITDPPGAKMYVGRQNAGETWHDITGNRSEPVVINSSEGGEFHVNGGSVSIV 480
QY 481 VQR 483
DB 481 VQR 483

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RESULT 9

US-10-146-327-4
Sequence 4, Application US/10146327
Publication No. US20030044954A1
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Jorgensen, Christel T.
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Kjaerulff, Soren
TITLE OF INVENTION: Alpha-Amylase Variants
FILE REFERENCE: 5886, 200-US
CURRENT APPLICATION NUMBER: US/10/146,327
CURRENT FILING DATE: 2002-05-15, 168
PRIOR APPLICATION NUMBER: US/09/537,168
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: PA 1999 00437
PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: 60/127,427
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-146-327-4

Query Match 100.0%; Score 2666; DB 14; Length 483;
Best Local Similarity 100.0%; Pred. No. 6.9e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANNGTLMQYFEWYMPNDGQWRLQNDSAIYLAHGTTAWIPPAKYGTSQADVYGAYD 60
DB 1 ANNGTLMQYFEWYMPNDGQWRLQNDSAIYLAHGTTAWIPPAKYGTSQADVYGAYD 60
QY 61 LYDGEFHQKGTATKTKGTGELQSAIKSLHSRDINVGDVVINKGADATEDVTAVEV 120
DB 61 LYDGEFHQKGTATKTKGTGELQSAIKSLHSRDINVGDVVINKGADATEDVTAVEV 120
QY 121 DPADNRNVIISGEHLIKAMTHFHPGSGTYSDFKMWYHFDGTDWDSRKLNRITYEQGK 180
DB 121 DPADNRNVIISGEHLIKAMTHFHPGSGTYSDFKMWYHFDGTDWDSRKLNRITYEQGK 180
QY 181 AMDWEVSNEGNNDYLMYADIDYDHPVAAEIKRWGTWYANLQDGFRLDAYKHIFSF 240
DB 181 AMDWEVSNEGNNDYLMYADIDYDHPVAAEIKRWGTWYANLQDGFRLDAYKHIFSF 240
QY 241 LRDWVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFHSVFDVPLHYQFHAASTQG 300
DB 241 LRDWVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFHSVFDVPLHYQFHAASTQG 300
QY 301 GYDWRKLLNGTVVSKHPLKSVTFVNDHNDTPQGSLSTVQWTFKPLAYAFILTRREGSYQ 360
DB 301 GYDWRKLLNGTVVSKHPLKSVTFVNDHNDTPQGSLSTVQWTFKPLAYAFILTRREGSYQ 360
QY 361 VFYGDMYGTKDGSOREIPALKHKIEPILKARKQYAGACHDYPDHDIVGWTREGDSSVA 420
DB 361 VFYGDMYGTKDGSOREIPALKHKIEPILKARKQYAGACHDYPDHDIVGWTREGDSSVA 420
QY 421 NSGLAALITDPPGAKMYVGRQNAGETWHDITGNRSEPVVINSSEGGEFHVNGGSVSIV 480
DB 421 NSGLAALITDPPGAKMYVGRQNAGETWHDITGNRSEPVVINSSEGGEFHVNGGSVSIV 480
QY 481 VQR 483
DB 481 VQR 483

```

RESULT 10

US-10-186-042-2
Sequence 2, Application US/10186042
Publication No. US20030171236A1
GENERAL INFORMATION:
APPLICANT: Borchert, Torben
APPLICANT: Svendsen, Allan
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796, 204-US
CURRENT APPLICATION NUMBER: US/10/186,042
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-186-042-2

Query Match 100.0%; Score 2666; DB 14; Length 483;
 Best Local Similarity 100.0%; Pred. No. 6.9e-239;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMOYFEWYMPNDGQHRRLQNDASAYLAHGTITAVWIPPAKGTSGADVGAYD 60
 DB 1 ANLNGTLMOYFEWYMPNDGQHRRLQNDASAYLAHGTITAVWIPPAKGTSGADVGAYD 60
 QY 61 LYDLGEFHOKGTVRTKYGKGLQSAIKSLHSRDINVGVINHGADATEDVTAVEV 120
 DB 61 LYDLGEFHOKGTVRTKYGKGLQSAIKSLHSRDINVGVINHGADATEDVTAVEV 120
 QY 121 DPADRNRVLSGHELLIKAWTHFHPFGSGSTYSDPKMWHYFDGTDWDESKLNRIYKFGQK 180
 DB 121 DPADRNRVLSGHELLIKAWTHFHPFGSGSTYSDPKMWHYFDGTDWDESKLNRIYKFGQK 180
 QY 121 DPADRNRVLSGHELLIKAWTHFHPFGSGSTYSDPKMWHYFDGTDWDESKLNRIYKFGQK 180
 DB 121 DPADRNRVLSGHELLIKAWTHFHPFGSGSTYSDPKMWHYFDGTDWDESKLNRIYKFGQK 180
 QY 181 AMDMEVSNENGVNDYLMVADIDYDHPDVALEIKRWGTWYANELQDGFRLDAVKIKRSEF 240
 DB 181 AMDMEVSNENGVNDYLMVADIDYDHPDVALEIKRWGTWYANELQDGFRLDAVKIKRSEF 240
 QY 241 LRDVNVHVEKTKGKEMFTVAEYQNDLGLNENYLNKTNFNSVFDVPLHYQFHAASGCG 300
 DB 241 LRDVNVHVEKTKGKEMFTVAEYQNDLGLNENYLNKTNFNSVFDVPLHYQFHAASGCG 300
 QY 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTFKPLAYAFILTRBSGYPO 360
 DB 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTFKPLAYAFILTRBSGYPO 360
 QY 361 VFYGDVYGTGDSOREIPALKKIEPILKARKQYAGAOHDYFDHDIYGMTRBGDSVA 420
 DB 361 VFYGDVYGTGDSOREIPALKKIEPILKARKQYAGAOHDYFDHDIYGMTRBGDSVA 420
 QY 421 NSGLAALLITDGPAGARMYVGRONAGETWHDITGNRSEBVVINSBGWGEFHNHNGSVSIY 480
 DB 421 NSGLAALLITDGPAGARMYVGRONAGETWHDITGNRSEBVVINSBGWGEFHNHNGSVSIY 480
 QY 481 VOR 483
 DB 481 VOR 483

RESULT 11

US-10-184-771-2
 ; Sequence 2, Application US/10184771
 ; Publication No. US20030170769A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Bisgaard-Frantzen, Henrik
 ; APPLICANT: Borchert, Torben Vedel
 ; TITLE OF INVENTION: Alpha-Amylase Mutants
 ; FILE REFERENCE: 0776/1P216-US2
 ; CURRENT APPLICATION NUMBER: US/10/184,771
 ; PRIOR FILING DATE: 2002-06-28
 ; PRIOR APPLICATION NUMBER: US/09/636,252
 ; PRIOR FILING DATE: 2000-08-10
 ; PRIOR APPLICATION NUMBER: 08/683,838
 ; PRIOR FILING DATE: 1996-07-18
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 512
 ; TYPE: PRT
 ; ORGANISM: B. licheniformis
 ; US-10-184-771-2

Query Match 100.0%; Score 2666; DB 14; Length 512;
 Best Local Similarity 100.0%; Pred. No. 7.5e-239;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMOYFEWYMPNDGQHRRLQNDASAYLAHGTITAVWIPPAKGTSGADVGAYD 60
 DB 30 ANLNGTLMOYFEWYMPNDGQHRRLQNDASAYLAHGTITAVWIPPAKGTSGADVGAYD 89

QY 61 LYDLGEFHOKGTVRTKYGKGLQSAIKSLHSRDINVGVINHGADATEDVTAVEV 120
 DB 90 LYDLGEFHOKGTVRTKYGKGLQSAIKSLHSRDINVGVINHGADATEDVTAVEV 149
 QY 121 DPADRNRVLSGHELLIKAWTHFHPFGSGSTYSDPKMWHYFDGTDWDESKLNRIYKFGQK 180
 DB 150 DPADRNRVLSGHELLIKAWTHFHPFGSGSTYSDPKMWHYFDGTDWDESKLNRIYKFGQK 209
 QY 181 AMDMEVSNENGVNDYLMVADIDYDHPDVALEIKRWGTWYANELQDGFRLDAVKIKRSEF 240
 DB 210 AMDMEVSNENGVNDYLMVADIDYDHPDVALEIKRWGTWYANELQDGFRLDAVKIKRSEF 269
 QY 241 LRDVNVHVEKTKGKEMFTVAEYQNDLGLNENYLNKTNFNSVFDVPLHYQFHAASGCG 300
 DB 270 LRDVNVHVEKTKGKEMFTVAEYQNDLGLNENYLNKTNFNSVFDVPLHYQFHAASGCG 329
 QY 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTFKPLAYAFILTRBSGYPO 360
 DB 330 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTFKPLAYAFILTRBSGYPO 389
 QY 361 VFYGDVYGTGDSOREIPALKKIEPILKARKQYAGAOHDYFDHDIYGMTRBGDSVA 420
 DB 390 VFYGDVYGTGDSOREIPALKKIEPILKARKQYAGAOHDYFDHDIYGMTRBGDSVA 449
 QY 421 NSGLAALLITDGPAGARMYVGRONAGETWHDITGNRSEBVVINSBGWGEFHNHNGSVSIY 480
 DB 450 NSGLAALLITDGPAGARMYVGRONAGETWHDITGNRSEBVVINSBGWGEFHNHNGSVSIY 509
 QY 481 VOR 483
 DB 510 VOR 512

RESULT 12

US-10-189-922-2
 ; Sequence 2, Application US/10199922
 ; Publication No. US20030022346A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gist-brocades B.V.
 ; TITLE OF INVENTION: Alpha-amylase mutants
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Gist-brocades B.V.
 ; STREET: Wateringseweg 1
 ; CITY: Delft
 ; COUNTRY: The Netherlands
 ; ZIP: 2611 XT
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/199,922
 ; FILING DATE: 18-Jul-2002
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 512 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 ; US-10-189-922-2

Query Match 99.9%; Score 2663; DB 14; Length 512;
 Best Local Similarity 99.8%; Pred. No. 1.4e-238;
 Matches 482; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMOYFEWYMPNDGQHRRLQNDASAYLAHGTITAVWIPPAKGTSGADVGAYD 60
 DB 30 ANLNGTLMOYFEWYMPNDGQHRRLQNDASAYLAHGTITAVWIPPAKGTSGADVGAYD 89
 QY 61 LYDLGEFHOKGTVRTKYGKGLQSAIKSLHSRDINVGVINHGADATEDVTAVEV 120

Db 90 LYDLGEFHQKGVTRTKYTGKGLQSAIKSLHSRDINTVGDVIVNHKGADATEDVTAIEV 149
Qy 121 DPADRRRVISGEHLIKAWTHFFPGRGSTYSDFKMWTHFFDGTWDESKLRIRYKFGQK 180
Db 150 DPADRRRVISGEHLIKAWTHFFPGRGSTYSDFKMWTHFFDGTWDESKLRIRYKFGQK 209
Qy 181 AMDMEVSNENGVNDYLMYADIDYDHPDVAABIKRWGTAYANELQDGFRLDAVKIKESF 240
Db 210 AMDMEVSNENGVNDYLMYADIDYDHPDVAABIKRWGTAYANELQDGFRLDAVKIKESF 269
Qy 241 LRDWNVHREKTKGEMFTVAEYQNDLGALENYLNTKTNFNSVFPVPLHYQPHAASTQGG 300
Db 270 LRDWNVHREKTKGEMFTVAEYQNDLGALENYLNTKTNFNSVFPVPLHYQPHAASTQGG 329
Qy 301 GYDMKRLNGTVSKPLSKVTFVNDHDTQPGOSLESTVQTFKPLAFAFLITRESGYPO 360
Db 330 GYDMKRLNGTVSKPLSKVTFVNDHDTQPGOSLESTVQTFKPLAFAFLITRESGYPO 389
Qy 361 VFYGDWYGTGKDSOREIPALKKIEPIILKARQYAYGAQHDFDHHDIYGMTREGDSSVA 420
Db 390 VFYGDWYGTGKDSOREIPALKKIEPIILKARQYAYGAQHDFDHHDIYGMTREGDSSVA 449
Qy 421 NSGLAALITDGPQAGKMTVGRONAGETWHDITGNRSEPVVINSBGMEFHVNGGSVSIY 480
Db 450 NSGLAALITDGPQAGKMTVGRONAGETWHDITGNRSEPVVINSBGMEFHVNGGSVSIY 509
Qy 481 VQR 483
Db 510 VQR 512

RESULT 13
US-10-872-114
Sequence 114, Application US/10081872,
Publication No. US20030125534A1
GENERAL INFORMATION:
APPLICANT: Callen, Walter
APPLICANT: Richardson, Toby
APPLICANT: Frey, Gerhard
APPLICANT: Short, Jay M.
APPLICANT: Mathur, Eric J.
APPLICANT: Gray, Kevin A.
APPLICANT: Kerovo, Janne S.
APPLICANT: Sluscka, Malgorzata
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
FILE REFERENCE: 09010-108001
CURRENT FILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/270,495
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/291,122
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 321
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 114
LENGTH: 512
TYPE: PRT
ORGANISM: Environmental
US-10-081-872-114

Query Match 99.5%; Score 2654; DB 14; Length 512;
Best Local Similarity 99.4%; Pred. No. 9.8e-238;
Matches 480; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANINGTLMQYFEWYMPNDGQHRRLQNDASAYLAHEGITTAVWIPPAVKGTQSADVGYGAYD 60
Db 30 ANINGTLMQYFEWYMPNDGQHRRLQNDASAYLAHEGITTAVWIPPAVKGTQSADVGYGAYD 89
Qy 61 LYDLGEFHQKGVTRTKYTGKGLQSAIKSLHSRDINTVGDVIVNHKGADATEDVTAIEV 120

Db 90 LYDLGEFHQKGVTRTKYTGKGLQSAIKSLHSRDINTVGDVIVNHKGADATEDVTAIEV 149
Qy 121 DPADRRRVISGEHLIKAWTHFFPGRGSTYSDFKMWTHFFDGTWDESKLRIRYKFGQK 180
Db 150 DPADRRRVISGEHLIKAWTHFFPGRGSTYSDFKMWTHFFDGTWDESKLRIRYKFGQK 209
Qy 181 AMDMEVSNENGVNDYLMYADIDYDHPDVAABIKRWGTAYANELQDGFRLDAVKIKESF 240
Db 210 AMDMEVSNENGVNDYLMYADIDYDHPDVAABIKRWGTAYANELQDGFRLDAVKIKESF 269
Qy 241 LRDWNVHREKTKGEMFTVAEYQNDLGALENYLNTKTNFNSVFPVPLHYQPHAASTQGG 300
Db 270 LRDWNVHREKTKGEMFTVAEYQNDLGALENYLNTKTNFNSVFPVPLHYQPHAASTQGG 329
Qy 301 GYDMKRLNGTVSKPLSKVTFVNDHDTQPGOSLESTVQTFKPLAFAFLITRESGYPO 360
Db 330 GYDMKRLNGTVSKPLSKVTFVNDHDTQPGOSLESTVQTFKPLAFAFLITRESGYPO 389
Qy 361 VFYGDWYGTGKDSOREIPALKKIEPIILKARQYAYGAQHDFDHHDIYGMTREGDSSVA 420
Db 390 VFYGDWYGTGKDSOREIPALKKIEPIILKARQYAYGAQHDFDHHDIYGMTREGDSSVA 449
Qy 421 NSGLAALITDGPQAGKMTVGRONAGETWHDITGNRSEPVVINSBGMEFHVNGGSVSIY 480
Db 450 NSGLAALITDGPQAGKMTVGRONAGETWHDITGNRSEPVVINSBGMEFHVNGGSVSIY 509
Qy 481 VQR 483
Db 510 VQR 512

RESULT 14
US-10-105-733-8
Sequence 8, Application US/10105733,
Publication No. US20030138786A1
GENERAL INFORMATION:
APPLICANT: Callen, Walter
APPLICANT: Richardson, Toby
APPLICANT: Frey, Gerhard
APPLICANT: Miller, Carl
APPLICANT: Kazaoka, Martin
APPLICANT: Short, Jay
APPLICANT: Mathur, Eric
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
FILE REFERENCE: 09010-107002
CURRENT FILING DATE: 2002-03-22
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US/10105,733
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10/081,739
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/270,495
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/291,122
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 512
TYPE: PRT
ORGANISM: Environmental
US-10-105-733-8

Query Match 99.5%; Score 2654; DB 14; Length 512;
Best Local Similarity 99.4%; Pred. No. 9.8e-238;
Matches 480; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANINGTLMQYFEWYMPNDGQHRRLQNDASAYLAHEGITTAVWIPPAVKGTQSADVGYGAYD 60
Db 30 ANINGTLMQYFEWYMPNDGQHRRLQNDASAYLAHEGITTAVWIPPAVKGTQSADVGYGAYD 89

QY 61 LYDGEFHOKGTATKTKGTGKGELOSALKSLSHRDINYYGDDVINHKGGADATEDVTAVEV 120
 DB 90 LYDGEFHOKGTATKTKGTGKGELOSALKSLSHRDINYYGDDVINHKGGADATEDVTAVEV 149
 QY 121 DPADNRVYISGEHLIKAWTHFHPFGSGTYSDFKHWYHFDGTDWDSRKLNRIFYKQK 180
 DB 150 DPADNRVYISGEHLIKAWTHFHPFGSGTYSDFKHWYHFDGTDWDSRKLNRIFYKQK 209
 QY 181 AMDWEVSNENGNYYDLMYADIDYDHPVAAEIKKMGTYANELQDGFRLDAVGHIFSF 240
 DB 210 AMDWEVSNENGNYYDLMYADIDYDHPVAAEIKKMGTYANELQDGFRLDAVGHIFSF 269
 QY 241 LRDWNVHREKTKGEMFTVAEYMONDIALENYLNKTNFNSVDFPLHYQFHAASQGG 300
 DB 270 LRDWNVHREKTKGEMFTVAEYMONDIALENYLNKTNFNSVDFPLHYQFHAASQGG 329
 QY 301 GYDMRKLNGTVVSGHPLKSVTFVNDHDTOPQGSLESTVQTMFKPLAYAFILITRESGYPQ 360
 DB 330 GYDMRKLNGTVVSGHPLKSVTFVNDHDTOPQGSLESTVQTMFKPLAYAFILITRESGYPQ 389
 QY 361 VFYGDWYGTGKDSOREIPALKHKEPIIKARKQAYAGQHDYFDHDI VGMTRGDSVA 420
 DB 390 VFYGDWYGTGKDSOREIPALKHKEPIIKARKQAYAGQHDYFDHDI VGMTRGDSVA 449
 QY 421 NSGLAALITDGPAGAKRMVYGRQNGETWHDITGNRSEPVYINSEGWGEFHVNGGSVSIY 480
 DB 450 NSGLAALITDGPAGAKRMVYGRQNGETWHDITGNRSEPVYINSEGWGEFHVNGGSVSIY 509
 QY 481 VQR 483
 DB 510 VQR 512

RESULT 15
 US-10-081-739A-8
 / Sequence 8, Application US/10081739A
 / Publication No. US20030170634A1
 / GENERAL INFORMATION:
 / APPLICANT: Callen, Walter
 / APPLICANT: Richardson, Toby
 / APPLICANT: Frey, Gerald
 / APPLICANT: Miller, Carl
 / APPLICANT: Kazaoka, Martin
 / APPLICANT: Short, Jay
 / APPLICANT: Mathur, Eric
 / TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
 / TITLE OF INVENTION: AND METHODS OF USE THEREOF
 / FILE REFERENCE: 09010-107001
 / CURRENT APPLICATION NUMBER: US/10/081,739A
 / CURRENT FILING DATE: 2002-02-21
 / PRIOR APPLICATION NUMBER: 60/270,495
 / PRIOR FILING DATE: 2001-02-21
 / PRIOR APPLICATION NUMBER: 60/270,496
 / PRIOR FILING DATE: 2001-02-21
 / PRIOR APPLICATION NUMBER: 60/291,122
 / PRIOR FILING DATE: 2001-05-14
 / NUMBER OF SEQ ID NOS: 69
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 8
 / LENGTH: 512
 / TYPE: PRT
 / ORGANISM: Unknown
 / FEATURE:
 / OTHER INFORMATION: Obtained from an environmental sample
 US-10-081-739A-8

Query Match 99.5%; Score 2654; DB 14; Length 512;
 Best local similarity 99.4%; Pred. No. 9, 8e-238;
 Matches 480; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANINGTLMQYFEWYMDGCHRLQNDASVLAERGITAVWIPRAYKTSQADVGAYD 60
 DB 30 ANINGTLMQYFEWYMDGCHRLQNDASVLAERGITAVWIPRAYKTSQADVGAYD 89

QY 61 LYDGEFHOKGTATKTKGTGKGELOSALKSLSHRDINYYGDDVINHKGGADATEDVTAVEV 120
 DB 90 LYDGEFHOKGTATKTKGTGKGELOSALKSLSHRDINYYGDDVINHKGGADATEDVTAVEV 149
 QY 121 DPADNRVYISGEHLIKAWTHFHPFGSGTYSDFKHWYHFDGTDWDSRKLNRIFYKQK 180
 DB 150 DPADNRVYISGEHLIKAWTHFHPFGSGTYSDFKHWYHFDGTDWDSRKLNRIFYKQK 209
 QY 181 AMDWEVSNENGNYYDLMYADIDYDHPVAAEIKKMGTYANELQDGFRLDAVGHIFSF 240
 DB 210 AMDWEVSNENGNYYDLMYADIDYDHPVAAEIKKMGTYANELQDGFRLDAVGHIFSF 269
 QY 241 LRDWNVHREKTKGEMFTVAEYMONDIALENYLNKTNFNSVDFPLHYQFHAASQGG 300
 DB 270 LRDWNVHREKTKGEMFTVAEYMONDIALENYLNKTNFNSVDFPLHYQFHAASQGG 329
 QY 301 GYDMRKLNGTVVSGHPLKSVTFVNDHDTOPQGSLESTVQTMFKPLAYAFILITRESGYPQ 360
 DB 330 GYDMRKLNGTVVSGHPLKSVTFVNDHDTOPQGSLESTVQTMFKPLAYAFILITRESGYPQ 389
 QY 361 VFYGDWYGTGKDSOREIPALKHKEPIIKARKQAYAGQHDYFDHDI VGMTRGDSVA 420
 DB 390 VFYGDWYGTGKDSOREIPALKHKEPIIKARKQAYAGQHDYFDHDI VGMTRGDSVA 449
 QY 421 NSGLAALITDGPAGAKRMVYGRQNGETWHDITGNRSEPVYINSEGWGEFHVNGGSVSIY 480
 DB 450 NSGLAALITDGPAGAKRMVYGRQNGETWHDITGNRSEPVYINSEGWGEFHVNGGSVSIY 509
 QY 481 VQR 483
 DB 510 VQR 512

Search completed: May 3, 2004, 20:47:45
 Job time : 39.6066 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:44:58 ; Search time 34.365 Seconds

(without alignments)
4438.289 Million cell updates/sec

Title: US-10-644-187-2

Perfect score: 2666
Sequence: 1 AALNTLMQYFEMWMDNDQ.....SGWGEFHYNGSVSTYQR 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP_mhc:*
8: SP_organella:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2025	76.0	513	16	Q81AS4 bacillus ce
2	2021	75.8	519	2	Q9RQ78 cytophaga s
3	2021	75.8	533	2	Q9AQ54 bacillus me
4	1991	74.7	513	16	Q81YJ4 bacillus an
5	1909	71.6	516	2	Q82839 bacillus sp
6	1789.5	67.1	549	2	Q31193 bacillus sp
7	1784.5	66.9	521	2	P71034 bacillus sp
8	1784.5	66.9	549	2	Q9KXV6 bacillus st
9	1783.5	65.8	613	2	Q59222 bacillus sp
10	1783.5	64.6	501	2	Q93148 bacillus sp
11	1502.5	56.4	507	16	Q87HG6 vibrio para
12	1336	50.1	481	16	Q89YPI bacteroides
13	1262	47.3	493	2	Q03657 bacteroides
14	1244	46.7	492	16	Q8YU21 anabaena sp
15	1233	46.2	484	16	Q97049 streptococc
16	1230.5	46.2	484	2	Q50583 streptococc

17	1228	46.1	484	16	Q8DPC8	Q8DPC8 streptococc
18	1197.5	44.9	488	16	Q8E696	Q8E696 streptococc
19	1186.5	44.9	488	16	Q8E0M2	Q8E0M2 streptococc
20	1185.5	44.8	486	16	Q8DT08	Q8DT08 streptococc
21	1182.5	44.4	485	2	Q53786	Q53786 streptococc
22	1156.5	43.4	486	2	Q68875	Q68875 streptococc
23	1108	41.6	491	16	Q9CG59	Q9CG59 lactococcus
24	1091.5	40.9	506	16	Q8U916	Q8U916 agrobacteri
25	1053	39.5	484	16	Q82555	Q82555 salmonella
26	1048	39.3	485	16	Q85G18	Q85G18 escherichia
27	1047	39.3	495	16	Q8XBB6	Q8XBB6 escherichia
28	1037	38.9	495	16	Q7UAB0	Q7UAB0 shigella fl
29	1035	38.8	495	16	Q83R40	Q83R40 shigella fl
30	1018.5	38.2	529	3	Q877B1	Q877B1 aspergillus
31	1018.5	38.2	460	1	Q9P9L0	Q9P9L0 pyrococcus
32	1018.5	38.2	460	1	Q08452	Q08452 pyrococcus
33	1018.5	38.2	473	17	Q8U319	Q8U319 pyrococcus
34	1018.5	38.2	473	17	Q8U319	Q8U319 pyrococcus
35	1018.5	38.2	473	17	Q8U319	Q8U319 pyrococcus
36	1018.5	38.2	473	17	Q8U319	Q8U319 pyrococcus
37	1018.5	38.2	473	17	Q8U319	Q8U319 pyrococcus
38	1018.5	38.2	473	17	Q8U319	Q8U319 pyrococcus
39	1018.5	38.2	473	17	Q8U319	Q8U319 pyrococcus
40	1018.5	38.2	473	17	Q8U319	Q8U319 pyrococcus
41	1018.5	38.2	473	17	Q8U319	Q8U319 pyrococcus
42	1018.5	38.2	473	17	Q8U319	Q8U319 pyrococcus
43	1018.5	38.2	473	17	Q8U319	Q8U319 pyrococcus
44	1018.5	38.2	473	17	Q8U319	Q8U319 pyrococcus
45	1018.5	38.2	473	17	Q8U319	Q8U319 pyrococcus

ALIGNMENTS

RESULT 1	Q81AS4	PRELIMINARY:	PRT:	513 AA.
ID	Q81AS4	Q81AS4		
AC	Q81AS4	Q81AS4		
DT	01-JUN-2003	(TRENDS) 24, Created		
DT	01-JUN-2003	(TRENDS) 24, Last sequence update		
DT	01-OCT-2003	(TRENDS) 25, Last annotation update		
DE	Glucan 1,4-alpha-maltotetraose (EC 3.2.1.98)			
GN	BC3482			
OC	Bacillus cereus (strain ATCC 14579 / DSM 31)			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus			
OK	NCBI_TaxID=226900			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=22608415; PubMed=12721630			
RX	Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,			
RA	Kapitel V., Bhattacharya A., Reznik G., Mikhailova N., Lapidis A.,			
RA	Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Malinas T.,			
RA	Grechkin Y., Pusch G., Goltzman E., Larsen N., D'Souza M., Malinas T.,			
RA	Overbeek R., Kyrpides N.,			
RT	"Genome sequence of Bacillus cereus and comparative analysis with			
RT	Bacillus anthracis",			
RL	Nature 423:87-91(2003).			
EMBL	AE017009; AAP10417.1			
DR	GO; GO:0004556; F:alpha-amyase activity; IEA.			
DR	GO; GO:0001678; F:hydrolyase activity, acting on glycosyl bonds; IEA.			
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.			
DR	InterPro; IPR006047; Alpha_ami_cat.			
DR	InterPro; IPR006589; Alp_ami_cat_sub.			
DR	Pfam; PF00128; alpha-amyase; 1.			
DR	SMART; SM00642; Amy; 1			
KW	Glycosidase; Hydrolase; Complete proteome.			
SC	SEQUENCE 513 AA; 58306 MW; 05C4611CBFF9F6 CRC64;			
Query Match	76.0%; Score 2025; DB 16; Length 513;			
Best Local Similarity	74.5%; Pred. No. 2,4e-140;			
Matches 359; Conservative 49; Mismatches 72; Indels 2; Gaps 1;				
QY	4 NOTLQYFEMWMDNDQ...RLQNDSDAYLAHGLTAWIPAYKGTSGADVGAYADLYD 63			

Db	32	NGILTMFEYVYVANDGNNHRLRTDVENLAEIGITSVWIPRAYKQTTQNDIDVGYADLLYD	91
Qy	64	LGEFHQKGVTRTKYGTGKGSJQSAIKSLHSRJDINVTGDAVINKGADATEDVTVAVEVDP	123
Db	92	LGEENQGVTRTKYGTGAQLKSAIDLHKKNIDVGDVVMNHKGADVTEVTVAVEVDP	151
Qy	124	DRNVSISGEHLIKAMTHFEHPPRGGSYSDPFKMMHWFPDGTOWDESRIKNIYKQ--GKA	181
Db	152	NRNVEVSGDYIEISMGCFNPGRGDSYSPFKMMHWFPOTOWDESRKNIYKRGIGKA	211
Qy	182	MDWVSVENNNYUYVYADIDYDHPVAAEIRMGWYANELQDGFPLDVVKIKTSFL	241
Db	212	MDWVSVENNNYDILMADIDPHDPVAAEMKMGWYANELNDLGFPLDVVKIIDHEYL	271
Qy	242	RDWVNHRETKGEMFTVAEYWCNDJGALENTLNTFNHSYFDVPLHYOFAASTQGG	301
Db	272	RDWVNHRCQGTGEMFVAEYWCNDIQTLNNYLAKNNYQSYFDPLNHNHYASTQGN	331
Qy	302	YDMKILNGVVSCHPLKSTFVDNHDQPGQSLSTVQTMKPAAYAFILTRBSGYOV	361
Db	332	YDMKILKGVYVANHPLAVTLVYENDSQPGQSLSVSPMFKPLAYFILTREGYPSV	391
Qy	362	FYDGNITKQDSQREIPALKEKTEPILKARKOYVGAOHDPFHNDIVGWTRECDSSVAN	421
Db	392	FYGGYVTKNSYVEIPALNDKIDPLITLARKKFAVGTQADYFDHDPVIGWTRBCDSYHAN	451
Qy	422	SGLAALITTDPGGAKMNVGRQVAGEYWDITDGNSESPVINSBEKMBEFHNGGSVSIY	481
Db	452	SGLATILISDQPGGAKMNDVGRKNNAGSVWVDIDGNQNTVYTIINKQMGQFVYSGGSVSIY	511
Qy	482	QR 483	
Db	512	QQ 513	

RESULT 2			
ID	OSROT8	PRELIMINARY;	PRT; 519 AA.
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, last annotation update)		
DE	Raw starch digesting amylase precursor.		
OS	Cytophaga sp.		
OC	Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;		
OC	Flexibacteriaceae; Cytophaga.		
OX	NCBI_TaxID=29535;		
RM	[1]		
RA	SEQUENCE FROM N.A.		
RA	Jeang C.L., Chan L.S., Chen M.Y.;		
RL	Submitted (May-1998) to the EMBL/GenBank/DBD databases.		
DR	EMBL; AF067653; AAF00567.1; -		
DR	HSSP; P06278; 1VTS.		
DR	GO: GO:0004556; F.alpha-amylase activity; IEA.		
DR	GO: GO:0005975; P.carbohydrate metabolism; IEA.		
DR	InterPro: IPR006047; Alpha-amyl_cat.		
DR	InterPro: IPR006589; Alp_amyl_cat_sub.		
DR	InterPro: IPR006046; Glyco_hydro_13.		
DR	Pfam; PF00128; alpha-amylase; 1.		
DR	PRINTS; PR00110; ALPHAMYLASE.		
DR	SMART; SM00642; Amy; 1.		
KW	Signal.		
FT	SIGNAL		
FT	CHAIN 1 57	POTENTIAL	
FT	CHAIN 58 510	RAW STARCH DIGESTING AMYLASE.	
SO	SEQUENCE 519 AA; 56337 MW; 3E6B8A4DF98B163 CRC64;		

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Query March      75.8%; Score 2021; DB 2; Length 519;  
Best Local Similarity 73.4%; Pred. No. 4.6e-140;  
Matches 356; Conservative 60; Mismatches 67; Indels 2; Gaps 1.  
  
QY      1 ANINGTLMGVEFKYMNDGCHNRRLONDSAYLAHGHTAAWVIPPAYKGTSDADVGCAVD 60  
| | | | | | | | | | | | | | : | : | : | | | | | | | | | | | |
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Dh	33	AA	NTNGNMQYFEMVYENSDQGNRLRLTDAFLYSVIGITAWTPRAYKSTQALVGYGFXD	94
Qy	61	LY	DGEFHOKTVPRTKGTGKELGSAIKLSLRDINYYGDPVJNHKGAATEDVTAVEY	120
Dh	95	LY	DGEFHNKGVRKRTGTGKELSAVNTLSNGICVYGDVNMHKGADYTERNAVEX	154
Qy	121	DP	ADRNRVITSGHLLIKAMTHFHPERGSTYSDFKMHYHEDGTDWDSRKLNIYKFO--	178
Dh	155	NP	ENRQETSGSYNIQAWTGFFPBRGTYTSENFKOMFHFEGTDMDSRSLSRFKRGST	214
Qy	179	GK	AMDEVENENGANDYLYMADIDVDHEDVAAEIKRGWTYANELQDGEFLDAVKIKF	238
Dh	215	GK	AMDEVESEKGNADYLYMADIDVDHEDVNMKKGVMTANVSGDGRLLDAVKIKF	274
Qy	239	SF	RDVWNHYREKTKGEMPTAEVYQNDLGALTEYLNKTNENHSVFPVPLHYOFLASTQ	298
Dh	275	SF	KDWYDAPARAATKEMPTVQETQVQNDLGALNNYLAKANNOSLFLAPLHYNVAASTG	334
Qy	299	GG	STDKRLNGTVYSKAPLSVTFVNDHDPQGSLESTYQYMFKFLAALFILTBSGY	358
Dh	335	GG	YDRENLLNLTVAASPTKAVTLVENHDQPOQSLESTVQPMFKFLAALFILTBSGY	384
Qy	359	PO	FYDMTGTQDSOREIPALKNKIEBILYARKOYAVGAOHDFDHDIVGWTREGSS	418
Dh	395	PS	FYDMTGTGTTRRELPAKLSKIEBILYARKDYAVGTORDYIDBVDIGWTRREBST	454
Qy	419	VA	SGALAITTOPGAKRMVYGRONAGETNHDITGRNRPVJNSGMEEFHNQGSVS	478
Dh	455	KAS	SGALAITTOPGSRKMVYGTGNABEIMYDITGNRTDILITGSDGYATFPNGGSVS	514
Qy	479	IT	YTOR 483	
Dh	515	VM	QO 519	

```

RESULT 3
09A054
ID 09A054 PRELIMINARY; PRT; 533 AA.
AC 09A054;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 14, Last annotation update)
DE Alpha-amylose.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1404;
[1]
RP SEQUENCE FROM N.A.
RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,
RA Park K.-H.;
RT "Cloning of maltopentaose-producing amylose from Bacillus megaterium
RT KSM B-404."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220440; AAK00598.1; -.
DR HSSP; P06278; 1VJ38.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR005889; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amylose; 1.
DR SMART; SM00642; Ramy; 1.
SQ SEQUENCE 533 AA; 60557 MW; 789CED6A19C7DDE CRC64;

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	Query Match	75.8%;	Score 20.1;	Length 533;
	Best Local Similarity	74.3%;	Pred. No. 4.9e-140;	
	Matches 358;	Conservative 49;	Mismatches 73;	Indels 2; Gaps 1
QY	4	NGTLMQYFFEMYNPNOGHWRSLQNDASALAHGTTAAVPIPAYKGTQADVGYGAYVLYD	63	
Db	52	NGTLMQYFEMYNPNOGHWRSLQNDASALAHGTTAAVPIPAYKGTQADVGYGAYVLYD	111	
QY	64	LGFHFQKGYVTRKYKQKSELQSAIKSLNSRDINYGADVIVHKKGAATEDVTAVEVDFPA	123	

Db 112 LGFEHQKGTVRTKGTGKAQLKSAIDALHKKNIDYGVVNMHKGADYETVTAVERDPS 171
 Qy 124 DNRNVIAGEHLIKAMTHFHPGSGTSPDFKMWYHFDGTDWDESKLRNRYKFO--GKA 181
 Db 172 NRVVSGDYELISANTGFRPGSGSYSPFKMKWHFPGTDWDESKLRNRYKFRGIGKA 231
 Qy 182 WMEVSNENGNNDYLYADIDYDHPVAALIKRWGTWYANIELDGFRLDAVGHIFSEFL 241
 Db 233 WMEVSNENGNNDYLYADIDYDHPVAALIKRWGTWYANIELDGFRLDAVGHIFSEFL 291
 Qy 242 RDMVNHVRKTKGEMFTVAEYQNDLGALNTNKTENHSHVDFVPLHYOFHAASFGCG 301
 Db 292 RDMVNHVRKTKGEMFTVAEYQNDLGALNTNKTENHSHVDFVPLHYOFHAASFGCG 351
 Qy 302 YDMRKLNGTVYSKHEPKSVTVFVNDHDTQPGSLESSTVQWTKPLAYAFILTRREGYPOV 361
 Db 352 YDMRKLNGTVYSKHEPKSVTVFVNDHDTQPGSLESSTVQWTKPLAYAFILTRREGYPOV 411
 Qy 362 FYGDMYGTGDSQREIPALKHKEIPILKARKQYAGAHDPDHDHIVGWTREGSSVAN 421
 Db 412 FYGDMYGTGDSQREIPALKHKEIPILKARKQYAGAHDPDHDHIVGWTREGSSVAN 471
 Qy 422 SGLAALITDGPAGAKMYVGRVAGETWHDITGNRSEPVINSSENGEFTVNGSSVSIY 481
 Db 472 SGLAALITDGPAGAKMYVGRVAGETWHDITGNRSEPVINSSENGEFTVNGSSVSIY 531
 Qy 482 QR 483
 Db 532 QR 533
 RESULT 4
 ID 081Y04 PRELIMINARY; PRT; 513 AA.
 AC 081Y04;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Alpha-amyase.
 GN AMYS OR BA3551.
 OS Bacillus anthracis (strain Ames).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=198094;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2608414; PubMed=12721629;
 RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
 Nelson K.B., Tetrelin H., Fouts D.E., Eisen J.A., Gill S.R.,
 Holtzapple E.K., Ostad O.A., Helgason E., Ralston J., Wu M.,
 Kolonay J.F., Beaman W.J., Dodson R.J., Brinkac L.M., Galin M.,
 Deboy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 Nelson M.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
 Barton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
 Berry K.J., Plant R.D., Wolf A.M., Watkins K.L., Niemeyer W.C.,
 Haren A., Cline R., Redmond C., Thwaiter J.E., White O., Salzberg S.L.,
 Thompson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
 Fraser C.M.;
 RA "The genome sequence of Bacillus anthracis Ames and comparison to
 RT closely related bacteria.";
 RL Nature 423:81-86(2003).
 RL EMBL; AB017035; AAP27311.1; -
 DR TIGR; BA3551;
 DR GO; GO:0004556; F:alpha-amyase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_aml1_cat.
 DR InterPro; IPR006589; Alp_aml1_cat_sub.
 DR Pfam; PF00128; alpha-amyase; 1.
 DR SMART; SM00642; Amy; 1.
 KM Complete proteome.
 SQ SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;

Query Match 74.7%; Score 1991; DB 16; Length 513;
 Best Local Similarity 73.0%; Pred. No. 7, 5e-138;

Matches 352; Conservative 51; Mismatches 77; Indels 2; Gaps 1;
 Qy 4 NGTLMQYFEWYAPSDNNHNRLLTDAENLAKQKITSVWIPPAVKGTQNDVYGADYLD 63
 Db 32 NGTLMQYFEWYAPSDNNHNRLLTDAENLAKQKITSVWIPPAVKGTQNDVYGADYLD 91
 Qy 64 LGFEHQKGTVRTKGTGKAQLKSAIDALHKKNIDYGVVNMHKGADYETVTAVERDPS 123
 Db 92 LGFEHQKGTVRTKGTGKAQLKSAIDALHKKNIDYGVVNMHKGADYETVTAVERDPS 151
 Qy 124 DNRNVIAGEHLIKAMTHFHPGSGTSPDFKMWYHFDGTDWDESKLRNRYKFO--GKA 181
 Db 152 NRVVSGDYELISANTGFRPGSGSYSPFKMKWHFPGTDWDESKLRNRYKFRGIGKA 211
 Qy 182 WMEVSNENGNNDYLYADIDYDHPVAALIKRWGTWYANIELDGFRLDAVGHIFSEFL 241
 Db 212 WMEVSNENGNNDYLYADIDYDHPVAALIKRWGTWYANIELDGFRLDAVGHIFSEFL 271
 Qy 242 RDMVNHVRKTKGEMFTVAEYQNDLGALNTNKTENHSHVDFVPLHYOFHAASFGCG 301
 Db 272 RDMVNHVRKTKGEMFTVAEYQNDLGALNTNKTENHSHVDFVPLHYOFHAASFGCG 331
 Qy 302 YDMRKLNGTVYSKHEPKSVTVFVNDHDTQPGSLESSTVQWTKPLAYAFILTRREGYPOV 361
 Db 332 YDMRKLNGTVYSKHEPKSVTVFVNDHDTQPGSLESSTVQWTKPLAYAFILTRREGYPOV 391
 Qy 362 FYGDMYGTGDSQREIPALKHKEIPILKARKQYAGAHDPDHDHIVGWTREGSSVAN 421
 Db 392 FYGDMYGTGDSQREIPALKHKEIPILKARKQYAGAHDPDHDHIVGWTREGSSVAN 451
 Qy 422 SGLAALITDGPAGAKMYVGRVAGETWHDITGNRSEPVINSSENGEFTVNGSSVSIY 481
 Db 452 SGLAALITDGPAGAKMYVGRVAGETWHDITGNRSEPVINSSENGEFTVNGSSVSIY 511
 Qy 482 QR 483
 Db 512 QR 513
 RESULT 5
 ID 082839 PRELIMINARY; PRT; 516 AA.
 AC 082839;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Amyase.
 OS Bacillus sp.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1409;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=KSM-1378;
 RC MEDLINE=98342096; PubMed=9675143;
 RA Igarashi K., Hatada Y., Ikawa K., Arai H., Oawa T., Kobayashi T.,
 Ozaki K., Ito S.;
 RA "Improved thermostability of a Bacillus alpha-amyase by deletion of
 RT an arginine-glycine residue is caused by enhanced calcium binding.";
 RL Biochem Biophys Res Commun. 248:372-377(1998).
 RL EMBL; AB067653; BA32431.1; -
 DR HSSP; P06278; IVS.
 DR GO; GO:0004556; F:alpha-amyase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_aml1_cat.
 DR InterPro; IPR006589; Alp_aml1_cat_sub.
 DR Pfam; PF00128; alpha-amyase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 SQ SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;

Query Match 71.6%; Score 1909; DB 2; Length 516;
 Best Local Similarity 69.1%; Pred. No. 8e-132;

Matches 335; Conservative 68; Mismatches 72; Indels 10; Gaps 4;

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QY 4 NGTLMQYFEWYMPNDGQWRRLONDASAYLAEHGITAWMIPPAKGTSGADVGAYD 63
DB 37 NGTMMQYFEWYHLPDNDGHNRLDPAANLKSIGITAWIPPAWKGTSGQNDVGAYDLYD 96
QY 64 LGEPHQGTGTRTKYGTGELQSAIKSLHSRDINVGDVVINKGADATDVTAYEVD 123
DB 97 LGEPHQGTGTRTKYGTGELQSAIKSLHSRDINVGDVVINKGADATDVTAYEVD 156
QY 124 DRRNVIAGEHLIKMTFHFHFGRGSTYSDFKMWHYHFDGTDMDSEKLT-NRIYKPO--GK 180
DB 157 NRNGEISGEYTIEMTKEFDFPGRGNTHSNFKMRHYHFDGTDMDQSQLOKIKYFGTCK 216
QY 181 AMDWEVSENGNNDYLYMADIDYHPDYAAEIKRWGTVYANELQDGFRLDAVKIKF 240
DB 217 AMDWEVSENGNNDYLYMADIDYHPDYAAEIKRWGTVYANELQDGFRLDAVKIKF 276
QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLTKTNPNHSVDPVLYHQFHAASQTQ 300
DB 277 TRDMLTHVRNTGKPMFAVAEFPWQNDLAIENTYLNKTSNMHSVPDVLHNLVNAANSQ 336
QY 301 GYDMRKLINGTVSKHPLKSVTFVNDHDTOPQSGLESTVQTKPLAYAFILIREGYP 360
DB 337 YEDMRNLINGSVQKHPHATFVDNHDSPGSEALBSFVQSWFKPLAYALILIREGYP 396
QY 361 VFYGDWYGT--TKGDSOREIPALKEIPILKARKQYVGAOHDFDHDIVGWTREGDS 418
DB 397 VFYGDWYGT--TKGDSOREIPALKEIPILKARKQYVGAOHDFDHDIVGWTREGDS 451
QY 419 VANSGLAALITDGPCKAMTVGRONAGETWHDITGNRSEPVVINSGEWFEHNGSV 478
DB 452 HPNSGLATIMSDGPGKMTYVGRONAGETWHDITGNRSEPVVINSGEWFEHNGSV 511
QY 479 IYVQR 483
DB 512 VWVQR 516

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RESULT 6

031193 PRELIMINARY; PRT; 549 AA.

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AC 031193 (1)
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Alpha amylase.
OS AMT.
OC Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 31195;
RA da Silva A.C.R., Fernandes E., Pueyo M.T.;
RT Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
DB EMBL; AF032864; AAB6961.1; --
DB PIR; A54541; A5451.
DB HSSP; P06278; IVUS.
DB GO; GO:0004556; F:alpha-amylase activity; IEA.
DB GO; GO:0005975; P:carbohydrate metabolism; IEA.
DB InterPro; IPR006047; Alpha_cat.
DB InterPro; IPR006589; Alp_cat.
DB InterPro; IPR006046; Glyco_hydro_13.
DB Pfam; PF00128; alpha-amylase; 1.
DB PRINTS; PR00110; ALPHAAMYLASE.
DB SMART; SM00642; Amy; 1.
SQ SEQUENCE 549 AA; 62651 MW; 2CA689EDACC4D262 CRC64;

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Query Match 67.1%; Score 1789.5; DB 2; Length 549;
 Best Local Similarity 64.9%; Pred. No. 5.2e-123;
 Matches 315; Conservative 67; Mismatches 98; Indels 5; Gaps 2;

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QY 1 ANGLTMOYFEWYMPNDGQWRRLONDASAYLAEHGITAWMIPPAKGTSGADVGAYD 60
DB 36 APNGTMMQYFEWYHLPDNDGHNRLDPAANLKSIGITAWIPPAWKGTSGQNDVGAYD 95
QY 61 LGDGEFHQGTGTRTKYGTGELQSAIKSLHSRDINVGDVVINKGADATDVTAYEVD 120
DB 96 LGDGEFHQGTGTRTKYGTGELQSAIKSLHSRDINVGDVVINKGADATDVTAYEVD 155
QY 121 DPADNRVISEHILIKMTFHFHFGRGSTYSDFKMWHYHFDGTDMDSEKLT-NRIYKPO-- 178
DB 156 NPSDNEISETGYIQMTKEFDFPGRGNTHSNFKMRHYHFDGTDMDSEKLT-NRIYKPO-- 215
QY 179 GKAMDWEVSENGNNDYLYMADIDYHPDYAAEIKRWGTVYANELQDGFRLDAVKIKF 238
DB 216 GKAMDWEVSENGNNDYLYMADIDYHPDYAAEIKRWGTVYANELQDGFRLDAVKIKF 275
QY 239 SFLDVNVHREKTKGEMFTVAEYQNDLGALENYLTKTNPNHSVDPVLYHQFHAASQTQ 298
DB 276 SFDPWMLSYVSQTKGKPLFVGEYWSYDINKLHNYITKNGTSLFAPLHNTKFTASKS 335
QY 299 GGGYDMRKLINGTVSKHPLKSVTFVNDHDTOPQSGLESTVQTKPLAYAFILIREGYP 358
DB 336 GGGYDMRKLINGTVSKHPLKSVTFVNDHDTOPQSGLESTVQTKPLAYAFILIREGYP 395
QY 359 POFYFGDMYGTGKDSOREIPALKEIPILKARKQYVGAOHDFDHDIVGWTREGDS 418
DB 396 POFYFGDMYGTGKDSOREIPALKEIPILKARKQYVGAOHDFDHDIVGWTREGDS 452
QY 419 VANSGLAALITDGPCKAMTVGRONAGETWHDITGNRSEPVVINSGEWFEHNGSV 478
DB 453 KPGSLAALITDGPCKAMTVGRONAGETWHDITGNRSEPVVINSGEWFEHNGSV 512
QY 479 IYVQR 483
DB 513 VWVQR 517

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RESULT 7

P71034 PRELIMINARY; PRT; 521 AA.

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AC P71034 (1)
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Alpha amylase precursor.
OS Bacillus sp. MK 716.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=54116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MK 716;
RA Sidhu G.S., Chakrabarti T.;
RT "Molecular cloning and expression of the gene encoding for
  thermostable alpha-amylase of a thermophilic bacterial isolate.";
RT Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
DB EMBL; U75445; AAB18785.1; --
DB HSSP; P06278; IVUS.
DB GO; GO:0004556; F:alpha-amylase activity; IEA.
DB GO; GO:0005975; P:carbohydrate metabolism; IEA.
DB InterPro; IPR006047; Alpha_cat.
DB InterPro; IPR006589; Alp_cat.
DB InterPro; IPR006046; Glyco_hydro_13.
DB Pfam; PF00128; alpha-amylase; 1.
DB PRINTS; PR00110; ALPHAAMYLASE.
DB SMART; SM00642; Amy; 1.
DB SIGNAL.
DB POTENTIAL.
FT CHAIN 35 521 ALPHA-AMYLASE.
SQ SEQUENCE 521 AA; 58311 MW; 5612A8596D922E1 CRC64;

```

Query Match 66.9%; Score 1784.5; DB 2; Length 521;
 Best Local Similarity 64.7%; Pred. No. 1.1e-122;
 Matches 314; Conservative 67; Mismatches 99; Indels 5; Gaps 2;

```

QY 1 ANLNGTLMQYFEMWMPNDGQHRRLONDSAYLAEGHTAVWIPRAYKGTSGOADVGYAD 60
DB 36 APFNGTMQYFEMWLPDDGTLMTKRVANENANSSLGITRLMLPRAYKGTSSSDVGYGYD 95
QY 61 LYLGEFHOKGTVRTKGTGKGLQSAIKSLHSRDINVGDDVYINHGADATEDVTAVEV 120
DB 96 LYLGEFNOGKTVRTKGTGKGLQSAIKSLHSRDINVGDDVYINHGADATEDVTAVEV 155
QY 121 DPADRNRVISEGHLIKAMTHFHPGSGTSDFKMWHYFDGTDWDESRKLNRIYKFO-- 178
DB 156 NPSDRNGEISGTQIQAMTKFDPFGKNTYSSFKRMWHYFDGTDWDESRKLNRIYKFOGI 215
QY 179 GKAMDVEVSNENGVNLYMTADIDYDHPVAALIKRGTWYANELQDGFRLDAVGHKIF 238
DB 216 GKAMDVEVDTEENGVNLYMTADIDYDHPVAALIKRGTWYANELQDGFRLDAVGHKIF 275
QY 239 SFLRDVNVHREKTKGEMFTVAEYQNDLGALENTKNTFNHVSFVDPVLAHQFHAASQ 298
DB 276 SFFPDMLSYRSQTKGLFTVGEYMSYDINKLHNYITKNGTMSLFDALHNKFTYAKS 335
QY 299 GGGYDKRLKNGTVSKHPLKSVTFVNDHDTOPGQSLSTVQTWKPLAVAFILTBESGY 358
DB 336 GGAEDKRLKNGTVSKHPLKSVTFVNDHDTOPGQSLSTVQTWKPLAVAFILTBESGY 395
QY 359 POVEYGMGTGKDSOREIPALKHKIEPIKAKOYAGAHDPFHNDIYGMTRREGSS 418
DB 396 PCVFGDYGI---PQYNIPSLKSKIDPILIRRDVAIGTDYDHDSDIIGMTREGYTE 452
QY 419 VANSGLAALITDGPAGAKMTYGRONAGETMDITGNRSEPVYINSEGEFHYNGGSVS 478
DB 453 KPSSGLAALITDGPAGAKMTYGRONAGETMDITGNRSDTYITNSDGEFHYNGGSVS 512
QY 479 IYVOR 483
DB 513 VWVPR 517

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RESULT 8

```

Q9KMY6 PRELIMINARY; PRT; 549 AA.
ID 09KMY6
AC 09KMY6;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DB Alpha-amylase (SC 3.2.1.1).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_Taxid=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US100;
RA Bejar S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y11557; CAB93517.1; -.
DR PIR; A54541; A54541.
DR HSSP; P06278; IVS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolyase activity; acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amyy; 1.
KW Glycosidase; Hydrolyase.
SQ SEQUENCE 549 AA; 62582 MW; 8DA3B6DF9120BCE CRC64;

```

Query Match 66.3%; Score 1784.5; DB 2; Length 549;
 Best Local Similarity 64.7%; Pred. No. 1.2e-122;
 Matches 314; Conservative 67; Mismatches 99; Indels 5; Gaps 2;

```

QY 1 ANLNGTLMQYFEMWMPNDGQHRRLONDSAYLAEGHTAVWIPRAYKGTSGOADVGYAD 60
DB 36 APFNGTMQYFEMWLPDDGTLMTKRVANENANSSLGITRLMLPRAYKGTSSSDVGYGYD 95
QY 61 LYLGEFHOKGTVRTKGTGKGLQSAIKSLHSRDINVGDDVYINHGADATEDVTAVEV 120
DB 96 LYLGEFNOGKTVRTKGTGKGLQSAIKSLHSRDINVGDDVYINHGADATEDVTAVEV 155
QY 121 DPADRNRVISEGHLIKAMTHFHPGSGTSDFKMWHYFDGTDWDESRKLNRIYKFO-- 178
DB 156 NPSDRNGEISGTQIQAMTKFDPFGKNTYSSFKRMWHYFDGTDWDESRKLNRIYKFOGI 215
QY 179 GKAMDVEVSNENGVNLYMTADIDYDHPVAALIKRGTWYANELQDGFRLDAVGHKIF 238
DB 216 GKAMDVEVDTEENGVNLYMTADIDYDHPVAALIKRGTWYANELQDGFRLDAVGHKIF 275
QY 239 SFLRDVNVHREKTKGEMFTVAEYQNDLGALENTKNTFNHVSFVDPVLAHQFHAASQ 298
DB 276 SFFPDMLSYRSQTKGLFTVGEYMSYDINKLHNYITKNGTMSLFDALHNKFTYAKS 335
QY 299 GGGYDKRLKNGTVSKHPLKSVTFVNDHDTOPGQSLSTVQTWKPLAVAFILTBESGY 358
DB 336 GGAEDKRLKNGTVSKHPLKSVTFVNDHDTOPGQSLSTVQTWKPLAVAFILTBESGY 395
QY 359 POVEYGMGTGKDSOREIPALKHKIEPIKAKOYAGAHDPFHNDIYGMTRREGSS 418
DB 396 PCVFGDYGI---PQYNIPSLKSKIDPILIRRDVAIGTDYDHDSDIIGMTREGYTE 452
QY 419 VANSGLAALITDGPAGAKMTYGRONAGETMDITGNRSEPVYINSEGEFHYNGGSVS 478
DB 453 KPSSGLAALITDGPAGAKMTYGRONAGETMDITGNRSDTYITNSDGEFHYNGGSVS 512
QY 479 IYVOR 483
DB 513 VWVPR 517

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RESULT 9

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Q59222 PRELIMINARY; PRT; 613 AA.
ID 059222
AC 059222;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DB Alpha-amylase (EC 3.2.2.1).
GN AMY.
OS Bacillus sp. TS-23.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=38441;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TS-23;
RA Lin L.-L.; Chu W.S.; Hsu W.H.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U22045; AAA63900.1; -.
DR HSSP; P06278; IVS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolyase activity; acting on glycosyl bonds; IEA.
DR GO; GO:0008777; F:purine nucleosidase activity; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF00686; CBM_20; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR PRODOM; PD001368; CBD_4; 1.
DR SMART; SM00642; Amyy; 1.
KW Glycosidase; Hydrolyase.
SQ SEQUENCE 613 AA; 69537 MW; 14684A30FC2895E8 CRC64;

```

Query Match 65.8%; Score 1755.5; DB 2; Length 613;

Best Local Similarity 64.1%; Pred. No. 1,9e-120; Matches 311; Conservative 68; Mismatches 101; Indels 5; Gaps 2;

```

OY 1 ANLNGTMOYFEWYMNDCGHWRLONDSAYLAHGHTAVWIPPAKGTSGQADVGAYDLY 60
D 33 APINEMTMOYFEMWLPBPDGLMTKVKRKAANLSLGLTALMPPAYKGTSGSDVGAYD 92
OY 61 LYDGEFHQKGTVRTKTKYGTGKELQSAIKSLHSRDINVGDVVINKGADATEDVTAVEY 120
D 93 LYDGEFHQKGTVRTKTKYGTGKTOYIOAIQAAAGMUYADVFNHKAAGATEFVDAVEY 152
OY 121 DPABNRVTSGEHILKATMTHFHPGRGSTYSDFKMHYHPGDTWDSRLNIYKPO-- 178
D 153 DPSNRNGTSTGTQIOAWTKFDFPKRGNTISSFKRHYHEDGIDMDSRKLNIRKST 212
OY 179 GKAMDVEVSNNGVDYLMVADIDYDHPDVAEIKRMGTWYANELQDGFELDAVYKIF 238
D 213 GKAMDVEVDTEGNYDYIMFADLMDHBEVTELEKNGTWVNTNIDGFLDAVYKIKY 272
OY 239 SELDMVNVHVEKTKGEMFTVAEYQNDLGLNLYLNKTNHNSVFPVPLHYOPHAATQ 298
D 273 SFPDMLYYKXQKSKNLFAYGEFNSYDVKLNHYITKNGSNLFPADLHNNFYTKSKS 332
OY 299 GGGYDMRKLNGTVVSKAPLKSVTVDNHDTPQGSLESTVQTFKPLAAYAFILTRBSGY 358
D 333 SGYFDMRYLNNITLMKQPSLAVTLVDNHDTPQGSLSQWEPWFKELAYAFILTRBSGY 392
OY 359 PQVFGDMYGTGKDSQREIIPALKIEPILKARKOYAGAOHDFDHDIVGTRBDS 418
D 393 PCVFYGDYGI--PKYNIPLKSKIDPLIARDYAGTGRDIDHODLIGWTRBGI 449
OY 419 VANSGLALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSSEGSEFHVNGSVS 478
D 450 KPNSSLALITDGPAGSKMYVYKKAHAKYVYDLGNRSDIVTINADGWGSEFHVNGSVS 509
OY 479 TYVQR 483
D 510 IWVAK 514

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RESULT 10

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ID 093148 PRELIMINARY; PRT; 501 AA.
AC 093148;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Amylase.
GN AMYK38.
OS Bacillus sp. KSM-K38.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=129736;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-K38;
RA Hayashi Y.;
RT Submitted (NOV-2000) to the EMBL/GenBank/DBD databases.
RL EMBL: AB051102; BAB71820.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; alpha-amylase; 1.
SQ SEQUENCE 501 AA; 57485 MW; 1240F46739A5CC11 CRC64;

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Query Match 64.6%; Score 1723.5; DB 2; Length 501; Best Local Similarity 62.8%; Pred. No. 3.2e-118; Matches 302; Conservative 72; Mismatches 104; Indels 3; Gaps 1;

```

OY 3 ANLNGTMOYFEWYMNDCGHWRLONDSAYLAHGHTAVWIPPAKGTSGQADVGAYDLY 62
D 24 LAGTMOYFEMWLPBPDGLMTKVKRKAANLSLGLTALMPPAYKGTSGSDVGAYDLY 83

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OY 63 DLGEFHQKGTVRTKTKYGTGKELQSAIKSLHSRDINVGDVVINKGADATEDVTAVEVP 122
D 84 DLGEFHQKGTVRTKTKYGTGKTOYIOAIQAAAGMUYADVFNHKAAGATEFVDAVEVP 143
OY 123 ADNRNVISGEHILKATMTHFHPGRGSTYSDFKMHYHPGDTWDSRLNIYKPOKAW 182
D 144 TNRMQDLSGATLTIDMTGFDPGSGNNAYSDPKRMWFFHNGVDMDQRYOEHNIFFRANTNW 203
OY 183 DMEVSNNGVDYLMVADIDYDHPDVAEIKRMGTWYANELQDGFELDAVYKIFKESFLR 242
D 204 MNRVDEENGNVDYLLGNSIDSHPEVDELKOWSWEFTDELDDGYRDAIKHLPWYTS 263
OY 243 DVNVHVEKTKGEMFTVAEYQNDLGLNLYLNKTNHNSVFPVPLHYOPHAATQGGGY 302
D 264 DVNVHVEKTKGEMFTVAEYQNDLGLNLYLNKTNHNSVFPVPLHYOPHAATQGGGY 323
OY 303 DMEKLLNGTVVSKAPLKSVTVDNHDTPQGSLESTVQTFKPLAAYAFILTRBSGY 362
D 324 DMRNITRQSLVFAHMAVTVVDNHDTPQGSLSWADWFKPLAVATILTRBSGY 383
OY 363 YGDMYGTGKDSQREIIPALKIEPILKARKOYAGAOHDFDHDIVGTRBDSVANS 422
D 384 YGDMYGTGKDSQREIIPALKIEPILKARKOYAGAOHDFDHDIVGTRBDSVANS 440
OY 423 GLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSSEGSEFHVNGSVSY 482
D 441 GLATMSNGPGSKMYVYKKAHAKYVYDLGNRSDIVTINADGWGSEFHVNGSVSY 500
OY 483 R 483
D 501 Q 501

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RESULT 11

```

ID 087H6 PRELIMINARY; PRT; 507 AA.
AC 087H6;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN VPA0999.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
OC NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K., Iijima Y., Naito M., Nakano M., Yamashita A., Kubota Y., Kimura S., Yasunaga T., Honda T., Shingawa H., Hattori W., Tida T.;
RT "genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL; AP005087; BAC62342.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; alpha-amylase; 1.
KW Complete proteome.
SQ SEQUENCE 507 AA; 58428 MW; 91B549E2BE0700BD CRC64;

```

Query Match 56.4%; Score 1502.5; DB 16; Length 507; Best Local Similarity 55.8%; Pred. No. 5.6e-102; Matches 271; Conservative 81; Mismatches 125; Indels 9; Gaps 7;

```

OY 1 ANLNGTMOYFEWYMNDCGHWRLONDSAYLAHGHTAVWIPPAKGTSGQADVGAYDLY 59
D 23 AGONGTMOYFEMWLPBPDGLMTKVKRKAANLSLGLTALMPPAYKGTSGSDVGAYDLY 82
OY 60 DYDGEFHQKGTVRTKTKYGTGKELQSAIKSLHSRDINVGDVVINKGADATEDVTAVE 119

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[illegible][illegible]

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Db      124 DRTKISPEFLEGTKTTFPRGQGYSSFTKNSHFGTDPDAREERTGFRLAGENK 183
Qy      182 WMEVSNENGVNDYIMVADIDYDPVAEIKRWGTAYANELQDGFRLDAVKIKSFL 241
Db      184 WMEVNDDEFGVNDYIMVADIDYDPVAEIKRWGTAYANELQDGFRLDAVKIKSFL 243
Qy      242 RDWVNHVEKTKGKEMFTVAEYKNDIGALEYLNKTNPHNSVFPVPLHYOPHAASTOGG 301
Db      244 KEFAEMTRKQGDYIVGEFNSNLDACREPLDVIDYQIDFLFVSLHYKHEMSLGRD 303
Qy      302 YDMRLKLTGVTSKPLKSVTFVNDHDTQPGQSLSTVQTFKPLAYAFILITRESGYPQV 361
Db      304 PLSKIPDITVQTPHTAHTFVDNHDSDQPHALESMIGDFKPSAYALTLLRRDGYFVV 363
Qy      362 FPGDVMYGTGK-----DSQREPALKHKIEPLKARQYAYGAOHDFPHDIDVGMTREDS 417
Db      364 FPGDVMYGTGK-----DSQREPALKHKIEPLKARQYAYGAOHDFPHDIDVGMTREDS 417
Qy      418 SVANGSLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVINSSEMGEPHYNGSV 477
Db      418 EIEGGCAVVISNGDGEKMFIEGRAGEVWVDLTKSCDQITIEEDGMATFVCGGV 477
Qy      478 STY 480
Db      478 SVM 480

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RESULT 14

08YU21 PRELIMINARY; PRT; 492 AA.

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ID 08YU21 PRELIMINARY; PRT; 492 AA.
AC 08YU21;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DT Alpha-amyase.
GN ALR2190.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2159285; PubMed=11759840;
RA Kaneo T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,
RA Matenabe A., Iritiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsumoto A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213 (2001).
DR EMBL: AP003588; BAB73889.1;
DR PIR: AH2079; AH2079.
DR GO: GO:0004556; F:alpha-amyase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amyase; 1.
DR PRINTS: PR00110; ALPHAAMYLAASE.
KM Complete proteome.
SQ SEQUENCE 492 AA; 57063 MW; 11B5D6CF2F1828 CRC64;

```

Query Match 46.7%; Score 1244; DB 16; Length 492;
 Best Local Similarity 47.5%; Pred. No. 5, 2e-83;
 Matches 234; Conservative 84; Mismatches 161; Indels 14; Gaps 6;

```

Qy      1 ANLNGLMQYFEWVNDGCHRRRLONDSAYLAERHITVWIPPAVKG-TSQADYGVAY 59
Db      2 AQMGNGMAYFHYIINDGNLMSKVASAPELADAGFTMLPAPYKAGASFDYGVY 61
Qy      60 DLYDGEFHQKGVTRTKYGTGKLGSAISLSRSDINVGDAVINHKSGADTEPVTAVE 119
Db      62 DLYDGEFHQKGVTRTKYGTGKLGSAISLSRSDINVGDAVINHKSGADTEPVTAVE 121

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```

Qy      120 VDPADNRNVTSGEHLIKAMTHPEPRGSTYSDFKMHYFDGTDWDESRKLR--LYKF 177
Db      122 FPDODRLNKGGLQITIKTYTHNFRGROKTSNPFMMHMDADVADYNEVNSGDSSTYLL 181
Qy      178 OGRAMDVEVSNENGVNDYIMVADIDYDPVAEIKRWGTAYANELQDGFRLDAVKIKSFL 237
Db      182 EGRNFDYVALKGNFAYLMGCDLDFONBWVGEVTVGKVCCLTTKYDGRIRDAIKIS 241
Qy      238 FSTLRDWNVHVEKTKGKEMFTVAEYKNDIGALEYLNKTNPHNSVFPVPLHYOPHAAS 297
Db      242 TWFFPMDALRRHAKGLDFWGEYVNDINTLLMYAVAKRMSVDFVPLHYNHQS 301
Qy      298 OGGYDMRLKLTGVTSKPLKSVTFVNDHDTQPGQSLSTVQTFKPLAYAFILITRESG 357
Db      302 SGGNYDMRLITDGTWVQGRFTHAVTFVENHDSQPLQALLESVYEPWFKPLAYAILLRQEG 361
Qy      358 YPQVFGDMYGTGK-----GDSQRE--IPALKHKIEPLKARQYAYGAOHDFPHDIDV 409
Db      362 YPQVFGDMYGTGK-----GDSQRE--IPALKHKIEPLKARQYAYGAOHDFPHDIDV 421
Qy      410 GMTREDSVANSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVINSSEMGEP 469
Db      422 GMTREGLDAD-HPGMAVIMSDSGEGIKMEVEGKPT--KFIDLTBIKEAVYTNEMGWGE 478
Qy      470 FHYNGSVSTLYQ 482
Db      479 FRCLGGSVSWVQ 491

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RESULT 15

097049 PRELIMINARY; PRT; 484 AA.

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ID 097049 PRELIMINARY; PRT; 484 AA.
AC 097049;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DT Alpha-amyase.
GN SP1382.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX Streptococcus.
NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC BAA-334 / TIGR4;
RC MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radding D.,
RA Holtzapfel E., Khouli H., Wolf A.M., Uetzel T.R., Hansen C.J.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae."
RL Science 293:498-506 (2001).
DR EMBL: AE007435; AAK75480.1;
DR PIR: G95160; G95160.
DR TIGR: SP1382;
DR GO: GO:0004556; F:alpha-amyase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006046; Alp_amy1_cat_sub.
DR Pfam: PF00128; alpha-amyase; 1.
DR PRINTS: PR00110; ALPHAAMYLAASE.
DR SMART: SM00642; Amy; 1.
KM Complete proteome.
SQ SEQUENCE 484 AA; 55918 MW; 4E90A450A90E8B8C CRC64;

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Query Match 46.2%; Score 1233; DB 16; Length 484;

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Page 9

Best Local Similarity 48.6%; Pred. No. 3.3e-82; Matches 234; Conservative 72; Mismatches 167; Indels 8; Gaps 4;

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QY 4 NCTLMQYFEMWPNNDGQHRRLQNDQSAVLAENHGTAWMPPRAYKGTQADVGAYDYD 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 NCTLMQYFEMWLPHQGHTRLAENAPHLALGISHWMPFAFKATNEDVGAYDYD 62
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 LGFFHQKGTVRKTYKIGKGLQSAIKSLHRDINVGDVYINKGADATEDVTAENVDA 123
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 LGFFHQKGTVRKTYKIGKGLQSAIKSLHRDINVGDVYINKGADATEDVTAENVDA 122
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 124 DRKRVISGEHLIKAWTHFFPGSGSTYSDFKWMTYHFDGTWDESRKLNRIYKFG--KA 181
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 DRVLEGEPTINGWTSFTFDGRQDTYNGFHHWHTFTGTDYDARKSKSGIYLIGDNKG 182
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 182 WQWE--VSNENGYDYLTADIDYDHPVAAEIKKNGTYANELQDGFRLDAVKHIFS 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 WANEELVDNENGYDYLTADIDYDHPVAAEIKKNGTYANELQDGFRLDAVKHIDSF 242
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 FLBDWVNHVREKTKGKEMFTVAEYQNDLGALENYLNKTNFNHSVPDPLHYQFHAAS 299
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 243 FMRNFTRDKKEKGDYDFYVGFGEFNPDKRANPDYLEKTEHFDYDVLHQNLFEASQAG 302
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 300 GGYDKRKLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTFEKLAYAFILTRSGYP 359
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 303 ANYDLRGIFTDLSVELPKPKAVTFVDNHDTPQGSLESTVQTFEKLAYAFILTRSGYP 362
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 360 QVYSGMYGKTKGDSOREIPALKKIEPIKARQVAYGAQHDYFDHHDIVGWTREGDS 419
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 363 CVFYGDYIGSQYAOE--DFKEILDRLAIRKDLAYGEONDIYFDHANCIGWVRSGAEN- 419
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 420 ANSGLAALITDGPQAKRWYVGRQNAGETWHDITGNRSEPVYINSGWGEFHVNGSVSI 479
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 420 -QSPYAVLISNDQENKSMFVGQEWNTQTFVDILGNHQGVITIDEGYQGFVVSARSVSV 478
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 480 Y 480
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 479 W 479
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Search completed: May 3, 2004, 20:53:12
Job time : 38.3365 secs

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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:36:03 ; Search time 11.1361 Seconds
(without alignments)
2403.363 Million cell updates/sec

Title: US-10-644-187-6
Performance: 2847
Sequence: 1 AAFNGTMMQGFYFWYLPDDG.....TTREPTGSEFVRWTEPRLVAN 514

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2780	97.6	549	1	AMT_BACST
2	1874.5	65.8	518	1	AMT6_BACST
3	1797.5	63.1	512	1	AMT_BACLI
4	1773.5	62.3	514	1	AMT_BACAM
5	1110.5	39.0	494	1	AMT2_SALTU
6	1074.5	37.7	495	1	AMT2_ECOLI
7	313	11.0	713	1	CDGT_BACSP
8	307	10.8	1196	1	AMT6_PABPO
9	302.5	10.6	440	1	AMT3_ORYSA
10	302	10.6	713	1	CDGT_BACSB
11	300	10.5	713	1	CDGT_BACCI
12	286.5	10.1	712	1	CDGT_BAC93
13	286	10.0	718	1	CDGT_BACLI
14	284.5	10.0	713	1	CDGT_BACSO
15	283	9.9	421	1	AMT4_VIGMU
16	282	9.9	718	1	CDGT_BACSS
17	280	9.8	413	1	AMT3_WHEAT
18	278	9.8	718	1	CDGT_BACCI
19	275.5	9.7	564	1	AMT4_SCHPO
20	274.5	9.6	438	1	AMT3_ORYSA
21	274.5	9.6	528	1	AMT_BACCI
22	273	9.6	710	1	CDGT_THETU
23	272.5	9.5	428	1	AMT3_ORYSA
24	271.5	9.5	437	1	AMT3_ORYSA
25	268.5	9.4	438	1	AMT1_HORVU
26	268	9.4	711	1	CDGT_BACST
27	266.5	9.4	429	1	AMT6_HORVU
28	266	9.3	435	1	AMT3_ORYSA
29	262.5	9.2	427	1	AMT2_HORVU
30	262	9.2	703	1	CDGT_BACSS2
31	258.5	9.1	368	1	AMT3_HORVU
32	257.5	9.0	437	1	AMT3_ORYSA
33	253.5	8.9	494	1	AMT1_SACFI

34	249	8.7	443	1	AMT2_ORYSA	P27935
35	248	8.7	498	1	AMT6_ASPAW	Q02905
36	248	8.7	499	1	AMT6_ASPAW	Q02906
37	247	8.7	499	1	AMT6_ASPSH	P10292
38	245	8.6	499	1	AMT6_ASPOR	P10529
39	244	8.6	519	1	AMT_STRLI	P05884
40	242	8.5	445	1	AMT2_ORYSA	P27941
41	238.5	8.4	498	1	AMT3_DICTH	P14899
42	236	8.3	581	1	AMT1_SCHPO	Q09840
43	230.5	8.1	713	1	CDGT_PABPO	P31835
44	224.5	7.9	704	1	CDGT_BACOR	P27036
45	224	7.9	624	1	AMT1_LIPRO	Q01117

ALIGNMENTS

RESULT 1
ID AMT_BACST STANDARD; PRT; 549 AA.
AC P06279; Q45519;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-FEB-1996 (Rel. 33, last sequence update)
DT 15-MAR-2004 (Rel. 43, last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMYS.
OC Bacillus stearothermophilus.
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxId=1422;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.
RX MEDLINE=65234394; PubMed=3924897;
RA Nakajima K., Imanaka T., Aiba S.;
RT "Nucleotide sequence of the Bacillus stearothermophilus alpha-amylase
RT gene."
RL J. Bacteriol. 163:401-406(1985).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=DV5/PHI300.
RX MEDLINE=66008166; PubMed=3876333;
RA Ihara H., Sasaki T., Tsuboi A., Yamagata H., Tsukagoshi N., Ueda S.;
RT "Complete nucleotide sequence of a thermophilic alpha-amylase gene:
RT homology between prokaryotic and eukaryotic alpha-amylases at the
RT active sites."
RL J. Biochem. 98:95-103(1985).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NG-3;
RX MEDLINE=66195857; PubMed=3009417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
CA Carmona C., Reuquard C.;
RT "Structural genes encoding the thermophilic alpha-amylases of
RT Bacillus stearothermophilus and Bacillus licheniformis."
RL J. Bacteriol. 166:635-643(1986).
RN [4]
RP SEQUENCE FROM N.A.
RA Suominen I., Karp M., Lautamo J., Knowles J., Mantseelae P.;
RT "Thermostable alpha amylase of Bacillus stearothermophilus: cloning,
RT expression, and secretion by Escherichia coli."
RL (in) Chaloupka J., Krumphanz V. (eds.);
RL Extracellular enzymes of microorganisms, pp.129-137, Plenum Press,
RL New York (1987).
RN [5]
RP SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48.
RC STRAIN=DV-5;
RX MEDLINE=66059211; PubMed=2999073;
RA Tsukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H.,
RA Iida Y., Yamagata H., Ueda S.;
RT "Efficient synthesis and secretion of a thermophilic alpha-amylase by
RT protein-producing Bacillus brevis 47 carrying the Bacillus
RT stearothermophilus amylase gene."
RL J. Bacteriol. 164:1182-1187(1985).
RL

RN [6]
 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RA MEDLINE=21125602; PubMed=11226887;
 RA Stud D., Fujimoto Z., Takase K., Matsumura M., Mizuno H.;
 RT "Crystal structure of Bacillus stearothermophilus alpha-amylase:
 RL J. Biochem. 129:461-468(2001).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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 DR EMBL; M1450; AAA22235.2; -;
 DR EMBL; X02769; CAA26547.1; -;
 DR EMBL; M57457; AAA22227.1; -;
 DR EMBL; M13255; AAA22241.1; -;
 DR PIR; A24436; A24436.
 DR PIR; A91999; ALBSF.
 DR PDB; 1HVX; 05-AUG-03.
 DR InterPro; IPR006589; Alpha amyl cat. sub.
 DR InterPro; IPR006047; Alpha amyl cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 KW Signal; 3D-structure.
 FT CHAIN 1 34
 FT SIGNAL 1 34
 FT ACT_SITE 35 549 ALPHA-AMYLASE.
 FT ACT_SITE 272 272
 FT ACT_SITE 365 365
 FT METAL 139 139
 FT METAL 196 196
 FT METAL 218 218
 FT METAL 220 220
 FT METAL 231 231
 FT METAL 237 237
 FT METAL 238 238
 FT METAL 239 239
 FT METAL 272 272
 FT METAL 337 337
 FT METAL 339 339
 FT METAL 440 440
 FT METAL 441 441
 FT METAL 464 464
 FT CONFLICT 13 13
 FT CONFLICT 19 19
 FT CONFLICT 23 23
 FT CONFLICT 31 31
 FT CONFLICT 107 107
 FT CONFLICT 167 167
 FT CONFLICT 179 179
 FT CONFLICT 251 251
 FT CONFLICT 260 260
 FT CONFLICT 284 284
 FT CONFLICT 312 312
 FT CONFLICT 338 338
 FT CONFLICT 342 342
 FT CONFLICT 346 346
 FT CONFLICT 376 376
 FT CONFLICT 526 527
 FT CONFLICT 527 527
 FT CONFLICT 535 535
 D -> V (IN REF. 3).
 L -> W (IN REF. 3).
 L -> S (IN REF. 2 AND 3).
 P -> H (IN REF. 2 AND 5).
 A -> T (IN REF. 2 AND 3).
 T -> I (IN REF. 4).
 P -> N (IN REF. 2).
 S -> N (IN REF. 2, 3 AND 4).
 TNI -> RTL (IN REF. 4).
 D -> Y (IN REF. 4).
 M -> T (IN REF. 2 AND 4).
 T -> A (IN REF. 2 AND 3).
 R -> S (IN REF. 3).
 T -> N (IN REF. 3).
 V -> C (IN REF. 2 AND 3).
 WS -> RP (IN REF. 2).
 D -> G (IN REF. 2 AND 3).

SQ SEQUENCE 549 AA; 62670 MW; 3A2DD93A955E79D3 CRC64;
 Query March 97.6%; Score 2780; DB 1; Length 549;
 Beest Local Similarity 98.1%; Pred. No. 3.2e-190;
 Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 1 AAPNGTMOQFEWYLPDDGTTKTVANEANNISLSGITLMLPFAVKGTSRSDVGVY 60
 DB 35 AAPNGTMOQFEWYLPDDGTTKTVANEANNISLSGITLMLPFAVKGTSRSDVGVY 94
 QY 61 DLYLGEFNQKGTATRYKGTAKOYLQAIQAHAAGQVADVVFEDHKGADGETWDAVE 120
 DB 95 DLYLGEFNQKGTATRYKGTAKOYLQAIQAHAAGQVADVVFEDHKGADGETWDAVE 154
 QY 121 VNPSPRNGEISGTVOIQAMTFDFPGRGNTYSSFKRWYHFDGVDDDESKLSRIYFRG 180
 DB 155 VNPSPRNGEISGTVOIQAMTFDFPGRGNTYSSFKRWYHFDGVDDDESKLSRIYFRG 214
 QY 181 IGRAMDWEVDTEENGVYIMVADLDMDHPEVYIELKMGKMYVNTTIDGFRIDAVGHK 240
 DB 215 IGRAMDWEVDTEENGVYIMVADLDMDHPEVYIELKMGKMYVNTTIDGFRIDAVGHK 274
 QY 241 FSEFPDMLSYVRSGTKRPLFVGEYNSYDINKLHNYITKTGTSLEFADLANKFYTASK 300
 DB 275 FSEFPDMLSDVRSQTKRPLFVGEYNSYDINKLHNYITKTGTSLEFADLANKFYTASK 334
 QY 301 SGGAFAVATLTNTLTKDQPLATFVDNHDTEFGQALQSWDPWFEFLAVAFILTRQEG 360
 DB 335 SGGFEDMTNTLNTLTKDQPLATFVDNHDTEFGQALQSWDPWFEFLAVAFILTRQEG 394
 QY 361 YPCVFGDYGIPIQYNIPSLKSKIDPLLIARDVAYGTQHDYDHSIDIGMTGEGTEKP 420
 DB 395 YPCVFGDYGIPIQYNIPSLKSKIDPLLIARDVAYGTQHDYDHSIDIGMTGEGTEKP 454
 QY 421 GSGLAALITDPPGSGKMYTVGKQAGVFDLTGNRSQTYTINSNGEGRKVGSGSYVW 480
 DB 455 GSGLAALITDPPGSGKMYTVGKQAGVFDLTGNRSQTYTINSNGEGRKVGSGSYVW 514
 QY 481 VPKXTVSTIARPIITRPMTGEFVRMTPEPLVAV 514
 DB 515 VPKXTVSTIARPIITRPMTGEFVRMTPEPLVAV 548
 RESULT 2
 ID AMT6_BACS7 STANDARD; PRT; 518 AA.
 AC P19571;
 DT 01-FEB-1991 (rel. 17, Created)
 DT 01-FEB-1991 (rel. 17, Last sequence update)
 DT 10-OCT-2003 (rel. 42, Last annotation update)
 DE Glucan 1,4-alpha-maltohexosidase precursor (EC 3.2.1.98) (66-amylase)
 DE (Maltotetraose-producing amylase) (Exo-maltotetraohydrolase).
 OS Bacillus sp. (strain 707).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1416;
 RN (1)
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.
 RX MEDLINE=88162814; PubMed=3258152;
 RA Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;
 RT "Nucleotide sequence of the maltotetraose-producing amylase gene from
 RT an alkalophilic Bacillus sp. #707 and structural similarity to
 RT liquefying type alpha-amylases";
 RL Biochem. Biophys. Res. Commun. 151:25-31(1988).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages
 CC in amylicaceous polysaccharides so as to remove successive
 CC maltotetraose residues from the non-reducing chain ends.
 CC -1- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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CC or send an email to license@ebi.ac.uk).

CC EMBL; M18862; AAA2231.1; -
CC PIR; A27705; A27705.
DR HSP; P06278; 1VCS.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alp_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KM Hydrolase; Glycosidase; Carbohydrate metabolism; signal.
FT SIGNAL 1 33
FT CHAIN 1 33
FT ACT_SITE 34 518
FT ACT_SITE 269 269
FT ACT_SITE 273 273
FT ACT_SITE 366 366
FT METAL 139 139
FT METAL 196 196
FT METAL 219 219
FT METAL 221 221
FT METAL 232 232
FT METAL 238 238
FT METAL 240 240
FT METAL 242 242
FT METAL 273 273
SQ SEQUENCE 518 AA; 59009 MM; 3A961E21612682C4 CRC64;
Query Match 65.8%; Score 1874.5; DB 1; Length 518;
Best Local Similarity 67.2%; Pred. No. 6; 6e-126;
Matches 321; Conservative 76; Mismatches 80; Indels 1; Gaps 1;

QY 5 NCTMMQYFENYLPDQGLMTKXANNNSSGITALMPPRYKGTSSRDVGYVLYD 64
DB 39 NGTMMQYFENYLPDQGLMTKXANNNSSGITALMPPRYKGTSSRDVGYVLYD 98
QY 65 LGEFNQKGTVRTKYGKTAQYLAIOAAHAAQVYADVVDHKGAGDGTWDAVEVNP 124
DB 99 LGEFNQKGTVRTKYGKTAQYLAIOAAHAAQVYADVVDHKGAGDGTWDAVEVNP 158
QY 125 DRNGEISGTQIOAWTKRPPRGNGYTSFKRWYHFDQVDESRKL-SRTYKRGYIK 183
DB 159 NRRQEVYGTETLEAWRFPFGNGHSSFKRWYHFDQVDESRKL-SRTYKRGYIK 218
QY 184 AMDMEVTEGNVNDYLMYADLMDHBEVTEKMGKWTYNTNIDGRLDAVKIKESF 243
DB 219 AMDMEVTEGNVNDYLMYADLMDHBEVTEKMGKWTYNTNIDGRLDAVKIKESF 278
QY 244 FPDWLSYVSQSGKPLFTYGEWYSYDINKLHYITTDGTMLEPDAFLNRYTSKSG 303
DB 279 TRDMINHVSAATGKNMFAVAEFKNDLGAIENTLOKTNHNSHVPDPLNLYNASKSG 338
QY 304 AFPMRTIMNTLMKQDPTLAATVFDNDHTEPGALQSWDPMPKPLAVALITRDEGYP 363
DB 339 NYMNRIFNGCTVQRRPASHAVTFVDHDSQPEALSFPEWFKPLAVALITRDEGYP 398
QY 364 VFPGDYVYGPQNTIBSKYIDPLLAARDYAVGTHVDLHSDIGMTRGEGTEKPSG 423
DB 399 VFPGDYVYGPQNTIBSKYIDPLLAARDYAVGTHVDLHSDIGMTRGEGTEKPSG 458
QY 424 LAALLIDDPGSGSWMYVYGGKQAKVYFDYLGKNSDVTINSQDWGKFXNKGVSVMV 481
DB 459 LAALLIDDPGSGSWMYVYGGKQAKVYFDYLGKNSDVTINSQDWGKFXNKGVSVMV 516
RESULT 3

AMY BACLI STANDARD; PRT; 512 AA.
ID AMY BACLI
AC P06278; Q84171;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amy1ase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase) (BLA).
GN AMYS OR AMYL.
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxId=1402;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27811.
RX MEDLINE=8611694; PubMed=2418011;
RA Yuki T., Nomura T., Tezuka H., Teuboi A., Yamagata H.,
RA Tsukagoshi N., Uda S.;
RT "Complete nucleotide sequence of a gene coding for heat- and
RT pH-stable alpha-amy1ase of Bacillus licheniformis: comparison of the
RT amino acid sequences of three bacterial liquefying alpha-amy1ases
RT deduced from the DNA sequences."
RL J. Biochem. 98:1147-1156(1985).
RN 2
RP SEQUENCE FROM N.A.
RX MEDLINE=86195857; PubMed=3009417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
RA Carmona C., Reznach C.;
RT "Structural genes encoding the thermophilic alpha-amy1ases of
RT Bacillus stearotherophilus and Bacillus licheniformis."
RL J. Bacteriol. 166:635-643(1986).
RN 3
RP SEQUENCE FROM N.A.
RA Shihoseini M., Ziaei A.A., Ghaemi N., Pourbaeai A.A.;
RT "An unusual DNA sequence encoded a hyperthermostable alpha-amy1ase."
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN 4
RP SEQUENCE OF 1-104 FROM N.A.
RX MEDLINE=8418455; PubMed=6609154;
RA Stephens M.A., Ortlepp S.A., Ollington J.F., McConnell D.J.;
RT "Nucleotide sequence of the 5' region of the Bacillus licheniformis
RT alpha-amy1ase gene: comparison with the B. amy1oliquefaciens gene."
RL J. Bacteriol. 158:369-372(1984).
RN 5
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=89213924; PubMed=2540150;
RA Iacide B.M., Chambliss G.H., McConnell D.J.;
RT "Bacillus licheniformis alpha-amy1ase gene, amy1, is subject to
RT promoter-independent catalytic repression in Bacillus subtilis."
RL J. Bacteriol. 171:2435-2442(1989).
RN 6
RP SEQUENCE OF 30-47.
RX MEDLINE=82098050; PubMed=6172418;
RA Kuhn H., Fietzek P.P., Lampen J.O.;
RT "N-terminal amino acid sequence of Bacillus licheniformis
RT alpha-amy1ase: comparison with Bacillus amy1oliquefaciens and
RT Bacillus subtilis enzymes."
RL J. Bacteriol. 149:372-373(1982).
RN 7
RP SEQUENCE OF SUBSTRATE-BINDING SITE.
RX MEDLINE=21992788; PubMed=11997021;
RA Kandra L., Gyeant G., Remenyik J., Hovanzki G., Liptak A.;
RT "Action pattern and substrate mapping of Bacillus licheniformis
RT alpha-amy1ase (BLA) with modified maltotriosecarbohydrate substrates."
RL PDBS Lett. 518:79-82(2002).
RN 8
RP MUTAGENESIS OF HIS-64; HIS-162; HIS-276; HIS-322; HIS-435 AND HIS-479.
RX STRAIN=ATCC 6598;
RA MEDLINE=90368748; PubMed=2394736;
RA Declerck N., Joyet P., Galliardin C., Masson J.M.;
RT "Use of amber suppressors to investigate the thermostability of
RT Bacillus licheniformis alpha-amy1ase. Amino acid replacements at 6
RT histidine residues reveal a critical position at His-123."

RL J. Biol. Chem. 265:15481-15488(1990).
RN [9]
RP MUTAGENESIS OF ALA-238.
RC STRAIN=ATCC 6598;
RX MEDLINE=96367070; PubMed=8771184;
RA Declerck N., Joyet P., Trosser J.Y., Garnier J., Galliardin C.;
RT "Hyperthermostable mutants of Bacillus licheniformis alpha-amylase:
RT multiple amino acid replacements and molecular modelling.",
RL Protein Eng. 8:1029-1037(1995).
RN [10]
RP MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;
RP ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-298; GLU-300; GLN-359
RP AND GLU-365.
RC STRAIN=ATCC 6598;
RX MEDLINE=20425100; PubMed=10966804;
RA Declerck N., Machius M., Wiegand G., Huber R., Galliardin C.;
RT "Probing structural determinants specifying high thermostability in
RT Bacillus licheniformis alpha-amylase.",
RL J. Mol. Biol. 301:1041-1057(2000).
RN [11]
RP MUTAGENESIS OF GLN-293 AND ASN-294.
RC STRAIN=ATCC 6598;
RX MEDLINE=22622182; PubMed=12736372;
RA Declerck N., Machius M., Joyet P., Wiegand G., Huber R.,
RA Galliardin C.;
RT "Hyperthermostabilization of Bacillus licheniformis alpha-amylase and
RT modulation of its stability over a 50 degrees C temperature range.",
RL Protein Eng. 16:287-293(2003).
RN [12]
RP MUTAGENESIS OF TRP-292 AND VAL-315.
RC STRAIN=ATCC 27811;
RX MEDLINE=22797417; PubMed=12915728;
RA Rivera M.H., Lopez-Munguia A., Soboron X., Saab-Rincon G.;
RT "Alpha-amylase from Bacillus licheniformis mutants near to the
RT catalytic site: effects on hydrolytic and transglycosylation
RT activity",
RL Protein Eng. 16:505-514(2003).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RC STRAIN=ATCC 27811;
RX MEDLINE=95182462; PubMed=7877175;
RA Machius M., Wiegand G., Huber R.;
RT "Crystal structure of calcium-depleted Bacillus licheniformis alpha-
RT amylase at 2.2-A resolution.",
RL J. Mol. Biol. 246:545-559(1995).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=98212915; PubMed=9515151;
RA Machius M., Declerck N., Huber R., Wiegand G.;
RT "Activation of Bacillus licheniformis alpha-amylase through a
RT disorder-to-order transition of the substrate-binding site mediated
RT by a calcium-sodium-calcium metal triad.",
RL Structure 6:281-292(1998).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 330-512.
RX MEDLINE=20384196; PubMed=10924103;
RA Brzezowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Prantzen H.,
RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
RT "Structural analysis of a chimeric bacterial alpha-amylase.
RT High-resolution analysis of native and ligand complexes.",
RL Biochemistry 39:9099-9107(2000).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT
RP H162V/N219F/A238V/Q293S/N294Y.
RC STRAIN=ATCC 6598;
RX MEDLINE=22538505; PubMed=12540849;
RA Machius M., Declerck N., Huber R., Wiegand G.;
RT "Kinetic stabilization of Bacillus licheniformis alpha-amylase through
RT introduction of hydrophobic residues at the surface.",
RL J. Biol. Chem. 278:11546-11553(2003).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.

CC -1- SUBUNIT: Monomer.
CC -1- BIOTECHNOLOGY: Used in the food industry for high temperature
CC liquefaction of starch-containing mashers and in the detergent
CC industry to remove starch. Sold under the name Termamyl by
CC Novozymes.
CC -1- MISCELLANEOUS: Able to work at relatively high (alkaline) pH
CC values (up to pH 11) and at high temperatures (up to 100 degrees
CC Celsius).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC -----
CC EMBL: X03236; CAA26981.1; -
CC EMBL: M38570; AAA22226.1; -
CC EMBL: M13256; AAA22240.1; -
CC EMBL: K01984; AAA22193.1; -
CC EMBL: AF38149; AA026743.1; -
CC EMBL: M26412; AAA22237.1; -
CC EMBL: A17930; CAA01355.1; -
CC FIR; A91997; ALBSL.
CC PDB: 1BPL; 23-MAR-99.
CC PDB: 1BPL; 17-AUG-96.
CC PDB: 1E3X; 21-JUN-01.
CC PDB: 1E3Z; 24-JUN-03.
CC PDB: 1E40; 24-JUN-03.
CC PDB: 1E43; 21-JUN-01.
CC PDB: 1O80; 03-APR-03.
CC PDB: 1V0S; 12-MAR-97.
CC InterPro: IPR006589; Alp_amy1_cat_sub.
CC InterPro: IPR006047; Alpha_amy1_cat.
CC InterPro: IPR006046; Glyco_hydro_13.
CC Pfam: PF00128; Alpha-amylase; 1.
CC PRINTS: PR00110; ALPHA-AMYLASE.
CC SMART: SM00642; Amy; 1.
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
CC KM Signal; 3D-structure.
CC FT SIGNAL 1 29
CC FT CHAIN 30 512
CC FT ACT_SITE 260 260
CC FT ACT_SITE 264 264
CC FT ACT_SITE 357 357
CC FT METAL 133 133
CC FT METAL 190 190
CC FT METAL 210 210
CC FT METAL 212 212
CC FT METAL 223 223
CC FT METAL 229 229
CC FT METAL 231 231
CC FT METAL 233 233
CC
CC Query Match 63.1%; Score 1797.5; DB 1; Length 512;
CC Best Local Similarity 65.0%; Pred. No.1.9e-120;
CC Matches 316; Conservative 69; Mismatches 96; Indels 5; Gaps 2;
CC
CC 1 AAFPNGTQVQYFPMYLPDDCTIMTKVANNANLSLSIGTALMLPPAYKSTSDVGYGY 60
CC AANLNTGLNQYFPMYWPNDGQHWKRLQNDASVLAHGIYAVIPAYKSTSDADVGKAY 88
CC
CC 29
CC
CC 61 DLYDLGFNQKGTATRTKYGKAYLQALQAAHAGQVYADVVPFHKGAGDGTENVDAVE 120
CC DLYDLGFNQKGTATRTKYGKAYLQALQAAHAGQVYADVVPFHKGAGDGTENVDAVE 148
CC
CC 89 DLYDLGFNQKGTATRTKYGKAYLQALQAAHAGQVYADVVPFHKGAGDGTENVDAVE 148
CC
CC 121 VNSDNRQELSGTYQQAATKTPDFPFGKNTYSSFFKRWHPFGVMDSESRKLSRIYKFG 180
CC VNSDNRQELSGTYQQAATKTPDFPFGKNTYSSFFKRWHPFGVMDSESRKLSRIYKFG 207
CC
CC 149 VDPADRRNRVYSGHRIKAWHFFHPGSGSYDFKRWYHFGDTWDSRKLNRITKFO- 207
CC
CC 181 IGRAMPWEVDTEGNQNDYLMYADLDMDHPEVYTELQNGMKWYVNTNIDGFRILDAVRIK 240
CC

DB 422 FSRSGTEENP---GCVVVLNSGDDGKTLTLLGDVANKTWBPLGNBDEYVVTNDGEATF 479
QY 471 KUNGSVSVMV 481
DB 480 FCNAGSVSMV 490

RESULT 6
AMY2_ECOLI STANDARD; PRT; 495 AA.
ID AMY2_ECOLI
AC P26612; P78072;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
GN AMYA OR B1927.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Jall;
RC MEDLINE=93015717; PubMed=1400215;
RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
RL J. Bacteriol. 174:6644-6652(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12; MG1655;
RC MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RC MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kikukawa M., Kikigawa M.,
RA Makino S., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampaio G., Seki Y., Sivasubramanian S., Tagami H.,
RA Takekoshi J., Takekoshi K., Wada C., Yamamoto Y., Horikuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [4]
RP SEQUENCE OF 1-5 FROM N.A.
RC STRAIN=Jall;
RC MEDLINE=92407478; PubMed=1527488;
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes.";
RL J. Gen. Microbiol. 138:1051-1065(1992).
RN [5]
RP SEQUENCE OF 475-495 FROM N.A.
RC STRAIN=Jall;
RC MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIIa and IIib, including a
RT large non-coding region.";
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
CC EMBL; L01642; AAA23810.1; --
CC DR EMBL; AE000285; AAC74994.1; --
CC DR EMBL; D90833; BAA15755.1; --
CC DR EMBL; M85240; -; NOT ANNOTATED_CDS.
CC DR EMBL; L13279; AAA82575.1; --
CC DR PIR; D64956; A45738.
CC DR HSP; P06278; 1YUS.
CC DR EcoGene; EG11387; amyA.
CC DR InterPro; IPR006589; Alp_amy1_cat_sub.
CC DR InterPro; IPR006047; Alpha_amy1_cat.
CC DR Pfam; PF00128; alpha-amylase; 1.
CC DR SMART; SMO0642; Amyy; 1.
CC KW Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;
CC Complete proteome.
CC FT ACT_SITE 235 235 BY SIMILARITY.
CC FT ACT_SITE 265 265 BY SIMILARITY.
CC FT ACT_SITE 332 332 BY SIMILARITY.
CC FT METAL 104 104 CALCIUM (BY SIMILARITY).
CC FT METAL 239 239 CALCIUM (VIA CARBOXYL OXYGEN) (BY
CC SIMILARITY).
CC FT CONFLICT 19 20 KL -> SS (IN REF. 1).
CC FT CONFLICT 109 109 A -> V (IN REF. 1).
CC FT CONFLICT 149 149 Q -> E (IN REF. 1).
CC FT CONFLICT 234 234 L -> I (IN REF. 1).
CC SQ SEQUENCE 495 AA; 56639 MW; 26AFF6797DA54d6 CRC64;
Query Match 37.7%; Score 1074.5; DB 1; Length 495;
Best Local Similarity 42.9%; Pred. No. 4,3e-69;
Matches 210; Conservative 83; Mismatches 182; Indels 15; Gaps 4;
QY 5 NGTMQYFEWYLPDDGLTMTKTVANEANNTSSLCITLMMPAYKTSRS-DVIGYVYDY 63
DB 3 NPTLLCFHMYPEEGGLMPELBRADGFNDIDINWVLPAYKAGSGVSGYSDYDLF 62
QY 64 DLGSENGKGVTRTKYTGKRAQYLAIOAANAAGQYVADYVFDHKGAGDGTWDAVEVP 123
DB 63 DLGSEFDKGSIPKIGKAKQLAIDLKRNDAVLVDVYVNHKMGADKDEAARQRYNA 122
QY 124 SDRNOEISGTQYLOAWTKFPDPGNGNTYSSPKRWYHFDGVDMDESKTSRIYKFG-1 181
DB 123 DRRQIDEBIEEGCGWTRYPFARAGYSGFIMDFKCFSGIDHLENDEDEGIFKIVNDYT 182
QY 182 GKAMDWEVDNENGVYDILAMADLDMDHREYVTELKMGSKYVNTNIDGRFLAVKHXF 241
DB 183 GEGANDVDDELGFMDLMBENIDFRNHAATEELKARWVMEQTCDCGRDLDAVKH1PA 242
QY 242 SFPDMLSYVRSQTKELFTVGEWYSYDINKLHNYIKTKDTGMSLFDAPLANKFYTASKS 301
DB 243 WFKYEMIEHVGVAKFLFVIAEYWSHEVDKLTQYIDQVGGKMTLFDAPLOMKFHEASRM 302
QY 302 GGADMETLMTNTLMKQOPLTAVFVNNDHTEPQALQSVVDMPKFLAFAFLITREGY 365
DB 303 GRDYDMQIFGTGLVEADPFPAVTLVANHDTOPQALAEAVPEVFKFLAYALLIRENGV 362
QY 362 PCVFEGYVYGIPQYNIPS-----LXSKIDPLLIARDVAYGTHDYLDSHDIIGW 411
DB 363 PSVFYPLDYGANHYDVGDDGQTVFIDWPILEQDELILAROFAGVQTLFFDHPCIAF 422
QY 412 TREGTEKPSGLAALLITDDEGSGKMYVGVKQHGAKFYDLTGRSDTYVINSGWKEFK 471
DB 423 SRSQTDERP---GCVVAVNSGDDGKTHLGENYGNKTRWPLGNRQRYVTVDENGEATFF 480

QY 472 VNGSVSVWV 481
 DB 481 CNGSVSVWV 490
 RESULT 7
 CDGT_BACSP STANDARD; PRT; 713 AA.
 ID CDGT_BACSP PRT; 713 AA.
 AC P30921.
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
 DE (Cyclodextrin-glucosyltransferase) (Gtase).
 GN CGT.
 OS Bacillus sp. (strain 17-1).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxId=1409;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-44.
 RX MEDLINE=90257592; PubMed=253460; Kudo T, Horikoshi K;
 RA Kaneo T., Song K.B., Hamamoto T., Kudo T, Horikoshi K;
 RT "Construction of a chimeric series of Bacillus cyclomaltodextrin
 glucanotransferases and analysis of the thermal stabilities and pH
 optima of the enzymes."
 RL J. Gen. Microbiol. 135:1447-1457(1989).
 CC -1 CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
 of a 1,4-alpha-D-glucosidic bond.
 CC -1 COFACTOR: Binds 2 calcium ions per subunit (By similarity).
 CC -1 SUBUNIT: Monomer.
 CC -1 MISCELLANEOUS: GTPASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
 IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
 IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
 ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
 ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
 MALTOOLIGOSACCHARIDE PRODUCED.
 CC -1 SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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 or send an email to license@sib-sib.ch).
 CC EMBL: M28053; AAA2310.1; -.
 DR HSSP: P43379; ICDS.
 DR InterPro: IPR006589; Alp_amy1_cat_sub.
 DR InterPro: IPR006048; Alp_amy1_C.
 DR InterPro: IPR006047; Alp_amy1_cat.
 DR InterPro: IPR002044; CBD_4.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR002909; IPT_TIG.
 DR Pfam: PF00128; alpha-amy1ase_1.
 DR Pfam: PF02806; alpha-amy1ase_C_1.
 DR Pfam: PF06886; CBW_20_1.
 DR Pfam: PF01833; TIG_1.
 DR PRINTS: PR00110; ALPHAMYLASE.
 DR PRODOM: PD001568; CBD_4; 1.
 DR SMART: SM00642; Amy; 1.
 DR SMART: SM00632; Amy; C; 1.
 KM Transferrase; Glycosyltransferase; Calcium-binding; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 713
 FT DOMAIN 28 165
 FT DOMAIN 166 229
 FT DOMAIN 230 433
 FT DOMAIN 434 522
 FT DOMAIN 523 609
 FT DOMAIN 610 713
 FT ACT_SITE 256 256
 BY SIMILARITY.

FT ACT_SITE 284 284 BY SIMILARITY.
 FT ACT_SITE 355 355 BY SIMILARITY.
 FT METAL 54 54 CALCIUM 2 (BY SIMILARITY).
 FT METAL 56 56 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
 SIMILARITY).
 FT METAL 59 59 CALCIUM 2 (BY SIMILARITY).
 FT METAL 60 60 CALCIUM 2 (BY SIMILARITY).
 FT METAL 78 78 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
 SIMILARITY).
 FT METAL 80 80 CALCIUM 2 (BY SIMILARITY).
 FT METAL 166 166 CALCIUM 1 (BY SIMILARITY).
 FT METAL 217 217 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
 SIMILARITY).
 FT METAL 226 226 CALCIUM 1 (BY SIMILARITY).
 FT METAL 260 260 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
 SIMILARITY).
 FT DISULFID 70 77 BY SIMILARITY.
 SQ SEQUENCE 713 AA; 77389 MW; D13AEF6C507FE45E CRC64;
 Query Match 11.0%; Score 313; DB 1; Length 713;
 Best local Similarity 24.7%; pred. No. 8.6e-15;
 Matches 135; Conservative 82; Mismatches 188; Indels 142; Gaps 29;
 QY 19 DQTL-----WTKYANENNN--LSLGTALMLPP---AYKGRSRSDVGVVDL 62
 DB 67 DQCTNLRLYCGSDWQGIINKINDYLTGKGVTAIWSQPVNTYSVINYSGVNNITVHG 126
 QY 63 YDLGEFNQKTVRTKGYKAYQYLQIAAQAQVADVVDHKGGA--DGTENVDAVE 120
 DB 127 YNARDPK--INPAYGTLADPQNLIAAHAKNIVITIDFAPNHTSPASLDQSFENGK 183
 QY 121 VNPSDRNQSISGTQIQANTKDFPGRKNITSSFKKRYTHRDGVWDSRKLSTRYKRG 180
 DB 184 LYNGRDE--GGY-----INDTNLF--HNGGDFG----- 211
 QY 181 IGAAMDWEVDTEGNVYDYL--YADLMDHEVVELKMGKMYVTNTIDGRDLDAVGI 239
 DB 212 -----TENGIKYKLYDLADLNHNSTYDYLKAIKRWLD-LIDGIRMDAVGEM 261
 QY 240 KFSFEDWLSYVRSQTKPLFTVGEYSYDINKL--HNYITDTGMSLFDAPLHNKRYT 297
 DB 262 PFGWQSFMAVYNNY--KVFTEGE--WELGVNEVAENHKEFANVSGMSLDFRFAQXKRO 318
 QY 298 ASK--SGCAFMDRTMTNLT-----MKDQPLTAAVFVNDHDE--PGQALQWVDPWFK 347
 DB 319 VFKDNTNNYGLSMLEGSATDYAQMEDQ---VFPIHDHMERHNNANRKLQ--- 371
 QY 348 PLVAFILTRQEGYPCVFYGDYGIPOY-----NIFS-----LKSRIPL 387
 DB 372 --ALAFTLT--SRGVPAI-----YGTQVYMSGNDPDRARIPSFITTAAYGVSKLAFL 424
 QY 388 LIRRDYAYGTQHDYDHDIDIIQMTREGTE-----KPGGLALITDGPQSGKW 437
 DB 425 RKNPAINVGTTOERNINDVLYERKFFANNVAIVANRNVTASITGLVSLPAGS-- 482
 QY 438 MYVGKHAGKVFYDLGN--RSDPTVINSNDGCE--FKVNGSVSVW--VERKTVSTIAR 492
 DB 483 -----YDVAGGLNGNLTVSGGSAIFTLAAGTAWQYTTAAPTIGHV 531
 QY 493 -PITTRP 498
 DB 532 GPMWAKP 538
 RESULT 8
 AMYB_PABPO STANDARD; PRT; 1196 AA.
 ID AMYB_PABPO
 AC P21543;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Beta/alpha-amy1ase precursor [Includes: Beta-amy1ase (EC 3.2.1.2);
 Alpha-amy1ase (EC 3.2.1.1)].

OS Paenibacillus polymyxa (Bacillus polymyxa).
 OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
 NCBI_TaxID=1406;
 RN [1]
 RP SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=72;
 RX MEDLINE=87165765; PubMed=2435707;
 RA Kawazu T., Nakamishi Y., Uozumi N., Sasaki T., Yamagata H.,
 RT Tsukagoshi N., Udaoka S.;
 RT "Cloning and nucleotide sequence of the gene coding for enzymatically
 active fragments of the Bacillus polymyxa beta-amylose.";
 RL J. Bacteriol. 169:1564-1570(1987).
 RN [2]
 RP SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=72;
 RX MEDLINE=89123046; PubMed=2464578;
 RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,
 RT Tsukagoshi N., Udaoka S.;
 RT "A single gene directs synthesis of a precursor protein with beta-
 and alpha-amylose activities in Bacillus polymyxa.";
 RL J. Bacteriol. 171:375-382(1989).
 RN [3]
 RP SEQUENCE OF 1-776 FROM N.A.
 RC STRAIN=ATCC 8523;
 RX MEDLINE=87231094; PubMed=2438660;
 RA Rhodes C., Strasser J., Friedberg F.;
 RT "Sequence of an active fragment of B. polymyxa beta amylose.";
 RL Nucleic Acids Res. 15:3934-3934(1987).
 RN [4]
 RP DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES.
 RX MEDLINE=91215008; PubMed=1827035;
 RA Uozumi N., Matsuda T., Tsukagoshi N., Udaoka S.;
 RT "Structural and functional roles of cysteine residues of Bacillus
 polymyxa beta-amylose.";
 RL Biochemistry 30:4594-4599(1991).
 CC -1- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO
 PRODUCE MULTIFORM BETA-AMYLASES AND A 48 KDA ALPHA-AMYLASE AFTER
 SECRETION.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in
 polysaccharides so as to remove successive maltose units from the
 non-reducing ends of the chains.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 linkages in oligosaccharides and polysaccharides.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: In the N-terminal section; belongs to family 14 of
 glycosyl hydrolases.
 CC -1- SIMILARITY: In the C-terminal section; belongs to family 13 of
 glycosyl hydrolases.
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 CC EMBL, M15817; AAA65446.1; -
 CC EMBL, Y00150; AAG68344.1; -
 CC PIR, A29130; A29130.
 CC HSSP, P36924; 1892.
 DR InterPro; IPR006589; A1p_amy1_cat_sub.
 DR InterPro; IPR006048; Alpha_amy1_C.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR005085; CBM_25.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR InterPro; IPR001554; Glyco_hydro_14.
 DR Pfam; PF00128; alpha-amylose_1.1.
 DR Pfam; PF02806; alpha-amylose_C.1.
 DR Pfam; PF03423; CBM_25_2.
 DR Pfam; PF01373; Glyco_hydro_14_1.
 DR PRINTS; PRO0110; ALPHAMYLASE.
 DR PRINTS; PRO0750; BETAMYLASE.

DR SMART; SM00642; Amy; 1.
 DR SMART; SM00632; Amy_C; 1.
 DR PROSITE; PS00506; BETA_AMYLASE_1; 1.
 DR PROSITE; PS00679; BETA_AMYLASE_2; 1.
 DR Multifunctional enzyme: Hydrolase; Glycosidase; Signal;
 KM Polysaccharide degradation; Repeat.
 FT SIGNAL 1 35
 FT CHAIN 36 1196
 FT DOMAIN 36 454
 FT REPEAT 455 558
 FT REPEAT 565 668
 FT DOMAIN 669 1196
 FT DISULFID 118 126
 FT ACT_SITE 198 198
 FT ACT_SITE 394 394
 FT MUTAGEN 118 118
 FT MUTAGEN 126 126
 FT MUTAGEN 358 358
 FT CONFLICT 1 1
 FT CONFLICT 67 67
 FT CONFLICT 100 100
 FT CONFLICT 154 154
 FT CONFLICT 177 177
 FT CONFLICT 227 227
 FT CONFLICT 330 330
 FT CONFLICT 425 425
 FT CONFLICT 493 493
 FT CONFLICT 532 532
 FT CONFLICT 559 559
 FT CONFLICT 665 665
 FT CONFLICT 681 681
 FT CONFLICT 686 686
 FT CONFLICT 725 728
 FT CONFLICT 736 736
 FT CONFLICT 741 741
 FT CONFLICT 758 758
 SQ SEQUENCE 1196 AA; 130893 MW; A41E6B70F257064 CRC64;
 Query Match 10.84; Score 307; DB 1; Length 1196;
 Best Local Similarity 23.04; Pred. No. 4,3e-14;
 Matches 123; Conservative 68; Mismatches 186; Indels 158; Gaps 27;
 QY 4 FNGTMQYFEMVLPDDGLTWTKYANBANNSIGITATMLPPAYKQTSR-SDVGYGVYPL 62
 DB FNSNNSDQRKWH-----GDPQGIINKLDYIKKNGFAIWTPTWQKSEAYVGHYTYDF 825
 QY 63 YDLGEFQKGTAVTKYGTAKVYLAIOAAHAAQMOYVADVPDHKGADGTEVAVENV 122
 DB AVDGHLSIMDKLQELVKAHDKRIAYVADVNVNHTG----- 862
 QY 123 PSRDNQISGTYYQIAWTKEDF-PGRGNTYSSF-KRWYHFDG---VWDSRKLSRIY 176
 DB -----DQPGNGFAFAPDKADWYHNDITDGDYNSNNQ----- 897
 QY 177 KFRSIGANWEVDTEGNVADYLMVADLMDHBEVTELEKNWKKYVNTNIDGFLDAY 236
 DB -----WKI-ENG--DVAGLDLNNENPATNELCWMKMLNETGIDGLRDIV 943
 QY 237 KHIFSFPMLSVRSQTKPLFTVGEVWVSVDINKLHNYITKTDGMSLFDAPLHNKFY 296
 DB KHVPKGLKDF-----DQANFTFTGELPHGPAVAGDTRYLDAAL--DFPM--XY 991
 QY 297 TAAK-SGGAEDWRTL---MTNLMKDQPLATVFDNHT-----ERQALQSWV 342
 DB TIKDVFHDQSMRKIKRYSDDRYRDAQNGV-FIDNHVKRFLNDASGKPAHYDKW- 1049
 QY 343 DPFKPLAVAFILTRCGEPCVFGVGYGIPQVYNISLSKIDPLLIARRDYAYGTQHDY 402
 DB 1050 -POLK-AALGFTLL-SNGIPIITVGTGEGYSGDDPA-----NRENKMFNANHDL 1096
 QY 403 LDHSDITIGWREGTEFPGSGLAALITDPPGSKMKVYQGAHGVFYDL--TGNSSDIV 460
 DB 1097 YQYIAKLNYYNN-----HPALONGSQRKRV-----DSFYFSFQRKNGDEAI 1140

QY 461 TINSDBW-----GEF-----KUNGSVSVWV-PRKTYST 489
 Db 1141 VFINNSMNSQRTITGNFDNLNSGRRLTNLSNDSVQINNSITVTLAPKEVAKFT 1195

RESULT 9
 AM3A_ORYSA STANDARD; PRT; 440 AA.

AC P27932;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Alpha-amylase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
 GN AMY1.2 OR AMY3A.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euphyllophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphyllophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphyllophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC NCB1_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STEIN-CD Japonica M202; Tissue=Etisolated leaf;
 RA MEDLINE=91329892; PubMed=1714318;
 RA Sutilif T.D., Huang N., Lites J.C., Rodriguez R.L.;
 RT "Characterization of an alpha-amylase multigene cluster in rice,"
 RL Plant Mol. Biol. 16:579-591(1991).
 CC -1- FUNCTION: Important for breakdown of endosperm starch during germination.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- TISSUE SPECIFICITY: Most abundant in embryo-derived callus tissue.
 CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination in the aleurone cells under the control of the plant hormone gibberellic acid and in the developing grains at a low level.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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 CC -----
 CC EMBL; X56336; CAA39776.1; -
 CC DR PIR; S14958; S14958.
 CC DR HSSP; P04063; IAVA.
 CC DR Gramene; P27932; -
 CC DR InterPro; IPR006589; Alp_amy1_cat_sub.
 CC DR InterPro; IPR006047; Alpha_amy1_cat.
 CC DR InterPro; IPR006046; Glyco_hydro_13.
 CC DR Pfam; PF00128; alpha-amylase; 1.
 CC DR PRINTS; PR00110; ALPHAAMYLAASE.
 CC DR SMART; SMO0642; Aamy; 1.
 CC DR Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 CC KW Signal; Multigene family.
 CC FT SIGNAL 1 26
 CC FT CHAIN 27 440
 CC FT ACT SITE 207 440
 CC FT ACT SITE 207 440
 CC FT METAL 119 119
 CC FT METAL 145 145
 CC FT METAL 155 155
 CC FT METAL 166 166
 CC FT METAL 169 169
 CC FT METAL 170 170
 CC FT METAL 171 171

FT METAL 174 174
 FT METAL 176 176
 FT METAL 176 176
 SQ SEQUENCE 440 AA; 48872 MW; SE9B78C29AA91C2B CRC64;

Query Match 10.6%; Score 302.5; DB 1; Length 440;
 Best Local Similarity 28.4%; Pred. No. 2.6e-14; Indels 101; Gaps 21;
 Matches 117; Conservative 47; Mismatches 147;

QY 8 MNOYFEW-YLPDDGLTWKYVNEANLNSIGITALMLPARYKTSRSDVGYVYDYLQ 66
 Db 31 LFGQNMDSWKQGGWNTMLDQVGLASAGVTHVLPPTH--SVFQGYMPGLYDLN 88
 QY 67 EFNOKGVTRYTKYKQYLAIOAAAGQVADVDPDKGADGTEWDAVENSQR 126
 Db 89 -----ASKYKGAELKSLIAFAHAKIKCVADIVNRCADD----- 125
 QY 127 NOEISGVQIQAWKEDPGRGNTYSSFKRWYHFPDGDVNDSEKLSRIYFR-GIGKAW 185
 Db 126 -KQGRGVYCI-----FKGGGR-----GLDWPSPVICDDPDQYSDGTGR- 165
 QY 186 DMEVDTEGNYDYLMYADLDVDPPEVTELVKMGKATVNTNIDGFLDAVKHKSFFP 245
 Db 166 -----DT-----GADFAAPDIDHNLVQRELSDWLRDRDVGFGWRLDPAKGSAAVA- 217
 QY 246 DMLSVRSQTKPLFTVGEYV---SYD-----INKLHNYITKTDGTSLPDAP 290
 Db 218 -RTVV--QNPSPFVAEINNSLYDGDGKPAANOGQRELNVNWKQVGPATADFT 273
 QY 291 LHNKFTYASKSGAFDMETLMTNTLMKD-----OPTLVTFVNDHTEPQALQSW 341
 Db 274 TKGILQSAVC-GLBRKD-----KDGKAPGMIGWPEKAVFPVNHDT--GSTQRMW 323
 QY 342 VDPWFKP-LNVAFLTRDGEYPCVFGYVGIPOYNIPLSKRIDPLIAR 392
 Db 324 PFPSSKVLIGAVYILT-HPGVPCIFQGVF---DWN---LKOELNALAATRK 368

RESULT 10
 CDCT_BACS8 STANDARD; PRT; 713 AA.

AC P17652;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cyclomatodextrin glucanotransferase precursor (EC 2.4.1.19) (Cyclodextrin-glycosyltransferase) (CGTase) (Raw-starch-digesting amylase)
 DE Bacillus sp. (strain B1019)
 OS Bacillus; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
 OC NCB1_TaxID=1417;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-47.
 RX MEDLINE=90147765; PubMed=1689153;
 RA Itokor P., Tsukagoshi N., Ueda S.;
 RT "Nucleotide sequence of the raw-starch-digesting amylase gene from Bacillus sp. B1018 and its strong homology to the cyclodextrin glucanotransferase genes."
 RT Biochem. Biophys. Res. Commun. 166:630-636(1990).
 RL Biochem. Biophys. Res. Commun. 166:630-636(1990).
 CC -1- FUNCTION: This endo-type adsorbable amylase is capable to digest raw starch.
 CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation of a 1,4-alpha-D-glucosidic bond.
 CC -1- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; X56336; CAA39776.1; -
 CC DR PIR; S14958; S14958.
 CC DR HSSP; P04063; IAVA.
 CC DR Gramene; P27932; -
 CC DR InterPro; IPR006589; Alp_amy1_cat_sub.
 CC DR InterPro; IPR006047; Alpha_amy1_cat.
 CC DR InterPro; IPR006046; Glyco_hydro_13.
 CC DR Pfam; PF00128; alpha-amylase; 1.
 CC DR PRINTS; PR00110; ALPHAAMYLAASE.
 CC DR SMART; SMO0642; Aamy; 1.
 CC DR Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 CC KW Signal; Multigene family.
 CC FT SIGNAL 1 26
 CC FT CHAIN 27 440
 CC FT ACT SITE 207 440
 CC FT ACT SITE 207 440
 CC FT METAL 119 119
 CC FT METAL 145 145
 CC FT METAL 155 155
 CC FT METAL 166 166
 CC FT METAL 169 169
 CC FT METAL 170 170
 CC FT METAL 171 171

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CC or send an email to licensee@eb.ch).
CC -----
CC EMBL/ M33302; AAA2239.1;
DR EMBL/ D90112; BAA1440.1;
DR PIR/ S09196; S09196.
DR HSSP/ P43379; 1CDG.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006048; Alpha_amy1_C.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR002909; IPR_TIG.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR Pfam; PF02806; alpha-amy1ase_C; 1.
DR Pfam; PF00886; CBM_20; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PR00110; ALPHAMYLAASE.
DR ProDom; PD001568; CBD_4; 1.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy; C; 1.
DR Transferrase; Glycosyltransferase; Calcium-binding; signal.
FT SIGNAL 1 27
FT CHAIN 1 27
FT ACT SITE 28 713
FT ACT SITE 256 256
FT ACT SITE 284 284
FT ACT SITE 355 355
FT METAL 54 54
FT METAL 56 56
FT METAL 59 59
FT METAL 60 60
FT METAL 80 80
FT METAL 166 166
FT METAL 217 217
FT METAL 226 226
FT METAL 260 260
FT SEQUENCE 713 AA; 77420 MW; 85FB616DA687888 CRC64;
SQ
Query Match 10.6%; Score 302; DB 1; Length 713;
Best Local Similarity 24.7%; Pred. No. 5,2e-14;
Matches 156; Conservative 80; Mismatches 205; Indels 130; Gaps 29;
2 APENGTMOYFEWYLPDGLTWKANEANN--LSLIGTALMLPP---AYKTSRSDV 55
64 AAFDGTCTN-LRLYCGSD--WGIINKINDGLTGMGTALWISQVENIYSIIYSGV 119
56 GYGVYDLYLGEFNQGYRTKTKGTQAOYLQALQAHAAQMOYVADVFDHSGADGTEM 115
120 NNTAYGYVARDKK--TNPAVGTADFOQLAAHAAKIKITIDFANHSPPASSDOP 176
116 VDAVEVPSDRNOEISGTQCIQMTKFPDPGRGNTYSFKRWYHEDGVMDSEKRLSRI 175
177 SFENGRALVD-NETLLGGY-----TNDQNLFF---HHNGGDFDS----- 211
176 YKFRGIGKAMDEVDENNGNYDIPLATADLMDHPEVYTE--LKMKKKVYNTNTINDGFL 233
212 -----TTENGYYKNL--VDLADLNHNNSSTDVYLDAIKMWLD--LGIDGIM 255
234 DAVKHIKESFPDMLSVRSQTKPLFTVGEWYSYDINKL--HNYITKTIDGTSFLDAPL 291
256 DAYKHHPFGWQKSFMAVNNY--KPVYTFGE-WFLGVNEGRPNHMFANESGSLDFRF 312
292 HNYFYTA--SKSGAEDMRTLMNTL-----MDQPLAVTFPDNHTREGQLQSWDP 344
313 AOKRQGVFRDNTDNMYGKAKMLRGSADYAVDQDQ---VTFFDNHMERFHASNNRRK 368
345 WPKYLAFAFLTROEGVPCVFGDYGIPOY-----NIPSLKS-----KI 384
369 LEQALATLLILAR---VPAT-----YGTEDYMSGSDPDNRALPISSTSTTAYVIOQL 421

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QY 385 DPLLARRDYAYGTQHDYLDHSDIIGMTREGST-----EKPSSGAALITDPG 433
DB 422 APLKSNPAIAYGSGQERINNDVILYERKFSNVAVAVNRNLAPAS--ISGLVTSLPQ 480
QY 434 GSKRMVYGKQAHQKAFYDITGN--RSQVTLNSDG--WSEPKNGSVSW--VPRTITST 489
DB 481 GS-----YNDVGLGGLNGNLTVGSGGAASNFTLAAGTAVMOTATATPT 527
QY 490 IAR--PIITRP 498
DB 528 IGHVGPMAKP 538
RESULT 11
CDGU_BACCI STANDARD; PRT; 713 AA.
AC P43379;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cycloaldodecitrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cycloaldodecitrin-glycosyltransferase) (CGTase).
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
[1]
SEQUENCE FROM N.A., SEQUENCE OF 28-37, AND X-RAY CRYSTALLOGRAPHY (2.0
ANGSTROMS).
RP STRAIN=251;
RC MEDLINE=94149761; PubMed=8107143;
RX Lawson C.L., van Montfort R., Strokopytov B., Rozeboom H.J.,
RA Kalk K.H., de Vries G.E., Penninga D., Dijkhuizen L.,
RT "Nucleotide sequence and X-ray structure of cycloaldodecitrin
dependent crystal form."
RL J. Mol. Biol. 236:590-600(1994).
[2]
X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RP STRAIN=251;
RC MEDLINE=96094317; PubMed=7493956;
RX Knegetel R.M.A., Strokopytov B., Penninga D., Faber O.G.,
RA Rozeboom H.J., Kalk K.H., Dijkhuizen L., Dijkstra B.W.,
RT "Crystallographic studies of the interaction of cycloaldodecitrin
glycosyltransferase from Bacillus circulans strain 251 with natural
substrates and products."
RL J. Biol. Chem. 270:29256-29264(1995).
[3]
X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RP MEDLINE=97115811; PubMed=8955113;
RX Penninga D., van der Veen B.A., Knegetel R.M.A., van Hijum S.A.F.T.,
RA Rozeboom H.J., Kalk K.H., Dijkstra B.W., Dijkhuizen L.,
RT "The raw starch binding domain of cycloaldodecitrin glycosyltransferase
from Bacillus circulans strain 251."
RL J. Biol. Chem. 271:32777-32784(1996).
[4]
X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH INHIBITOR.
RP STRAIN=251;
RC MEDLINE=96264806; PubMed=8672460;
RX Strokopytov B., Knegetel R.M.A., Penninga D., Rozeboom H.J., Kalk K.H.,
RA Dijkhuizen L., Dijkstra B.W.,
RT "Structure of cycloaldodecitrin glycosyltransferase complexed with a
maltonase inhibitor at 2.6-A resolution. Implications for product
specificity."
RL Biochemistry 35:4241-4249(1996).
CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
of a 1,4-alpha-D-glucosidic bond.
CC -1- CORFACTOR: Binds 2 calcium ions per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- DOMAIN: May consist of two protein domains: the one in the amino-
terminal side cleaves the alpha-1,4-glucosidic bond in starch, and
the other in the C-terminal side catalyzes other activities,
including the reconstruction of an alpha-1,4-glucosidic linkage
for cyclizing the maltooligosaccharide produced.

```

CC -! SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X78145; CAAS5023.1; -
DR PIR: A58800; A58800
DR PDB: 1CDG; 08-MAR-95.
DR PDB: 1CGV; 27-FEB-95.
DR PDB: 1CGW; 27-FEB-95.
DR PDB: 1CGY; 07-FEB-95.
DR PDB: 1CGY; 07-FEB-95.
DR PDB: 1CXE; 15-DEC-95.
DR PDB: 1CXF; 15-DEC-95.
DR PDB: 1CXH; 15-DEC-95.
DR PDB: 1CXI; 15-DEC-95.
DR PDB: 1CXK; 07-FEB-00.
DR PDB: 1CXL; 03-SEP-99.
DR PDB: 1D3C; 22-DEC-99.
DR PDB: 1DTU; 06-MAR-00.
DR PDB: 1E05; 22-NOV-00.
DR PDB: 1E07; 22-NOV-00.
DR PDB: 1KCK; 16-JAN-02.
DR PDB: 1KCL; 16-JAN-02.
DR PDB: 1TCM; 21-APR-97.
DR PDB: 2CXG; 14-OCT-98.
DR PDB: 2DIJ; 13-JAN-99.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR InterPro: IPR006048; Alp_amy1_C.
DR InterPro: IPR006047; Alp_amy1_cat.
DR InterPro: IPR002044; CBD_4.
DR InterPro: IPR006046; Glyco_hydro_13.
DR InterPro: IPR007110; Ig-1ike.
DR InterPro: IPR002909; IPT_TIG.
DR Pfam: PF00128; alpha-amy1ase_1.
DR Pfam: PF02806; alpha-amy1ase_C_1.
DR Pfam: PF00686; CBK_20; 1.
DR Pfam: PF01833; TIG_1; 1.
DR PRINTS: PR00110; ALPHAMYLAASE.
DR PRODOM: PD001568; CBD_4; 1.
DR SMART: SM00642; Amy; 1.
DR SMART: SM00632; Amy; C; 1.
DR transferase; Glycosyltransferase; Calcium-binding; signal;
KM 3d-structure. 1
FT SIGNAL. 27
FT CHAIN 28 713
FT DOMAIN 28 165
FT DOMAIN 166 229
FT DOMAIN 230 433
FT DOMAIN 434 522
FT DOMAIN 523 609
FT DOMAIN 610 713
FT DISULFID 70 77
FT ACT_SITE 256 256
FT ACT_SITE 284 284
FT ACT_SITE 355 355
FT METAL 54 54
FT METAL 55 55
FT METAL 56 56
FT METAL 59 59
FT METAL 60 60
FT METAL 80 80
FT METAL 166 166
FT METAL 217 217
FT METAL 226 226
FT METAL 260 260
FT TURN 30 31
FT TURN 33 34
FT TURN 36 37
CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
A1.
B.
A2.
C.
D.
E.
NUCLEOPHILE.
PROTON DONOR.
SUBSTRATE BINDING.
CALCIUM 1.
CALCIUM 1 (VIA CARBOXYL OXYGEN).
CALCIUM 1.
CALCIUM 1.
CALCIUM 1.
CALCIUM 2.
CALCIUM 2 (VIA CARBOXYL OXYGEN).
CALCIUM 2 (VIA CARBOXYL OXYGEN).
CALCIUM 2 (VIA CARBOXYL OXYGEN).

FT TURN 40 41
FT STRAND 44 46
FT HELIX 49 52
FT HELIX 53 59
FT HELIX 57 63
FT STRAND 66 66
FT TURN 68 69
FT TURN 73 74
FT STRAND 76 76
FT HELIX 81 89
FT TURN 90 91
FT HELIX 92 96
FT TURN 97 97
FT STRAND 100 103
FT STRAND 107 109
FT STRAND 114 116
FT TURN 117 118
FT STRAND 119 121
FT TURN 124 125
FT STRAND 129 135
FT STRAND 137 139
FT TURN 142 154
FT HELIX 155 158
FT TURN 158 163
FT TURN 165 166
FT STRAND 167 170
FT TURN 173 174
FT TURN 175 177
FT TURN 179 182
FT STRAND 184 186
FT TURN 187 188
FT STRAND 189 192
FT TURN 195 196
FT STRAND 202 202
FT STRAND 207 207
FT HELIX 213 218
FT STRAND 220 220
FT STRAND 222 223
FT STRAND 224 227
FT TURN 229 230
FT HELIX 232 248
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FT STRAND 252 255
FT HELIX 258 260
FT HELIX 263 274
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FT HELIX 413 421
FT TURN 422 423
FT HELIX 424 427
FT HELIX 429 433

Query Match 10.5%; Score 300; DB 1; Length 713;
Best Local Similarity 24.8%; Pred. No. 7.2e-14;
Matches 138; Conservative 77; Mismatches 200; Indels 142; Gaps 30;

QY	APENGMMQGFENEYLLDDDLTMTKVAENKN--LSLSGTLTLMPE-----AYKSTSDV	55
Db	64 AADPGICTM..LRJYCGD---WGGIINKNDGTLGGMVTAIWISQPEVNIYSTINISGV <td>119</td>	119
QY	56 GYGVDYLLDGEFNQKGTAVKRYGTGAQYLAIOAHAAGQVAVDVFFDEKGGADGTEW <td>115</td>	115
Db	120 NNTAAYHGVMARDEPKK---TNPAVGTTADPQNTIAAHHAKNIKVIDPAPNTSTPSSDOP <td>176</td>	176
QY	116 VDAVENVNPSPRNOEISGTQIQAMTFDPDPKGNVYSSPKRWTHFPDGVDEDEKKSRI <td>175</td>	175
Db	177 SFAENGLRYD-NGTLIGY-----TNDIONLF---HNNGSTDS----- <td>211</td>	211
QY	176 YKFRGICKAMDWEVDIENGNYDYLM-YADLDMDHEVVVELKNMGKMYVNTTINIGREL <td>234</td>	234
Db	212 -----TTENGIRKYLVDLADLNHNNSFTVDYELKDAIKMMLD-LGIDGIRMD <td>256</td>	256
QY	235 AVHGIRKSFEPDMLSYRSTGKPELTIVGEWYSYDNLK--HNYLTKDGIMSLFDAPLH <td>292</td>	292
Db	257 AVKMPGPMQKSFPAAYNNY--KPEVTFGE-PELGNEVSPENHKFANESGKSLDPRFA <td>313</td>	313
QY	293 NKEFYTA--SKSGGAFDMKTLMTNTL-----MKDQPLATVPNDTDETPGQA----- <td>338</td>	338
Db	314 QKVAQVPRDNTDMWYGLKAMLBGSADVAQVDDQ---VTFLDNHDERPHASVANRKL <td>366</td>	366
QY	339 QSWDPMFKPLAFAFLITROEGYPCVCFYDGYGIRY-----NITSLS----- <td>382</td>	382
Db	370 EQ-----AAFLITL-SRGPAL-----YGTGQWMSGTDPDNRARIPSTSTTAY <td>415</td>	415
QY	383 ----KIDPLLIARDVAVGTQHDYLDHSDIIGMTREGT-----EKPGSGLAAL <td>427</td>	427
Db	416 QVIOKLAPLKKNCPRALAYGSTQGRWLNNDVLLYERFGSNVAVAVNKNLAPAS-ISGL <td>474</td>	474
QY	428 ITDPGSGSKMYVYCKQAGACVFDLTGN--RSQVTTINSDG-WGEFKYNGSVSYW-VPR <td>483</td>	483
Db	475 VTSUPOGS-----YNDVLGGLNGLNTLSVSGGAASNFTLAAGTAVWQYXTA <td>521</td>	521
QY	484 KTVSTVAR--PITTRP 498 <td></td>	
Db	522 ATATPTTIGHVGPMAK 538 <td></td>	

RESULT 12

ID	CDGT_BAC63	STANDARD;	PRT;	712 AA.
AC	P09121;			
DT	01-MAR-1989 (Rel. 10, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Cyclomaltoedextrin glucanotransferase precursor (EC 2.4.1.19)			
DE	(Cyclodextrin-glycosyltransferase) (CGTase).			
GN	CGT.			
OS	Bacillus sp. (strain 38-2).			
OC	Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxId=1412;			
RN	[1]			
RN	SEQUENCE FROM N.A., AND SEQUENCE OF 28-44.			
RX	MEDLINE=89036108; Pubmed=297812;			
RA	Kaneko T., Hamamoto T., Horikoshi K.;			
RT	"Molecular cloning and nucleotide sequence of the cyclomaltoedextrin			
RT	glucanotransferase gene from the alkalophilic Bacillus sp. strain no.			
RT	38-2."			
RL	J. Gen. Microbiol. 134:97-105(1988).			
RN	[2]			
RP	SEQUENCE OF 1-566 FROM N.A.			
RA	Hamamoto T., Kaneko T., Horikoshi K.;			
RT	"Nucleotide sequence of the cyclomaltoedextrin glucanotransferase			
RT	(CGTase) gene from alkalophilic Bacillus sp. strain No. 38-2."			
RL	Agric. Biol. Chem. 51:2019-2022(1987).			
CC	-) CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation			
CC	of a 1,4-alpha-D-glucosidic bond.			
CC	-) COFACTOR: Binds 2 calcium ions per subunit (By similarity).			
CC	-) SUBUNIT: Monomer.			

```

CC -1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GUCCOSIDIC BOND
CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
CC ALPHA-1,4-GUCCOSIDIC LINKAGE FOR CYCLIZING THE
CC MALTOOLIGOSACCHARIDE PRODUCED.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ch/announce/
CC or send an email to license@isb.ch).
CC -----
CC CC EMBL; M19680; AAA22309.1; -.
CC DR EMBL; D00129; BAA00077.1; -.
CC DR HSSP; P05618; IPAM.
CC DR InterPro; IPR006589; Alp_amy1_cat_sub.
CC DR InterPro; IPR006048; Alpha_amy1_C-
CC InterPro; IPR006047; Alpha_amy1_cat.
CC DR InterPro; IPR002044; CBD_4.
CC DR InterPro; IPK006046; Glyco_hydro_13.
CC DR InterPro; IPK007110; 1g_11ke.
CC DR Pfam; PF00128; alpha-amy1ase; 1.
CC DR Pfam; PF02806; alpha-amy1ase_C; 1.
CC DR Pfam; PF00666; CBM_20; 1.
CC DR Pfam; PF01833; TIG; 1.
CC DR PRINTS; PR00110; ALPHAMYLASE.
CC DR PRODOM; PD001568; CBD_4; 1.
CC DR SMART; SMO0642; Aamy; 1.
CC DR SMART; SMO0632; Aamy_C; 1.
CC KW Transferrase; Glycosyltransferase; Calcium-binding; signal.
CC -----
CC FT SIGNAL 1 27
CC FT CHAIN 28 712 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
CC FT DOMAIN 28 165 A1.
CC FT DOMAIN 166 229 B.
CC FT DOMAIN 230 433 A2.
CC FT DOMAIN 434 522 C.
CC FT DOMAIN 523 608 D.
CC FT DOMAIN 609 712 E.
CC FT ACT_SITE 256 256 BY SIMILARITY.
CC FT ACT_SITE 284 284 BY SIMILARITY.
CC FT ACT_SITE 355 355 BY SIMILARITY.
CC FT METAL 54 54 CALCIUM 2 (BY SIMILARITY).
CC FT METAL 56 56 CALCIUM 2 (VIA CARBOXYL OXYGEN) (BY
CC SIMILARITY).
CC FT METAL 59 59 CALCIUM 2 (BY SIMILARITY).
CC FT METAL 60 60 CALCIUM 2 (BY SIMILARITY).
CC FT METAL 78 78 CALCIUM 2 (VIA CARBOXYL OXYGEN) (BY
CC SIMILARITY).
CC FT METAL 80 80 CALCIUM 2 (BY SIMILARITY).
CC FT METAL 166 166 CALCIUM 1 (BY SIMILARITY).
CC FT METAL 217 217 CALCIUM 1 (VIA CARBOXYL OXYGEN) (BY
CC SIMILARITY).
CC FT METAL 226 226 CALCIUM 1 (BY SIMILARITY).
CC FT METAL 260 260 CALCIUM 1 (VIA CARBOXYL OXYGEN) (BY
CC SIMILARITY).
CC FT DISULFID 70 77 VPGRI -> SWRHL (IN REF. 2).
CC FT CONFLICT 582 586
CC FT SEQUENCE 712 AA; *78249 MW; 4FPA8F70BEF818F9 CRC64;
CC -----
CC Query Match 10.1%; Score 286.5; DB 1; Length 712;
CC Best Local Similarity 24.5%; Pred. No. 5.5e-13;
CC Matches 127; Conservative 75; Mismatches 190; Indels 127; Gaps 27
CC -----
CC 23 WTQVNEANN--LSELGITLALMP---AVKGTSRSDVGYGVVDLYDLGEFNGKGTVRT 76
CC | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC 81 WGIITNKINDGVLTGMSGITAIWISQPAENIISVNIYSGVNHNTAHCYVARDPKF---TNP 137
CC | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC 77 KYGTQAYQLAQLQAHAAGQGVVADVDFDHKGADGTEWVDAVEVNSDRNOELISGTQI 136

```


QY 333 EPGQALQSWDPWFKFLAVAFILITROGYCVFYGDYGIPOY-----NIPSLK 381
 DB 364 D--RFTSAVNNRRLQALAFITL-SRGVPAI-----YGTBQILITNGDPNRRGKMPSPS 416
 QY 382 -----SKIDPLLIARRDYAVG-TQHDYLD----- 404
 DB 417 KSTTAFNVISKLAPLKRKNPAIAYGSTQGWNNVDYIERKFGKSVAVVNRMLTPT 476
 QY 405 -----HSDIIGWTRGCGEKEKSGSLAALITDGPGRK-WMTVGNQ-----H 444
 DB 477 STNNLTSLPSSGYTVDLGGVLNGNNITSSGNISSFTLAAGTAVMOYTASETPTTGH 536
 QY 445 AGKAFYDLTGNRSDTYTINSDEGWGEFK-----VNGSVSVW--VPRKTTVSTIA 491
 DB 537 VGPVW-----GKPGNVVTLIDGRFGSAKGTFTYFTTAVTSATISWEDTQIKVTIPVA 590
 RESULT 14
 ID CDGT_BACSO STANDARD; PRT; 713 AA.
 AC P05618;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cyclomalodextrin glucanotransferase precursor (EC 2.4.1.19)
 GN (Cyclodextrin-glycosyltransferase) (Cgtase).
 OS Bacillus sp. (strain 1011).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87308036; PubMed=2957361;
 RA Kiuma K., Kataoka S., Ishii Y., Takano T., Yamane K.;
 RT "Nucleotide sequence of the beta-cyclodextrin glucanotransferase gene
 of alkalophilic Bacillus sp. strain 1011 and similarity of its amino
 acid sequence to those of alpha-amylases.";
 RT J. Bacteriol. 169:4399-4402(1987).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RA Harata K., Haga K., Nakamura A., Aoyagi M., Yamane K.;
 RT "X-ray structure of cyclodextrin glucanotransferase from alkalophilic
 Bacillus Sp. 1011. Comparison of two independent molecules at 1.8-A
 resolution.";
 RT Acta Crystallogr. D 52:1136-1145(1996).
 CC -1- CATALYTIC ACTIVITY: Degradates starch to cyclodextrins by formation
 of a 1,4-alpha-D-glucosidic bond.
 CC -1- COFACTOR: Binds 2 calcium ions per subunit.
 CC -1- SUBUNIT: Monomer.
 CC -1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
 IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
 IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
 ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
 ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
 MALTOLOGSACCHARIDE PRODUCED.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DB EMBL: M17366; AAA23308.1; -
 DB PIR: A26678; ALBSC3.
 DB PDB: 1D7F; 17-MAR-00.
 DB PDB: 1DED; 07-APR-00.
 DB PDB: 1175; 11-APR-01.
 DB PDB: 1PAM; 11-JAN-97.
 DB InterPro: IPR006589; Alp_amyl_cat_sub.

DR InterPro: IPR006048; Alpha_amyl_C.
 DR InterPro: IPR006047; Alpha_amyl_cat.
 DR InterPro: IPR002044; CBD_4.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR002909; IPT_TIG.
 DR Pfam: PF00128; alpha-amylase_1.
 DR Pfam: PF02806; alpha-amylase_C_1.
 DR Pfam: PF00686; CBM_20; 1.
 DR Pfam: PF01833; TIG_1.
 DR PRINTS: PR00110; ALPHAMYLASE.
 DR ProDom: PD001568; CBD_4; 1.
 DR SMART: SM00642; Amyy; 1.
 DR SMART: SM00632; Amyy_C; 1.
 KM Transferase; Glycosyltransferase; Calcium-binding; signal;
 KM 3D-structure.
 FT SIGNAL 1 27
 FT CHAIN 28 713
 FT DOMAIN 166 165
 FT DOMAIN 166 229
 FT DOMAIN 230 433
 FT DOMAIN 434 522
 FT DOMAIN 523 609
 FT DOMAIN 610 713
 FT ACT_SITE 256 256
 FT ACT_SITE 284 284
 FT ACT_SITE 355 355
 FT METAL 54 54
 FT METAL 54 54
 FT METAL 56 56
 FT METAL 59 59
 FT METAL 60 60
 FT METAL 80 80
 FT METAL 166 166
 FT METAL 217 217
 FT METAL 226 226
 FT METAL 260 260
 FT DISULFID 70 77
 FT TURN 30 31
 FT TURN 33 34
 FT TURN 33 34
 FT TURN 40 41
 FT STRAND 44 46
 FT HELIX 49 51
 FT TURN 52 52
 FT HELIX 57 59
 FT HELIX 63 65
 FT STRAND 66 66
 FT TURN 68 69
 FT TURN 73 74
 FT STRAND 76 76
 FT HELIX 81 89
 FT TURN 90 93
 FT HELIX 94 96
 FT TURN 97 97
 FT STRAND 100 103
 FT STRAND 107 109
 FT STRAND 114 116
 FT TURN 117 118
 FT STRAND 119 121
 FT STRAND 124 125
 FT STRAND 129 135
 FT TURN 137 139
 FT HELIX 142 154
 FT TURN 155 156
 FT STRAND 158 163
 FT TURN 165 166
 FT STRAND 167 170
 FT TURN 176 177
 FT TURN 179 182
 FT STRAND 184 186
 FT TURN 187 188
 FT STRAND 189 192
 FT TURN 195 196
 FT TURN 198 199
 CYCLOMALDODEXTRIN GLUCANOTRANSFERASE.
 A1.
 B.
 A2.
 C.
 D.
 E.
 CALCIDIUM 1.
 CALCIDIUM 1 (VIA CARBONYL OXYGEN).
 CALCIDIUM 1.
 CALCIDIUM 1.
 CALCIDIUM 1.
 CALCIDIUM 2.
 CALCIDIUM 2 (VIA CARBONYL OXYGEN).
 CALCIDIUM 2.
 CALCIDIUM 2 (VIA CARBONYL OXYGEN).

RA Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
RT "Nucleotide sequence of the alpha-amylase gene from *Vigna mungo*,";
RL Plant Physiol. 103:1459-1459(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X53049; CAA37217.1; -;
DR EMBL; X73301; CAA51734.1; -;
DR PIR; S10514; S10514.
DR HSSP; P04063; IAVA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLAZE.
DR SMART; SMO0642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KM Signal.
FT SIGNAL 1 23 PROBABLE.
FT CHAIN 24 421 ALPHA-AMYLASE.
FT ACT SITE 201 201 BY SIMILARITY.
FT ACT SITE 309 309 BY SIMILARITY.
FT METAL 113 113 CALCIUM 1 (BY SIMILARITY).
FT METAL 130 130 CALCIUM 2 (BY SIMILARITY).
FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).
FT METAL 135 135 CALCIUM 2 (BY SIMILARITY).
FT METAL 139 139 CALCIUM 2 (BY SIMILARITY).
FT METAL 149 149 CALCIUM 3 (BY SIMILARITY).
FT METAL 160 160 CALCIUM 3 (BY SIMILARITY).
FT METAL 168 168 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 170 170 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 421 AA; 46888 MW; 15CA0DAB3DB4656 CRC64;
Query Match 9.9%; Score 283; DB 1; Length 421;
Best Local Similarity 26.3%; Pred. No. 6,1e-13;
Matches 103; Conservative 48; Mismatches 142; Indels 98; Gaps 17;
QY 8 MMGYFEMYLDDDTLTWKVANEANNLSGITLMTLPAYKGTSRSDVGAVYDYLGE 67
DB 26 LFGGFHWESKKGKGNLSKNSIPDLANGITHWLP--PGQSVPBGITLRLYLDL- 82
QY 68 FNGKGVRTKYGTGAQYLAIQAAAGQYVAVVDFHKG--ADGETWDAVEVNPSP 125
DB 83 -----ASKYGSKNELKSLIAFHEKGIKCLADIVINHTAERKGRGIYCFEGGTPD 135
QY 126 RNGEIGTVOIAMTFDPFGRGNTYSPFKRWYHFDGVDWDSRKLRIYKFRGIGKAM 185
DB 136 SRQDMGSPFICRDTIYS--DGTGNDS-----GEGY 165
QY 186 DWEVDTENGNYDYLMYADLMDH--PEVYTELKNMGKMYVNTNIDGFRLLDAVKHKISF 243
DB 166 D-----AAPDIDLNPQVORELSEWNNMLKTEIGFGMRFDYK---GY 206
QY 244 FPDMLSVRSQTKPLFTVGEVY---SY-----DINK--LHNYITKTDGTMSLFD 288
DB 207 APS-ISKIYVQTKPFAVGEKWDISTYGQDGKPNYNQSHRGALVNWVESAGAITAPD 265
QY 289 -----APLNKFTYASKSGGAFDMRTLMTNTLLKDOPTLAVTFVDNHDTEPGQALQS 340
DB 266 FTTKGILOAVQGEIWLIDPNG-----KPPGMIQVKNPNAVTFIDNHDT--GSTQRL 316

QY 341 WVDPEFKPL-AYAFILTRQSGYPCVFYGDY 370
DB 317 WPFSDKVMQGYAYILT-HPGTSPSIFYDHPF 346

Search completed: May 3, 2004, 20:51:15
Job time : 12.1361 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:34:58 ; Search time 49.0521 Seconds
(without alignments)
2782.151 Million cell updates/sec

Title: US-10-644-187-2
Perfect score: 2666
Sequence: 1 ANLNGTLMQYEFWYVNDQ.....SEGNGEPHNGSVSYVQR 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_28Jan04.*
1: Geneseq19806.*
2: Geneseq19908.*
3: Geneseq20008.*
4: Geneseq20018.*
5: Geneseq20028.*
6: Geneseq20038.*
7: Geneseq20048.*
8: Geneseq20058.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2666	100.0	483	2 AAR72447	Aar72447 Bacillus
2	2666	100.0	483	2 AAR78267	Aar78267 Bacillus
3	2666	100.0	483	2 AAW31404	Aaw31404 Bacillus
4	2666	100.0	483	2 AAT15818	Aat15818 Bacillus
5	2666	100.0	483	2 AAT29852	Aat29852 Bacillus
6	2666	100.0	483	2 AAT07384	Aat07384 Wild type
7	2666	100.0	483	3 AAY97965	Aay97965 Bacillus
8	2666	100.0	483	3 AAY97945	Aay97945 B. lichen
9	2666	100.0	483	5 AAB06936	Aab06936 B. lichen
10	2666	100.0	483	5 AAT12152	Aat12152 Bacillus
11	2666	100.0	483	5 AAT26534	Aat26534 Bacillus
12	2666	100.0	483	5 AAB47853	Aab47853 Bacillus
13	2666	100.0	483	5 AAB76589	Aab76589 Terminus
14	2666	100.0	531	2 AAR98007	Aar98007 Peib sign
15	2666	100.0	630	2 AAW22523	Aaw22523 Alpha-amy
16	2666	100.0	630	2 AAW23603	Aaw23603 Alpha-amy
17	2666	99.9	483	2 AAR57985	Aar57985 Wild type
18	2666	99.9	483	2 AAR88438	Aar88438 B. lichen
19	2666	99.9	483	2 AAR81475	Aar81475 Wild type
20	2666	99.9	483	2 AAW14498	Aaw14498 Bacillus
21	2666	99.9	483	2 AAW39742	Aaw39742 B. lichen
22	2666	99.9	483	4 AAG65876	Aag65876 B. lichen
23	2666	99.9	487	2 AAR57987	Aar57987 A4 form a
24	2666	99.9	487	2 AAW80189	Aaw80189 A4 form o
25	2666	99.9	487	4 AAG65881	Aag65881 B. lichen

26	2663	99.9	512	1 AAR70753	Aar70753 pheA aroF
27	2663	99.9	512	2 AAW73509	Aaw73509 Alpha-amy
28	2663	99.9	512	2 AAY00769	Aay00769 B. lichen
29	2663	99.9	512	4 AAY07097	Aay07097 Bacillus
30	2663	99.9	512	4 AAG65875	Aag65875 B. lichen
31	2663	99.9	512	4 AAG65877	Aag65877 B. lichen
32	2661	99.8	483	5 AAT12165	Aat12165 Bacillus
33	2661	99.8	483	5 AAT12161	Aat12161 Bacillus
34	2660	99.8	483	2 AAR58000	Aar58000 M197L alp
35	2660	99.8	483	2 AAR58002	Aar58002 M304L alp
36	2660	99.8	483	2 AAR58735	Aar58735 M15L alp
37	2660	99.8	483	2 AAR57992	Aar57992 M15L alp
38	2660	99.8	483	2 AAW80192	Aaw80192 Bacillus
39	2660	99.8	483	5 AAT12162	Aat12162 Bacillus
40	2660	99.8	483	5 AAT12163	Aat12163 Bacillus
41	2660	99.8	487	2 AAW80215	Aaw80215 A4 form a
42	2660	99.8	487	2 AAW80191	Aaw80191 A4 form a
43	2660	99.8	653	2 AAW57437	Aaw57437 NAMI.0 fu
44	2659	99.7	483	2 AAR10576	Aar10576 Mutant a1
45	2659	99.7	483	2 AAR58007	Aar58007 M197L alp

ALIGNMENTS

RESULT 1
AAR72447
ID AAR72447 standard; protein; 483 AA.
XX
AC AAR72447;
XX
AC 25-MAR-2003 (revised)
DT 01-DEC-1995 (first entry)
DE
DE Bacillus licheniformis alpha amylase (mature protein).
XX
XX Alpha amylase; variant; enzyme; detergent; additive; dishwashing;
KW washing; Bacillus licheniformis; Bacillus amyloliquefaciens;
KW Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
KM thermostable.
XX
OS Bacillus licheniformis.
XX
XX NO9510603-AI.
PN
XX 20-APR-1995.
PD
XX 05-OCT-1994; 94MO-DK000370.
PF
XX 08-OCT-1993; 93DK-00001133.
PR 02-FEB-1994; 94DK-00000140.
PR
XX (NOVO) NOVO-NORDISK AS.
XX Borchert TV, Bisgard-Frantzen H, Svendsen A, Thellersen M;
PI Van Der Zee P;
PI WPI: 1995-161790/21.
XX N-PSDB; AAC88066.
DR
XX New Bacillus derived alpha-amylase variants - having amino acid
PT modifications to improve washing and/or dishwashing performance.
PT
XX Claim 6; Page 72; 105pp; English.
PS
XX Variant alpha amylase enzymes which have improved washing and/or as
CC detergent additives. The enzymes have one or more amino acid residues
CC added, deleted or substituted. The variants can also be used for textile
CC deizing prior to scouring, bleaching and dyeing. The variants have
CC improved thermostability, acid/alkaline stability, low temperature
CC optimum; pH optimum; higher hydrolysis velocity and improved tolerance to
CC other composition constituents, e.g. oxidation agents. (Updated on 25-MAR
CC -2003 to correct pn field.) (Updated on 25-MAR-2003 to correct pi field.)

XX Sequence 483 AA;
 SQ Query Match 100.0%; Score 2666; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSDAYLAHGGITAWIPPAKGTSGADVGYGAYD 60
 DB 1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSDAYLAHGGITAWIPPAKGTSGADVGYGAYD 60
 QY 61 LYDGEFHQKGTAVTKYGTGKGLQSAIKSLHSRDINYGVDVINHKGADATEDVTAVEV 120
 DB 61 LYDGEFHQKGTAVTKYGTGKGLQSAIKSLHSRDINYGVDVINHKGADATEDVTAVEV 120
 QY 121 DPADNRNVIAGEHLIKAWTHFHPGRGSTYSDFKMWHYHFDGTDWDSRKLNRITYKQSK 180
 DB 121 DPADNRNVIAGEHLIKAWTHFHPGRGSTYSDFKMWHYHFDGTDWDSRKLNRITYKQSK 180
 QY 181 AMDWEVSENGNNDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
 DB 181 AMDWEVSENGNNDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
 QY 241 LRDMVNHVREKTKGEMTVAEYMONDICALENTLNKTNHNSVFDVPLHQFHAASQGG 300
 DB 241 LRDMVNHVREKTKGEMTVAEYMONDICALENTLNKTNHNSVFDVPLHQFHAASQGG 300
 QY 301 GYDKRKLNGTVSGKPLKSVTFVDNHDTPQGSLSTVQTWKFLAYAFILTRSGYPO 360
 DB 301 GYDKRKLNGTVSGKPLKSVTFVDNHDTPQGSLSTVQTWKFLAYAFILTRSGYPO 360
 QY 361 VFYGDWYGTGKDSQREIPALKHKEIPILKARKOYAYAGOHYDFDHDIVGWTREGDSSVA 420
 DB 361 VFYGDWYGTGKDSQREIPALKHKEIPILKARKOYAYAGOHYDFDHDIVGWTREGDSSVA 420
 QY 421 NSGLAALITDGPQAKMYVGRONAGETWHDITGNRSEPVVINSBGGEFHVNGGSYSIY 480
 DB 421 NSGLAALITDGPQAKMYVGRONAGETWHDITGNRSEPVVINSBGGEFHVNGGSYSIY 480
 QY 481 VQR 483
 DB 481 VQR 483

RESULT 2
 AAR78267
 ID AAR78267 standard; protein; 483 AA.
 AC AAR78267;
 XX 17-JAN-1996 (first entry)
 DT
 DE Bacillus licheniformis alpha amylase (mature protein).
 XX
 KW Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch;
 KW thermostable; methionine; Bacillus licheniformis;
 KW Bacillus amyloliquefaciens; Bacillus stearothermophilus.
 XX
 OS Bacillus licheniformis.
 XX
 PN MO9521247-A1.
 XX
 PD 10-AUG-1995.
 XX
 PE 05-OCT-1994; 94MO-DK000371.
 XX
 PR 02-FEB-1994; 94DK-00000141.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Toft AH, Marcher D, Federsen HH, Nilesen TE;
 XX
 DR WPI; 1995-283767/37.

DR N-PSDB; AAQ95031.
 XX Use of an oxidation stable alpha-amylase - for simultaneous desizing and
 PT bleaching or scouring of fabrics contg. starch or starch derivs.
 XX Claim 6; Page 22; 37pp; English.
 PS
 CC Oxidation stable alpha amylases can be used for the simultaneous desizing
 CC and bleaching or scouring of a fabric comprising starch or starch
 CC derivatives. They exhibit a better heat stability, especially in the
 CC presence of oxidizing agents. They are obtained from a parent alpha
 CC amylase by replacing one or more methionine residues with any amino acid
 CC different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or
 CC Asp. The parent alpha amylase is derived from a Bacillus species. This is
 CC the wild type (unmodified) alpha amylase

XX Sequence 483 AA;
 SQ Query Match 100.0%; Score 2666; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSDAYLAHGGITAWIPPAKGTSGADVGYGAYD 60
 DB 1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSDAYLAHGGITAWIPPAKGTSGADVGYGAYD 60
 QY 61 LYDGEFHQKGTAVTKYGTGKGLQSAIKSLHSRDINYGVDVINHKGADATEDVTAVEV 120
 DB 61 LYDGEFHQKGTAVTKYGTGKGLQSAIKSLHSRDINYGVDVINHKGADATEDVTAVEV 120
 QY 121 DPADNRNVIAGEHLIKAWTHFHPGRGSTYSDFKMWHYHFDGTDWDSRKLNRITYKQSK 180
 DB 121 DPADNRNVIAGEHLIKAWTHFHPGRGSTYSDFKMWHYHFDGTDWDSRKLNRITYKQSK 180
 QY 181 AMDWEVSENGNNDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
 DB 181 AMDWEVSENGNNDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
 QY 241 LRDMVNHVREKTKGEMTVAEYMONDICALENTLNKTNHNSVFDVPLHQFHAASQGG 300
 DB 241 LRDMVNHVREKTKGEMTVAEYMONDICALENTLNKTNHNSVFDVPLHQFHAASQGG 300
 QY 301 GYDKRKLNGTVSGKPLKSVTFVDNHDTPQGSLSTVQTWKFLAYAFILTRSGYPO 360
 DB 301 GYDKRKLNGTVSGKPLKSVTFVDNHDTPQGSLSTVQTWKFLAYAFILTRSGYPO 360
 QY 361 VFYGDWYGTGKDSQREIPALKHKEIPILKARKOYAYAGOHYDFDHDIVGWTREGDSSVA 420
 DB 361 VFYGDWYGTGKDSQREIPALKHKEIPILKARKOYAYAGOHYDFDHDIVGWTREGDSSVA 420
 QY 421 NSGLAALITDGPQAKMYVGRONAGETWHDITGNRSEPVVINSBGGEFHVNGGSYSIY 480
 DB 421 NSGLAALITDGPQAKMYVGRONAGETWHDITGNRSEPVVINSBGGEFHVNGGSYSIY 480
 QY 481 VQR 483
 DB 481 VQR 483

RESULT 3
 AAM31404
 ID AAM31404 standard; protein; 483 AA.
 AC AAM31404;
 XX
 DT 17-OCT-2003 (revised)
 XX
 DT 11-MAY-1998 (first entry)
 XX
 DE Bacillus licheniformis [Termamy] alpha-amylase.
 XX
 KW [Termamy]; alpha-amylase; enzyme engineering; protein engineering; starch;
 KW liquefaction; saccharification; sweetener; textile desizing;
 KW detergent additive.

XX OS Bacillus licheniformis; strain ATCC 27811.
 XX PN WO9741213-A1.
 XX PD 06-NOV-1997.
 XX PF 30-APR-1997; 97MO-DK000197.
 XX PR 30-APR-1996; 96DK-00000515.
 XX PR 28-JUN-1996; 96DK-00000712.
 XX PR 11-JUL-1996; 96DK-00000775.
 XX PR 08-NOV-1996; 96DK-00001263.
 XX BA (NOVO) NOVO-NORDISK AS.
 XX PI Svendsen A, Borchert TV, Bisgaard-Frantzen H;
 XX DR WPI; 1997-549718/50.
 XX DR N-PSDB; AAV02471.
 XX PT Termamyl-like alpha-amylase variants with improved properties - e.g.
 XX PT increased stability at low pH and low calcium, useful as detergent
 XX PT additives and in industrial starch processing e.g. liquefaction.
 XX PS Claim 1; Page 82; 101pp; English.
 CC This protein comprises Termamyl alpha-amylase (see AAW31404) of Bacillus
 CC licheniformis ATCC 27811. The invention relates to novel variants
 CC (mutants) of Termamyl-like alpha-amylases that have alpha-amylase
 CC activity and exhibit an alteration in at least one property selected
 CC from: substrate specificity; binding or cleavage pattern; thermal
 CC stability; pH/activity or pH/stability profile; stability towards
 CC oxidation; Ca2+ dependency and specific activity. The variant has one or
 CC more mutations selected from: (a) the mutations A181E, D, Q, N, V; I201
 CC (bulkier amino acid) including I201W, F, L, Y203Q, Q9K, L, E; F11R, K, E;
 CC E120; D100N, L, V101H, R, K, D, E, F, V102A, T, I103H, K, N104R, K, D, I;
 CC H105R, K, D, E, W, F, I106R, K, D, E, F, Y, I121R, K, D, E, L230H, K, I;
 CC A232G, H, F, S, V; V233D, K234L, E, I236R, K, N, H, D, E; L241R, K, D, E,
 CC F, A260S; W263H; Q264R, D, K, E; N265K, R, D; A269R, K, D, E; L270R, K,
 CC H, D, E; V283H, D; F284H, D285N, L; V286R, K, H, D, E; Y290R, E, K;
 CC V312R, K, D, E; F323H; D325N; N326K, H, D, L; H327Q, N, E, D, F; Q220L, E
 CC ; G332D; Q333R, K, H, E, L; S334A, V, T, L, I, D; L335G, A, S, T, N, N,
 CC E336R, R337E, T337D, K, T338D, E, T338D, Q360K, R, E, D365N; G372D, R;
 CC (b) substitutions at positions H68, H91, H247, R305, K306, H382, K389,
 CC H405, H406, H450 or R483; (c) the mutations H140Y, H142Y, H145Y, H145D +
 CC H142R, H140K + H142D; or H142Y + H156Y; (d) deletion of 3 amino acids
 CC within the partial sequence from T369 to I377, including K370-D372 or
 CC D372-Q374; (e) replacement of T369-I377 by IPTHSV, IPTHGV or IPQYNI; (F)
 CC substitutions at positions R169 or R173, including R169I, L, F, T or
 CC R172I, L, F, T; (G) the mutations H156D, I201F, I212F, A209I or T, or
 CC V208I; (h) substitutions at positions N172, A181, N186, N190, H205, D207,
 CC A209, A210, E211, Q264 or N265, including N172R, H, K, A181T, N186T;
 CC N190L, F, H205C; D207Y; A209L, T, V; A210S, E211Q, Q264A, E, L, K, S, T;
 CC N265A, S, T, Y; or (O264S + N265Y); and (i) the mutations H156Y + A181T +
 CC A209V; H156Y + A181T + N190F + A209V + Q264S + L157 + M15T +
 CC R23K + S29A + A30E + Y31H + A33S + E34D + H35I + H156Y + A209V
 CC (where + indicates deletion of the amino acid residue); A1* + N2* + L3V +
 CC M15T + R23K + S29A + A30E + Y31H + A33S + E34D + H35I + H156Y + A181T +
 CC N90F + A205V; or A1* + N2* + L3V + M15T + R23K + S29A + A30E + Y31H +
 CC A33S + E34D + H35I + H156Y + A181T + N190F + A205V + Q264S. Also claimed
 CC are constructs comprising DNA (see AAV02471) encoding such a variant, and
 CC recombinant expression vectors and transformed cells containing the DNA.
 CC The alpha-amylase variant is useful as a detergent additive and can also
 CC be used in industrial starch processing e.g. liquefaction (claimed) or
 CC saccharification to produce sweeteners, and in textile desizing
 CC (claimed). (Updated on 17-OCT-2003 to standardise OS field)
 XX SQ

QY 1 ANLTGTLMOYFEWVMPNDGQHRRLQNDASVLAIEGHITAVWIPPAKYKSTQADYGYGAYD 60
 DB 1 ANLTGTLMOYFEWVMPNDGQHRRLQNDASVLAIEGHITAVWIPPAKYKSTQADYGYGAYD 60
 QY 61 LVDLGEFHQKGTVRTKYGTGKELQSAIKSLHSRDINVGDVVNHKKGADATEDVTAVEV 120
 DB 61 LVDLGEFHQKGTVRTKYGTGKELQSAIKSLHSRDINVGDVVNHKKGADATEDVTAVEV 120
 QY 121 DPADRRRVISGSHLKAQTHFFPGRGTSYSPFKMWHFPGTMDERKLNRIYKFGK 180
 DB 121 DPADRRRVISGSHLKAQTHFFPGRGTSYSPFKMWHFPGTMDERKLNRIYKFGK 180
 QY 181 AMDWEVSNENGVYDLYMADIDYDHPDVAALIKRNGTAYANELQDGRDLAVKHKFSF 240
 DB 181 AMDWEVSNENGVYDLYMADIDYDHPDVAALIKRNGTAYANELQDGRDLAVKHKFSF 240
 QY 241 LRDVNVHREKTKEMFTVAEYQNDLGALENYLNKTNFNSVFVPLHYQPHASTQGG 300
 DB 241 LRDVNVHREKTKEMFTVAEYQNDLGALENYLNKTNFNSVFVPLHYQPHASTQGG 300
 QY 301 GYDMRKLNGTVSKAPLKSATFVFNHNDTPQGSLESTVQTWFKELAYAFILTRSGYPQ 360
 DB 301 GYDMRKLNGTVSKAPLKSATFVFNHNDTPQGSLESTVQTWFKELAYAFILTRSGYPQ 360
 QY 361 VFYGDVYGTGDSQREIPALKEIEPIKARKQVYGAQHDYFDHHDYVGTREDDSSVA 420
 DB 361 VFYGDVYGTGDSQREIPALKEIEPIKARKQVYGAQHDYFDHHDYVGTREDDSSVA 420
 QY 421 NSGLAALITDGGPGAARMVVRONAGETWHDITGNRSEPVVINSBGGEFHVNGGSVSIY 480
 DB 421 NSGLAALITDGGPGAARMVVRONAGETWHDITGNRSEPVVINSBGGEFHVNGGSVSIY 480
 QY 481 VQR 483
 DB 481 VQR 483
 RESULT 4
 ID AAV15418 standard; protein; 483 AA.
 AC AAV15418;
 XX 22-JUL-1999 (first entry)
 DT 22-JUL-1999 (first entry)
 XX Bacillus licheniformis alpha-amylase protein.
 DE Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
 XX sweeter; ethanol; starch; textile desizing; starch liquefaction;
 KM saccharification process.
 XX Bacillus licheniformis.
 OS WO9923211-A1.
 XX 14-MAY-1999.
 XX 30-OCT-1998; 98MO-DK000471.
 XX 30-OCT-1997; 97DK-00001240.
 XX 14-JUL-1998; 98DK-00000936.
 XX (NOVO) NOVO-NORDISK AS.
 XX Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TV;
 PI Kjaerulff S;
 XX WPI; 1999-326987/27.
 XX New Termamyl-like alpha-amylase variants.
 PT Claim 38; Page 82-84; 115pp; English.
 PS

CC The specification describes termamyl-like alpha-amylase variants
CC that have altered amino acid sequences to improve properties. The variants are
CC produced by creating one or more of the following mutations in amino acid
CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F443,
CC D146, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,
CC A186, W189, S193, N195, H107, A108, G109, P166, W167, D168, Q169, S170,
CC R111, Q172, F173, F267, N270, D271, L272, G273, A274, L275,
CC K311, E346, K385, G455, N457, K458, P459, G460, T461, V462, T463. The
CC variants can be used for washing and/or dishwashing. They can also be
CC used in the production of sweeteners and/or starch. They can also be
CC used in the production of sizers and/or starch. They can also be
CC used in the production of starch liquefaction and/or saccharification
CC processes. The present amylase can function as the parent sequence in the
CC production of the variants of the invention

Sequence 483 AA;

Query Match	100.0%;	Score 2666;	DB 2;	Length 483;
Best Local Similarity	100.0%;	Pred. No. 1.7e-224;		
Matches 483;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	ANINGTLMQYFEENYPMNDGQHRRLONDSAYLAENGITAWMIPRAYGTSQADVGAYAD	60
Db	1 ANUNGITLMQYFEENYPMNDGQHRRLONDSAYLAENGITAWMIPRAYKTSQADVGAYAD	60
Qy	LYDGEFHQKGTVRKYGTGKELQSAIKSLHSRDINVGDVINHKGADATEDVTAVEY	120
Db	61 LYDGEFHQKGTVRKYGTGKELQSAIKSLHSRDINVGDVINHKGADATEDVTAVEY	120
Qy	121 DPADRRNVISGEHLIAYMTFHFPBGSGSYSPFKKMHWHFPGTMDSEKLNRYKQOK	180
Db	121 DPADRRNVISGEHLIAYMTFHFPBGSGSYSPFKKMHWHFPGTMDSEKLNRYKQOK	180
Qy	181 AMDMEVSNENGANDYLMATADIDYDHEDEVAAIEKMGTVAYANELQDGRFLDAVGHIEFSF	240
Db	181 AMDMEVSNENGANDYLMATADIDYDHEDEVAAIEKMGTVAYANELQDGRFLDAVGHIEFSF	240
Qy	241 LRDMVAHFREKTKGEMFTVAETWQNDGLALENYLKTPTNHSVDPVPLHYFPHAASTQOG	300
Db	241 LRDMVAHFREKTKGEMFTVAETWQNDGLALENYLKTPTNHSVDPVPLHYFPHAASTQOG	300
Qy	301 GYDMRKILNLTIVVSKRPKSVTFEVDNHDHPQOSQSESTVQTMFXPLAAFLITRESGYPQ	360
Db	301 GYDMRKILNLTIVVSKRPKSVTFEVDNHDHPQOSQSESTVQTMFXPLAAFLITRESGYPQ	360
Qy	361 VFVGDWMTGSDSQREIPALXKHIEBILAKRQVAYGQHDYFDHHDIVGMTREGBDSVA	420
Db	361 VFVGDWMTGSDSQREIPALXKHIEBILAKRQVAYGQHDYFDHHDIVGMTREGBDSVA	420
Qy	421 NSGLAALITDGPQAGAKMYVGRONAGETMHDITGNRSEPVVINSGEWGEFPHNGSGVSIV	480
Db	421 NSGLAALITDGPQAGAKMYVGRONAGETMHDITGNRSEPVVINSGEWGEFPHNGSGVSIV	480
Qy	481 VOR 483	
Db	481 VOR 483	

RESULT 5
AAV29852
ID AAV29852 standard; protein; 483 AA.

AC AAY29852;

DT 18-NOV-1999 (first entry)

Bacillus licheniformis Termamyli-like alpha-amylase Val54.

KW Alpha-amylase; Termamyl-like alpha-amylase; glucose syrup; starch.

OS Bacillus licheniformis.

PN WO9946399-A1.

XX 16-SEP-1999.
PD

PF 08-MAR-1999; 99WO-DK000114.

PR 09-MAR-1998; 98DK-00000321.

PA (NOVO) NOVO-NORDISK AS.

PI Norman BE, Hendriksen HV;

DR WPI; 1999-551422/46.

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A method has been developed for the preparation of a glucose syrup using a thermamyl-like alpha-amylase containing a substitution at Val 534. The glucose syrup obtained by the process is useful as an ingredient in food products. The thermamyl-like alpha-amylase facilitates the preparation of glucose syrups suitable for the food industry, previously only possible using acid hydrolysis. The present sequence represents *Bacillus licheniformis* thermamyl-like alpha-amylase

SQ Sequence 483 AA;

Query Match	100.0%;	Score 2666;	DB 2;	Length 483;
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Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANINGTLMQYFEWYMPNDGQHWRLQND SAYLAEHGITAVWIPPAYKGT SQADVGYGAYD 60

Db 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASAYLAHGITAWIPRAYKGTSGADVGYGAYD 60

QY 61 LYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVIHKGADATEDVTAVEV 12

Db 61 LYDLGEFHQKTVRTKYGTKGELQSAIKSLHSRDINVGDVINHHKGADATEDVTAVEV 12

QY 121 DPADNRVIGEHLIKAWTHFHPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQ GK 18

Db 121 DPADRNRVISGEHLIKAWTHFHPBGRGSTYSDFKWHYHFDGTDWDESRKLNRIYKFQ GK 18

QY 181 AMDMEVSNENGNYYDLYMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDVVKHKEFSF 24

Db 181 AMDWEVSNENGNYYDLMYADIDYDHPDVAAEIKRWGTYANELQLDGFRLDAVKHIFSF 24

241 LRDMVNHVREKTGKEMFTVAEYWONDGALENYLNKTNFNHVSFEDVPLHYQFHAAS TOGG 30

Db 241 LRDWNVHREKTGKEMFTVAEYWNDDGALENYLKNTNENHSVFDPVLIHYQFHAASDGG 30

0Y 301 GYDMRKLLNGTVSKHPIKSVTFEVDNHDTPGOSLESTVOTWFKPLAYAFILTRSGYPQ 36

Db 301 GYDMRKLLNGTVVSKHPDKSVTFVVDNHDTPGOSLESTVOTWFKPLAYAFILTRSGYPQ 36

OV 361 VFYGDMYGTKGDSOREIPALKKHKEPILKARKOYAYGAOHDFDHHDIVGWTREGDSSVA 42

Dh 361 VFEYGDMYGTGDSOREIPALKEKIEPILKARKOYAYGAOHDPEDHDI VGTREGDSSVA 42

421 NSGI.AA.ITDGPQAKRMVGRONAGETWHDITGNRSEPVINSEGWGEFHVNGGSVSIY 48

Dh 421 NSGTAAITTDGPGAKRMVYGRONAGETWHDITGNRSEPVYINSEGWGEFHVNGGSY 48

CV 481 YOB 483

481 VCF 483

RESULT 6
AAV07394

ID	AY07384	standard; protein; 483 AA.
YY		

AC AAY07384;
XX 16-JUL-1999 (first entry)
XX wild type Termamy1 (RTM)-like alpha-amylase protein #4.
XX
XX Variant; Termamy1; alpha-amylase; mutation; Bacillus; detergent;
XX dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;
XX ethanol.
XX
XX Bacillus sp.
XX
XX Key Location/Qualifiers
XX FH Misc-difference 190
XX FT /note="optionally altered to any amino acid except an
XX FT /note="asn residue"
XX FT Misc-difference 201
XX FT /note="optionally altered to any amino acid except an
XX FT /note="ile residue"
XX FT Misc-difference 211
XX FT /note="optionally altered to any amino acid except an
XX FT /note="asp residue"
XX FT Misc-difference 214
XX FT /note="optionally altered to any amino acid except a Glu
XX FT /note="residue"
XX FT Misc-difference 264
XX FT /note="optionally altered to any amino acid except a Glu
XX FT /note="residue"
XX PN W09919467-A1.
XX PD 22-APR-1999.
XX PF 13-OCT-1998; 98WO-DK000444.
XX PR 13-OCT-1997; 97DK-00001172.
XX PA (NOVO) NOVO-NORDISK AS.
XX PI Svendsen A, Borchert TV, Bisgard-Frantzen H;
XX DR WPI; 1999-277632/23.
XX Variant alpha-amylases - useful as detergents or for textile desizing or
XX starch liquefaction.
XX PT
XX PS Claim 1; Page 67-68; 93pp; English.
XX
XX This sequence represents the parent sequence for new variants of a parent
XX Termamy1-like alpha-amylase with alpha-amylase activity. The variants
XX comprise mutations in 2-6 regions/positions relative to an alpha-amylase
XX from either of two Bacillus species in W09526397, B. stearothermophilus,
XX B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-
XX amylase variants are detergent additives for use in detergents for
XX dishwashing, manual or automatic laundry. The variants can also be used
XX for textile desizing or starch liquefaction (e.g. for production of
XX sweeteners or ethanol).
XX
XX Sequence 483 AA;
SQ

Query Match 100.0%; Score 2666; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.7e-224; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0;

DB 121 DPADRNRVLSGEHLIKAWTHFFPGRGSTYSDFKMWHFPGTDWDESRKLNRIYKFGOK 180
QY 181 AMDMEVSNENGVYDILMADIDYDHPDVAELIKRMGTYYANELQDGRFLDAVKIKFSF 240
DB 181 AMDMEVSNENGVYDILMADIDYDHPDVAELIKRMGTYYANELQDGRFLDAVKIKFSF 240
QY 241 LRDVNVHVEKTKGKEMFTVAEYMONDLGALENYLNKTFNHSVPDPLHYQFAASTQCG 300
DB 241 LRDVNVHVEKTKGKEMFTVAEYMONDLGALENYLNKTFNHSVPDPLHYQFAASTQCG 300
QY 301 GYDMKLLNGTVYSKPLKSVTFVNDHDTQPOQSLSSTVQTFKPLAYFILTRESGYQ 360
DB 301 GYDMKLLNGTVYSKPLKSVTFVNDHDTQPOQSLSSTVQTFKPLAYFILTRESGYQ 360
QY 361 VFYGDWYGTGDSQREIPALKEIPLKARQYVGAOHDFDHDIVGWTREGDSVA 420
DB 361 VFYGDWYGTGDSQREIPALKEIPLKARQYVGAOHDFDHDIVGWTREGDSVA 420
QY 421 NSGLAALITDGPAGAKRMVYGRONAGETWDTTKRSEPVYINSRKGFFHNGGSVSY 480
DB 421 NSGLAALITDGPAGAKRMVYGRONAGETWDTTKRSEPVYINSRKGFFHNGGSVSY 480
QY 481 VQR 483
DB 481 VQR 483

RESULT 7
AAY9605
ID AAY9605 standard; protein; 483 AA.
XX
XX AC AAY9605;
XX DT 04-SEP-2000 (first entry)
XX
XX DE Bacillus licheniformis Termamy1 alpha-amylase.
XX KW Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
XX KW saccharification; muten; mutant; enzyme stability; hybrid.
XX OS Bacillus licheniformis.
XX PN W0200029560-A1.
XX PD 25-MAY-2000.
XX PF 16-NOV-1999; 99WO-DK000628.
XX PR 16-NOV-1998; 98DK-00001495.
XX PA (NOVO) NOVO-NORDISK AS.
XX PI Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;
XX DR WPI; 2000-387777/33.
XX DR N-PSDB; AAA48483.
XX Variant of parent termamy1-like alpha amylase useful for washing, textile
XX desizing and starch liquefaction, comprising alterations in one or more
XX solvent exposed amino acid residues.
XX
XX Claim 8; Page 58-59; 80pp; English.
XX
XX The present sequence is a parent alpha-amylase from which mutants with
XX increased stability at acidic pH, low calcium concentration and high
XX temperatures have been derived. The enzyme is commercially available as
XX Termamy1. A variant may contain mutations in one or more solvent exposed
XX amino acid residues to increase the overall hydrophobicity of the enzyme
XX or the overall number of methyl groups in the side chains of exposed
XX residues may be increased. The mutations can be incorporated by site-
XX directed mutagenesis or by random mutagenesis. As a result of their
XX increased stability, the variants are suitable for the industrial

CC processing of starch, i.e. starch liquefaction and saccharification. They
 CC may also be useful for washing, dishwashing and textile desizing. Hybrid
 CC alpha-amylases comprising partial amino acid sequences derived from two
 CC or more alpha-amylases have also been created in order to increase enzyme
 CC stability

XX Sequence 483 AA:

Query Match 100.0%; Score 2666; DB 3; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANNGTLMQFEPWMPNDGQHRRLQNDSDATLAHGHTAVWIPPAVYKTSQADVGAYD 60
 DB 1 ANNGTLMQFEPWMPNDGQHRRLQNDSDATLAHGHTAVWIPPAVYKTSQADVGAYD 60
 QY 61 LYDGEFHQKGTATKTKYGTGKELQSAIKSLHSRDINVGDVINHKGADATEDVAVEV 120
 DB 61 LYDGEFHQKGTATKTKYGTGKELQSAIKSLHSRDINVGDVINHKGADATEDVAVEV 120
 QY 121 DPADRNRTVSGEHLIKAWTHFHFPGSGTYSDFKMWYHFDGTDWDSRKLNRITKFGQK 180
 DB 121 DPADRNRTVSGEHLIKAWTHFHFPGSGTYSDFKMWYHFDGTDWDSRKLNRITKFGQK 180
 QY 181 AMDWEVSNGNNDYLYMADIDYDHPDVAAEIKMGTYANELQDGFRLDAVGHKFSF 240
 DB 181 AMDWEVSNGNNDYLYMADIDYDHPDVAAEIKMGTYANELQDGFRLDAVGHKFSF 240
 QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNHNSVDVLYHQFHAASQGG 300
 DB 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNHNSVDVLYHQFHAASQGG 300
 QY 301 GYDMRKLLNGTVVSKHPLKSVTFVNDHDTQPGQSLESTVQTFKPLAFAFILTRESGYPQ 360
 DB 301 GYDMRKLLNGTVVSKHPLKSVTFVNDHDTQPGQSLESTVQTFKPLAFAFILTRESGYPQ 360
 QY 361 VFYGDWYGTGKDSOREIPALKHIEPIIKARKQYAGACHDYFDHDI VGTWREGDSVA 420
 DB 361 VFYGDWYGTGKDSOREIPALKHIEPIIKARKQYAGACHDYFDHDI VGTWREGDSVA 420
 QY 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSBGMGEFHNQGSVSIT 480
 DB 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSBGMGEFHNQGSVSIT 480
 QY 481 VQR 483
 DB 481 VQR 483

RESULT 8
 AAY97545
 ID AAY97545 standard; protein; 483 AA.

XX AAY97545;

DT 12-FEB-2001 (first entry)

DE B. licheniformis termamyl-like alpha amylase.

XX Termamyl-like alpha-amylase; variant; starch liquefaction; fuel;
 XX detergent composition; laundry cleaning composition; ethanol production;
 XX dish washing cleaning composition; hard surface cleaning composition;
 XX industrial ethanol production; textile desizing.

OS Bacillus licheniformis.

XX WO200060059-A2.

PD 12-OCT-2000.

PF 28-MAR-2000; 2000WO-DK000148.

XX 30-MAR-1999; 99DK-00000437.

XX (NOVO) NOVO NORDISK AS.
 PA Andersen C, Jorgensen CT, Bisgard-Frantzen H, Svendsen A,
 PI Kjaerulf S;
 DR WPI: 2001-015656/02.
 XX N-PsDB; AAA37849.

PT New variants of parent Termamyl-like alpha-amylase, useful in starch
 PT liquefaction, in detergent compositions and in ethanol production,
 PT exhibit altered cleavage pattern relative to the parent.

Claim 1; Page 60-62; 78pp; English.

CC This sequence represents a termamyl-like alpha amylase. The invention
 CC relates to a variant (1) of parent Termamyl-like alpha-amylase comprising
 CC alteration at one or more of the positions M13, G48, T49, S50, Q51, A52,
 CC D53, V54, G57, G107, G108, A111, S168 and M197. The alterations in (1)
 CC are independently an insertion of an amino acid downstream of the amino
 CC acid which occupies the position of an amino acid downstream of the amino
 CC acid which occupies the position with a different amino acid. The variant
 CC has alpha-amylase activity (1) or compositions containing it are useful
 CC in starch liquefaction, in detergent compositions such as laundry, dish
 CC washing and hard surface cleaning compositions, ethanol production such
 CC as fuel, drinking and industrial ethanol production, desizing of
 CC textiles, fabrics or garments. (1) exhibits a reduced capability of
 CC cleaving a substrate close to the branching point, and further exhibits
 CC improved substrate specificity and/or improved specific activity relative
 CC to the parent alpha-amylase

XX Sequence 483 AA:

Query Match 100.0%; Score 2666; DB 4; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANNGTLMQFEPWMPNDGQHRRLQNDSDATLAHGHTAVWIPPAVYKTSQADVGAYD 60
 DB 1 ANNGTLMQFEPWMPNDGQHRRLQNDSDATLAHGHTAVWIPPAVYKTSQADVGAYD 60
 QY 61 LYDGEFHQKGTATKTKYGTGKELQSAIKSLHSRDINVGDVINHKGADATEDVAVEV 120
 DB 61 LYDGEFHQKGTATKTKYGTGKELQSAIKSLHSRDINVGDVINHKGADATEDVAVEV 120
 QY 121 DPADRNRTVSGEHLIKAWTHFHFPGSGTYSDFKMWYHFDGTDWDSRKLNRITKFGQK 180
 DB 121 DPADRNRTVSGEHLIKAWTHFHFPGSGTYSDFKMWYHFDGTDWDSRKLNRITKFGQK 180
 QY 181 AMDWEVSNGNNDYLYMADIDYDHPDVAAEIKMGTYANELQDGFRLDAVGHKFSF 240
 DB 181 AMDWEVSNGNNDYLYMADIDYDHPDVAAEIKMGTYANELQDGFRLDAVGHKFSF 240
 QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNHNSVDVLYHQFHAASQGG 300
 DB 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNHNSVDVLYHQFHAASQGG 300
 QY 301 GYDMRKLLNGTVVSKHPLKSVTFVNDHDTQPGQSLESTVQTFKPLAFAFILTRESGYPQ 360
 DB 301 GYDMRKLLNGTVVSKHPLKSVTFVNDHDTQPGQSLESTVQTFKPLAFAFILTRESGYPQ 360
 QY 361 VFYGDWYGTGKDSOREIPALKHIEPIIKARKQYAGACHDYFDHDI VGTWREGDSVA 420
 DB 361 VFYGDWYGTGKDSOREIPALKHIEPIIKARKQYAGACHDYFDHDI VGTWREGDSVA 420
 QY 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSBGMGEFHNQGSVSIT 480
 DB 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSEPVVINSBGMGEFHNQGSVSIT 480
 QY 481 VQR 483
 DB 481 VQR 483

RESULT 9
 ABB06936
 ID ABB06936 standard; protein; 483 AA.
 XX
 AC ABB06936;
 XX
 DT 19-JUN-2002 (first entry)
 XX
 DE B. licheniformis termamyl-like alpha-amylase protein SEQ ID NO:8.
 XX
 XX Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
 XX variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
 XX washing; sweetener; ethanol; starch.
 OS
 XX Bacillus licheniformis.
 XX
 XX MO20016712-A2.
 XX
 XX 13-SEP-2001.
 XX
 XX 07-MAR-2001; 2001MO-DK000144.
 XX
 XX 06-MAR-2000; 2000DK-00000376.
 XX
 XX 15-MAR-2000; 2000US-0189857P.
 XX
 XX 23-FEB-2001; 2001DK-00000303.
 XX
 XX 26-FEB-2001; 2001US-0271382P.
 XX
 XX (NOVO) NOVOZYMES AS.
 XX
 XX
 XX Andersen C, Borchert TV, Nielsen BR;
 XX
 XX WPI; 2002-239612/29.
 XX
 XX N-PSDB; ABL50567.
 XX
 XX Novel variant of parent termamyl-like alpha-amylase useful as a component
 XX PT in washing and dishwashing compositions, for textile desizing, for starch
 XX PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 XX
 XX Claim 8; Page 142-143; 153pp; English.
 XX
 XX The present invention describes a variant of a parent termamyl-like alpha
 XX CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
 XX CC positions of a group of 31 possible amino acid positions. The alteration
 XX CC in (I) may be at Arg28, Arg118, Arg174, Arg181, Gly182, Asp183, Gly184,
 XX CC Gly186, Trp189, Asn195, Met202, Tyr298, Leu302, Ser303, Asn305,
 XX CC Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
 XX CC Asn445, Lys446, Glu448, Arg458, Asn471, or Ser484. (I) can be used for
 XX CC washing and/or dishwashing, textile desizing, and starch liquefaction.
 XX CC (I) is useful as a component in hard surface cleaning detergent
 XX CC composition, and for producing sweeteners and ethanol from starch. (I)
 XX CC has altered solubility, preferably increased solubility, in particular
 XX CC under washing, dish washing or hard surface cleaning conditions. The
 XX CC present sequence represents a Bacillus licheniformis termamyl-like alpha-
 XX CC amylase which is used in the exemplification of the present invention.
 XX
 XX Sequence 483 AA.
 XX
 XX Query Match 100.0%; Score 2666; DB 5; Length 483;
 XX Best Local Similarity 100.0%; Pred. No. 1.7e-224;
 XX Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 ANINGTLMQFEWYMYNDGQHRRLONDSAYLAHSGITVWLPYAKTSGQSDVGYGYND 60
 XX
 DB 1 ANANGTLMQFEWYMYNDGQHRRLONDSAYLAHSGITVWLPYAKTSGQSDVGYGYND 60
 XX
 QY 61 LNDLGEFHOKGIVRTYKGTGKQSAIKSLASRDINVDVIVNKGADATEDVAVEV 120
 XX
 DB 61 LNDLGEFHOKGIVRTYKGTGKQSAIKSLASRDINVDVIVNKGADATEDVAVEV 120
 XX
 QY 121 DPADRKRIVISGEHLIKAMTHFHPGSGTYSDEPKMWMYFDGTDWDESKRNRIYKFGX 180
 XX
 DB 121 DPADRKRIVISGEHLIKAMTHFHPGSGTYSDEPKMWMYFDGTDWDESKRNRIYKFGX 180
 XX

RESULT 10
 AAU12152
 ID AAU12152 standard; protein; 483 AA.
 XX
 AC AAU12152;
 XX
 DT 09-APR-2002 (first entry)
 XX
 XX
 XX Bacillus TERMAMYL alpha-amylase.
 XX
 XX TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing;
 XX starch liquefaction; ethanol production; hard surface cleaner; sweetener;
 XX amylopectin; limit dextrin; NOVAMYL.
 XX
 XX
 XX Bacillus licheniformis.
 XX
 XX MO200188107-A2.
 XX
 XX 22-NOV-2001.
 XX
 XX 10-MAY-2001; 2001MO-DK000323.
 XX
 XX 12-MAY-2000; 2000DK-00000779.
 XX
 XX (NOVO) NOVOZYMES AS.
 XX
 XX Svendsen A, Jorgensen CT, Nielsen BR;
 XX
 XX WPI; 2002-106123/14.
 XX
 XX N-PSDB; AAS20025.
 XX
 XX New variant of parent Termamyl-like alpha-amylase for use as a component
 XX PT in washing and dishwashing compositions, for textile desizing, for starch
 XX PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 XX
 XX Claim 5; Fig 1; 84pp; English.
 XX
 XX The invention relates to a variant of parent TERMAMYL-like alpha- amylase
 XX CC comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,
 XX CC or at position 234, where the variant has alpha-amylase activity and each
 XX CC position corresponds to a position of a parent Termamyl-like alpha-
 XX CC amylase sequence having a Bacillus licheniformis alpha-amylase sequence
 XX CC of 483 amino acids, given in specification. The variant alpha- amylase, a
 XX CC detergent additive comprising the variant or a detergent composition
 XX CC comprising the variant, is useful for washing and/or dishwashing or
 XX CC textile desizing. The alpha-amylase is useful for starch liquefaction or
 XX CC ethanol production and as a component in a hard surface cleaning

CC detergent composition, and for producing sweeteners from starch. The
CC variant has altered alpha-1,6-D-glucosidic branch linkage cleavage
CC activity on amylopectin, preferably increased alpha-1,6-D-glucosidic
CC branch linkage cleavage activity of amylopectin or a limit dextrin
CC prepared by TERMAMYL (RTM) or NOVAMYL (RTM). The present sequence is the
CC TERMAMYL alpha-amylase upon which the variants of the invention are based
XX
SQ Sequence 483 AA;

Query Match	100.0%;	Score 2666;	DB 5;	Length 483;
Best Local Similarity	100.0%;	Pred. No. 1.7e-224;		
Matches 483;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ANINGTLMQYFEMWTMPNDQCEWRRLOJNDNSAYLAENHGTATWITPRAYUGTSQADYVGCAGD	60
Db	1	ANINGTLMQYFEMWTMPNDQCEWRRLOJNDNSAYLAENHGTATWITPRAYUGTSQADYVGCAGD	60
QY	61	LYDAGEFHQGTVRTKXGTGKGELOSAIKSLHSRDLINYGDVVJHNKGGATEDVTAYEV	120
Db	61	LYDGEFHQGTVRTKXGTGKGELOSAIKSLHSRDLINYGDVVJHNKGGATEDVTAYEV	120
QY	121	DPADRNRVISEHILIAWTHFHFPGRGSTYSDFKKNWTHFPGTWMDESRKLNITYFQOK	180
Db	121	DPADRNRVISEHILIAWTHFHFPGRGSTYSDFKKNWTHFPGTWMDESRKLNITYFQOK	180
QY	181	AMDEVENENGNANDYLMYADIDYDHPDYAAELIKRWGTVAANELOLDFRDLAYAKHIFKFS	240
Db	181	AMDEVENENGNANDYLMYADIDYDHPDYAAELIKRWGTVAANELOLDFRDLAYAKHIFKFS	240
QY	241	LRDMVAVHVRKTEKEMFTVAEYQNDLGALENYLTKTPNHSVDPDYLNHOFHAASTOGS	300
Db	241	LRDMVAVHVRKTEKEMFTVAEYQNDLGALENYLTKTPNHSVDPDYLNHOFHAASTOGS	300
QY	301	GYDMRKLNLTNVVSKRPLKSVTFVNDHNDPQSGSLSTVQVTFKPLAYAFLLTRESGYPQ	360
Db	301	GYDMRKLNLTNVVSKRPLKSVTFVNDHNDPQSGSLSTVQVTFKPLAYAFLLTRESGYPQ	360
QY	361	VFYEDMGTGDSORELPALKHIEBELTARQOYVYGOMHYEPHHDIYGMTREGDSVA	420
Db	361	VFYEDMGTGDSORELPALKHIEBELTARQOYVYGOMHYEPHHDIYGMTREGDSVA	420
QY	421	NSGLAALITDPPGAKRMVGRONAGEIWHDITGNRSEPVVINSGEWGEFHVNGSVSIT	480
Db	421	NSGLAALITDPPGAKRMVGRONAGEIWHDITGNRSEPVVINSGEWGEFHVNGSVSIT	480
QY	481	VOR 483	
Db	481	VOR 483	

XX	RESULT 11
XX	AAE26534
ID	AAE26534 standard; protein; 483 AA.
XX	
XX	AAE26534;
AC	
XX	
DT	13-DEC-2002 (first entry)
XX	
DE	Bacillus licheniformis alpha-amylase protein.
XX	
KM	Alpha amylase; alpha-1,4-glucan-4-glucanohydrolase; EC 3.2.1.1;
KM	dishwashing; textile desizing; detergent; paper; starch liquefaction;
KM	laundry; alcohol production; ethanol production; pulp; beer; brewing;
KW	sweetener; enzyme.
XX	
OS	Bacillus licheniformis.
XX	
PN	WO200231124-A2.
XX	
PD	18-APR-2002.
XX	
PF	12-OCT-2001; 2001WO-DK000665.
XX	

PR 13-OCT-2000; 2000DK-00001533
PR 23-OCT-2000; 2000US-0242692P.
PR 02-OCT-2001; 2001DK-00001442.
PR 03-OCT-2001; 2001US-0326752P.
XX
PA (NOVO) NOVOTIMES AS.

XX
PI Andersen C;
XX WPI; 2002-463264/49.
DR N-PSDB; AAD44363.
XY

XX KSM-K36 or KSM-K38 variant from *Bacillus* for cleaning dishes, textile
PT desizing, starch liquefaction and ethanol production has alpha-amylase
PT activity.

PS Disclosure; Page 60-62; 69pp; English

XX The present invention relates to KSM-K36 or KSM-K38 variant of parent
CC alpha-amylases (alpha-1,4-glucan-4-glucanohydrolases, EC 3.2.1.1) from
CC *Bacillus*. The variants have alpha-amylase activity and exhibit an amino
CC acid alteration such as an insertion, deletion or substitution of the
CC parent alpha-amylase. The variants are useful for washing and/or dish-
CC washing, textile desizing, starch liquefaction and alcohol production,
CC particularly ethanol production. They are also useful as components in
CC detergents for e.g. laundry, dishwashing and hard surface cleaning
CC detergent compositions, in pulp and paper production, in beer making or
CC brewing and in production of sweeteners. The present sequence is *Bacillus*
CC licheniformis alpha-amylase protein

Sequence 483 AA;
SQ

Query Match	100.0%;	Score 2666;	DB 5;	Length 483;
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Best Local Similarity 100.0%; Pred. NO. 1./e-24;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 ANLNGTLMOYFEWYMNDGQHWRLONDSAYLAHGITAVWIPPAYKGTSOADVGDAYD 60

Db 1 ANLNGTLMQYEMTYMPNDGQHRRLONDSAYLAEHGITAVWIPRAYKGTSGADVGYGAYD 60

61 IYDIGEEFHOKGTVRTYKTKGELQSAIKSLHSRDINTYGDVINHKGADATEDVTAVEV 120

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6 L L I D D E F H Q N G I V K A I N G I N O D D G H A W M I C I N C A T T 180

122 DPADRNKVISGEHLKAMIHFFPGKSIISLFNWMTHIFDGLDMDSNKNM... 200

121 DPADNRVTSGEHLIKAMTHFHPGSGTYSDFKMWYHFDGTDWDESKLNKRIKNGCA 180

181 AWDWEVSNENGNDYLMYADIDYDHPVAAEIKRWGTWYNELQDGRLLDAVKHKESF 240

181 AMDWEVSNENGNYYDLYMTADIDYDHPVAAEI KRWGTYWANELQLDGERLDAVKIKESF 240

241 LRDVNHREKTKGEMFTVAEYQNDICALENYLNTKNTNENHSVDVPLHYQFHAASQGG 300

Db 241 LRDWVNHVREKTGKEMFTVAEYQNDGALENYLKNNFNHSEVDVPLHYQFHAASIOGG 300

301 GYDMRKLTNGTWSKHPDKSVTFVDNHDTPQGSLESTWQTNEXELAYAFILITRESGYPO 360

301 CYDMEKIKTNGTWSKHPKSKVTFLVDNHDPTOGOSLESTVOETWEKPLAYAEILITRESCGYC 360

[illegible]

36. VEGDMIGKDSCKREI PAUNNLEI LINGNY IASIPYI I DANDI KUN I ABBBCCD... 430

Db 361 VFIDMNGTKGDSQREI PALKHKLEP LKAKKQYAIGAQHDFDHDI VSM INKGGSSVA 420

421 NSGLALITDGPAGAKRYVGRONAGETHDITGNRSEPVINSEGWGEFHVNGGSVSLY 480

421 NSGLALITDGPAGAKMYGRQNAGETWHDITGNRSEPVVINSBGWGEFFHVGGSVSIY 480C

QY 481 VQR 483

D_b 481 VQR 483

RESULT 12
 AAB47853
 ID AAB47853 standard; protein; 483 AA.
 XX
 AC AAB47853;
 XX
 DT 02-APR-2002 (first entry)
 XX
 DE Bacillus termamyli alpha amylase.
 XX
 KW Alpha amylase; Bacillus; Termamyli-like; maltodextrin; glucose syrup;
 KW starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;
 KW bakery; cereal bar; ice cream; coffee whitener; salad dressing;
 KW cured meat; fermented meat; spice.
 XX
 OS Bacillus licheniformis.
 XX
 PN WO200196537-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 13-JUN-2001; 2001WO-DK000404.
 XX
 PR 14-JUN-2000; 2000DK-00000917.
 XX
 PR 20-JUN-2000; 2000US-0212852P.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Nielsen BR, Welbye M;
 XX
 DR WPI; 2002-098064/13.
 XX
 DR N-PSDB; AAI72214.
 XX
 PT New modified alpha-amylase derived from the genus Bacillus and/or is a
 PT Termamyli-like alpha-amylase, which has been pre-oxidized for producing
 PT maltodextrin or glucose syrup.
 XX
 PS Claim 5; Page 36-37; 47pp; English.
 XX
 CC The sequences given in AAB47850-56 show modified alpha-amylases derived
 CC from the genus Bacillus. These alpha amylases are Termamyli-like alpha
 CC amylase and they have been pre-oxidized. The alpha amylase is useful for
 CC producing a maltodextrin or glucose syrup, by treating starch with a pre-
 CC oxidized alpha-amylase until a product with a DE between 5-45 has been
 CC provided and/or until a product with a molecular weight of between 5-30
 CC kDa has been provided. The product comprises a maltodextrin with a DE of
 CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kDa. The
 CC alpha amylase is useful for producing a maltodextrin or glucose syrup,
 CC where the glucose syrup is useful as an ingredient in food, feed or
 CC pharmaceuticals. Glucose syrup is useful in confectionery such as
 CC candies, beverages such as isotonic drinks, bakery such as cereal bars,
 CC dairy and ice cream such as coffee whiteners, conventional foods such as
 CC salad dressings, and food ingredients and preparations such as cured
 CC meat, fermented meat, spices and seasoning encapsulated flavours
 XX
 SQ Sequence 483 AA;
 XX
 Query Match 100.0%; Score 2666; DB 5; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 ANNGTMOYFEMMPDQGHMRLONSAYLAHEGTTAVIPPAKYSQADVGVGAND 60
 DB 1 ANNGTMOYFEMMPDQGHMRLONSAYLAHEGTTAVIPPAKYSQADVGVGAND 60
 QY 61 LYDGEFHQKGTAVTKGTGKGELOSALKSLSHRDINVGDVVNHKGGADATEDVAVAV 120
 DB 61 LYDGEFHQKGTAVTKGTGKGELOSALKSLSHRDINVGDVVNHKGGADATEDVAVAV 120
 QY 121 DPADRNVISGEHLIKAWTHFHPFGSGTSDRFEMWYHHDGTDWDSRLTANLYFQCK 180
 DB 121 DPADRNVISGEHLIKAWTHFHPFGSGTSDRFEMWYHHDGTDWDSRLTANLYFQCK 180

QY 181 ANDREVSNGNDYDMADIDYDHPDAAEIKRWGTWYANELQDGFELDAVKHIFSE 240
 DB 181 ANDREVSNGNDYDMADIDYDHPDAAEIKRWGTWYANELQDGFELDAVKHIFSE 240
 QY 241 LRDVNVHVEKTKGEMFTVAEYQNDLGALENYLNKTNFNHGVFDPVLPYQPHAASTOGG 300
 DB 241 LRDVNVHVEKTKGEMFTVAEYQNDLGALENYLNKTNFNHGVFDPVLPYQPHAASTOGG 300
 QY 301 GYDREKILNCTVVSKEPLKSVTFVDNHDTPQGSLESTVQTWFKPLAVAFILTRSGYQ 360
 DB 301 GYDREKILNCTVVSKEPLKSVTFVDNHDTPQGSLESTVQTWFKPLAVAFILTRSGYQ 360
 QY 361 VFYGDWYGTGDSQREIPALKEIPILKARKQYAGAGHDYFDHDIYGMTREGDSSVA 420
 DB 361 VFYGDWYGTGDSQREIPALKEIPILKARKQYAGAGHDYFDHDIYGMTREGDSSVA 420
 QY 421 NSGLAALITDGPAGAKRMVYGRQNAGETWHDITGNSEPVVINSBGWGFHYNGGSVSIY 480
 DB 421 NSGLAALITDGPAGAKRMVYGRQNAGETWHDITGNSEPVVINSBGWGFHYNGGSVSIY 480
 QY 481 VQR 483
 DB 481 VQR 483
 XX
 RESULT 13
 ABB76589
 ID ABB76589 standard; protein; 483 AA.
 XX
 AC ABB76589;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Termamyli-like alpha-amylase #4.
 XX
 KW Termamyli; alpha amylase; starch liquefaction; ethanol production;
 KW textile desizing; detergent; enzyme.
 XX
 OS Bacillus licheniformis.
 XX
 PN WO200210355-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 12-JUN-2001; 2001WO-DK000488.
 XX
 PR 01-AUG-2000; 2000DK-00001160.
 XX
 PR 12-SEP-2000; 2000DK-00001354.
 XX
 PR 10-NOV-2000; 2000DK-00001687.
 XX
 PR 26-APR-2001; 2001DK-00000655.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Thisted T, Kjaerulff S, Andersen C, Fuglsang CC;
 XX
 DR WPI; 2002-280633/32-
 XX
 DR N-PSDB; ABI96210.
 XX
 PT Variant of parent Termamyli-like alpha amylase, useful in detergent
 PT compositions, for starch liquefaction, ethanol production, washing and/or
 PT dish washing, and textile desizing.
 XX
 PS Claim 1; Fig 4; 90pp; English.
 XX
 CC This invention relates to variants of a parent Termamyli-like alpha-
 CC amylases. These are used for starch liquefaction, ethanol production,
 CC detergent, and textile desizing. The amylases have altered stability,
 CC particularly at high temperatures from 70-120plusoc and low pH in the
 CC range from pH 4.0-6.0. The present sequence is a termamyli-like-alpha-
 CC amylase
 XX
 SQ Sequence 483 AA;
 XX

Query Match 100.0%; Score 2666; DB 5; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.7e-224;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEWYMPNDGQWRLQNDSDAYLAHEGHTAVWIPPAKGTSGADVGYAYD 60
DB 1 ANLNGTLMQYFEWYMPNDGQWRLQNDSDAYLAHEGHTAVWIPPAKGTSGADVGYAYD 60
QY 61 LYDLGEFHQGTGVTATKGTGELQSAIKSLHSRDINVGVDVINNHKGADATEDVTAVEY 120
DB 61 LYDLGEFHQGTGVTATKGTGELQSAIKSLHSRDINVGVDVINNHKGADATEDVTAVEY 120
QY 121 DPADRNKRVISGEHLIKAMTHFHPFGSGTYSDFKHMWHFPGDGDWDSRKLNRITYKFGQK 180
DB 121 DPADRNKRVISGEHLIKAMTHFHPFGSGTYSDFKHMWHFPGDGDWDSRKLNRITYKFGQK 180
QY 181 AMDWEVSNGNNGNYITLMTADIDYHPVAAEIKRWGTWYANLQDGFRLDAVKHIFSF 240
DB 181 AMDWEVSNGNNGNYITLMTADIDYHPVAAEIKRWGTWYANLQDGFRLDAVKHIFSF 240
QY 241 LRDWNVNHRKTKGEMFTVAEYQNDLGALENYLNTKTNFNSVFDVPLHYQFHAASTOGG 300
DB 241 LRDWNVNHRKTKGEMFTVAEYQNDLGALENYLNTKTNFNSVFDVPLHYQFHAASTOGG 300
QY 301 GYDMRKILNGTVSKPKLSVTVDNHDTPQGSLSTVQTWFKPLAYAFILTRSGYPO 360
DB 301 GYDMRKILNGTVSKPKLSVTVDNHDTPQGSLSTVQTWFKPLAYAFILTRSGYPO 360
QY 361 VFYGDWYGTGDSOREIPALPKHKEIPILKAKQYAYGAOHDFPHNDIVGWTREGDSVA 420
DB 361 VFYGDWYGTGDSOREIPALPKHKEIPILKAKQYAYGAOHDFPHNDIVGWTREGDSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGWGFHNNGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGWGFHNNGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483

RESULT 14
AAR98007
ID AAR98007 standard; protein; 531 AA.
XX
AC AAR98007;
XX
DT 27-AUG-2003 (revised)
DT 16-OCT-1996 (first entry)
XX
DE PeB signal-Termamyl-leucine zipper.
XX
KW Allergen; allergy; self-oligomerizing polypeptide; Termamyl;
KW alpha-amylase; leucine zipper; detergent.
XX
OS Synthetic.
OS Unspecified organism.
OS Chimeric.
XX
FH Key Location/Qualifiers
FH Protein 1..482
FT /label= Termamyl
FT Region 483..489
FT /label= Linker
FT Domain 490..531
FT /label= leucine_zipper
XX
PN WO9616177-A1.
XX
PD 30-MAY-1996.
XX
PF 23-NOV-1995; 95WO-DK000463.
XX

PR 24-NOV-1994; 94DX-00001343.
XX
PA (NOVO) NOVO-NORDISK AB.
XX
PI Bjornvad ME, Prento A;
XX
DR WPI; 1996-266613/27.
XX
DR N-PEDB; AAT33228.
XX
PT Prodn. of self-oligomerising peptide(s) with reduced allergenicity - used
in household and personal cleaning prods., and in food and feeds etc.
XX
PS Disclosure; Page 61-63; 85pp; English.
XX
CC A polypeptide (AAR98007) is composed of Termamyl alpha-amylase, a linker
CC derived from the IgG3 hinge domain and a leucine zipper from the GCN4
CC yeast transcription factor. It was produced by PCR amplification of the
CC Termamyl gene and ligation of synthetic oligonucleotides (see also
CC AAT33228-32) encoding the leucine zipper and linker. Upon expression in
CC E.coli, using a vector including the leucine zipper sequence, the Termamyl
CC product self-oligomerised into a dimer that was secreted into the
CC periplasm. The method constitutes an industrially applicable process for
CC producing a biologically active polypeptide that self-oligomerises owing
CC to the presence of leucine zippers, the enlarged size of the resulting
CC polypeptide leading to a reduction in its allergenicity. (Updated on 27-
CC AUG-2003 to correct OS field.)
XX
SQ Sequence 531 AA;

Query Match 100.0%; Score 2666; DB 2; Length 531;
Best Local Similarity 100.0%; Pred. No. 1.9e-224;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEWYMPNDGQWRLQNDSDAYLAHEGHTAVWIPPAKGTSGADVGYAYD 60
DB 1 ANLNGTLMQYFEWYMPNDGQWRLQNDSDAYLAHEGHTAVWIPPAKGTSGADVGYAYD 60
QY 61 LYDLGEFHQGTGVTATKGTGELQSAIKSLHSRDINVGVDVINNHKGADATEDVTAVEY 120
DB 61 LYDLGEFHQGTGVTATKGTGELQSAIKSLHSRDINVGVDVINNHKGADATEDVTAVEY 120
QY 121 DPADRNKRVISGEHLIKAMTHFHPFGSGTYSDFKHMWHFPGDGDWDSRKLNRITYKFGQK 180
DB 121 DPADRNKRVISGEHLIKAMTHFHPFGSGTYSDFKHMWHFPGDGDWDSRKLNRITYKFGQK 180
QY 181 AMDWEVSNGNNGNYITLMTADIDYHPVAAEIKRWGTWYANLQDGFRLDAVKHIFSF 240
DB 181 AMDWEVSNGNNGNYITLMTADIDYHPVAAEIKRWGTWYANLQDGFRLDAVKHIFSF 240
QY 241 LRDWNVNHRKTKGEMFTVAEYQNDLGALENYLNTKTNFNSVFDVPLHYQFHAASTOGG 300
DB 241 LRDWNVNHRKTKGEMFTVAEYQNDLGALENYLNTKTNFNSVFDVPLHYQFHAASTOGG 300
QY 301 GYDMRKILNGTVSKPKLSVTVDNHDTPQGSLSTVQTWFKPLAYAFILTRSGYPO 360
DB 301 GYDMRKILNGTVSKPKLSVTVDNHDTPQGSLSTVQTWFKPLAYAFILTRSGYPO 360
QY 361 VFYGDWYGTGDSOREIPALPKHKEIPILKAKQYAYGAOHDFPHNDIVGWTREGDSVA 420
DB 361 VFYGDWYGTGDSOREIPALPKHKEIPILKAKQYAYGAOHDFPHNDIVGWTREGDSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGWGFHNNGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSBGWGFHNNGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483

RESULT 15
AAM22523
ID AAM22523 standard; protein; 630 AA.

XX AAM2523;
 AC 17-OCT-2003 (revised)
 DT 08-FEB-1998 (first entry)
 XX Alpha-amylase-CenA cellulose binding domain hybrid enzyme.
 XX Desizing; cellulose; fabric; enzyme hybrid; Termamyl; alpha-amylase;
 KM cellulose binding domain; CenA; Bacillus licheniformis;
 KM Cellulomonas film; protein secretion.
 XX Bacillus licheniformis.
 OS Cellulomonas film; strain ATCC 484.
 OS Chimeric.
 XX
 FH Key
 FT Peptide
 FT /label= Sig_peptide
 FT /note= "Termamyl signal peptide"
 FT Protein
 FT /label= Mal protein
 FT /note= "CBD (aa29-147)-Termamyl (aa148-630) hybrid"
 XX
 PN WO9728256-A1.
 PD 07-AUG-1997.
 XX
 XX 29-JAN-1997; 97WO-DK000041.
 PF 29-JAN-1997; 96DK-00000093.
 XX
 PR 29-JAN-1996; 96DK-00000093.
 XX
 XX (NOVO) NOVO-NORDISK AS.
 PA
 XX Von Der Oosten C, Bjornvad M, Vind J, Rasmussen MD;
 PI MPI, 1997-402610/37.
 DR N-PSDB; AAT77063.
 XX
 PT Desizing cellulose-containing fabric or textile using an enzyme hybrid -
 PT which comprises a catalytically active amino acid sequence of a non-
 PT cellulolytic enzyme linked to an amino acid sequence comprising a
 PT cellulose binding domain.
 XX
 XX Example 3; Page 60; 72pp; English.
 PS
 XX This protein sequence comprises a hybrid enzyme in which Bacillus
 CC licheniformis alpha-amylase (Termamyl) signal peptide is linked to the
 CC cellulose binding domain (CBD) of Cellulomonas film CenA, which is
 CC further linked to mature Termamyl polypeptide. The CBD-Termamyl fusion
 CC has been expressed and secreted as an approx. 85 kDa protein in Bacillus
 CC subtilis p12306 transformants. A claimed process for desizing cellulose-
 CC containing fabric or textile comprises treating the fabric or textile
 CC with a modified enzyme (enzyme hybrid) comprising a non-cellulolytic
 CC enzyme linked to a CBD. The process gives improved enzyme performance by
 CC modifying the enzyme so as to increase its affinity for cellulose
 CC fabric. A desizing composition suitable for use in the process comprises
 CC the enzyme hybrid and a wetting agent. (Updated on 17-OCT-2003 to
 CC standardise OS field)
 CC
 XX
 SQ Sequence 630 AA;

Query Match 100.0%; Score 2666; DB 2; Length 630;
 Best Local Similarity 100.0%; Pred. No. 2,5e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANINGTLMQYFFWYMNPDGQHWRLQNDGAYLAHGTAVWIPPAKGTSGADVGAYD 60
 DB 148 ANINGTLMQYFFWYMNPDGQHWRLQNDGAYLAHGTAVWIPPAKGTSGADVGAYD 207
 QY 61 LYLGEFHQKGVRTYKGTGKGLQSAIKSLHSRDINVGQVWLNHGAGADATEDVTAAYV 120
 DB 208 LYLGEFHQKGVRTYKGTGKGLQSAIKSLHSRDINVGQVWLNHGAGADATEDVTAAYV 267

QY 121 DPADNRNRYISGEHLIKAMTHFHPGRGSTYSDFFKRWTHFPGDTWDESRKLNRYKQOK 180
 DB 266 DPADNRNRYISGEHLIKAMTHFHPGRGSTYSDFFKRWTHFPGDTWDESRKLNRYKQOK 327
 QY 181 AMDWEVSNENGVYDYLMAADIDYDHPDVAAEIKKMGTYANELQDGFRLDAVKIKFSF 240
 DB 328 AMDWEVSNENGVYDYLMAADIDYDHPDVAAEIKKMGTYANELQDGFRLDAVKIKFSF 387
 QY 241 LRDMVNVHREKTKEMFTVAEYQNDLGALENYLNKTNFNHSPVDPVLYHGFHAATGCG 300
 DB 388 LRDMVNVHREKTKEMFTVAEYQNDLGALENYLNKTNFNHSPVDPVLYHGFHAATGCG 447
 QY 301 GYDMRLTLNGTVVSKHPKSVTFVNNHTOPQOSLESTVQTFKFLAYAFILTRSGYPO 360
 DB 448 GYDMRLTLNGTVVSKHPKSVTFVNNHTOPQOSLESTVQTFKFLAYAFILTRSGYPO 507
 QY 361 VFYGDWYGTGKDSOREIPALKEIPIIKARKQAYGAQHDYFDDHDIVGWTRGDSVA 420
 DB 508 VFYGDWYGTGKDSOREIPALKEIPIIKARKQAYGAQHDYFDDHDIVGWTRGDSVA 567
 QY 420 NSGLAALITDGPQAKRMVYGRQNGETWHDITGNRSEPVYVNSGMEFFHNGGSVSIY 480
 DB 568 NSGLAALITDGPQAKRMVYGRQNGETWHDITGNRSEPVYVNSGMEFFHNGGSVSIY 627
 QY 481 VQR 483
 DB 628 VQR 630

Search completed: May 3, 2004, 20:50:29
 Job time : 53.0521 secs

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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:44:58 ; Search time 34.1233 Seconds
(without alignments)
4436.289 Million cell updates/sec

Title: US-10-644-187-4
Perfect score: 2624
Sequence: 1 VNGTLMQYEWYTPNDGQHM.....KIGSDQWGEFHNDSVSIRY 480

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MNC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_XVIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2061	78.5	519	2 Q9ROT8	Q9ROT8 cytophaga s
2	1947	74.2	513	16 Q81AS4	Q81AS4 bacillus ce
3	1946	74.2	533	2 Q9AQ54	Q9AQ54 bacillus me
4	1914	72.9	513	16 Q81YJ4	Q81YJ4 bacillus an
5	1836	70.0	516	2 Q82839	Q82839 bacillus sp
6	1767.5	67.4	549	2 Q31193	Q31193 bacillus st
7	1766.5	67.3	549	2 Q9KXV6	Q9KXV6 bacillus st
8	1762.5	67.2	521	2 P71034	P71034 bacillus sp
9	1749.5	66.7	613	2 Q59222	Q59222 bacillus sp
10	1614.5	56.2	501	2 Q93148	Q93148 bacillus sp
11	1474.5	56.2	507	16 Q87H66	Q87H66 vibrio para
12	1359	51.8	481	16 Q89YPI	Q89YPI bacteroides
13	1253	47.8	493	2 Q03657	Q03657 bacillus ci
14	1217	46.4	484	16 Q97049	Q97049 streptococc
15	1212	46.2	484	16 Q8DPC8	Q8DPC8 streptococc
16	1206.5	46.0	488	16 Q8E96	Q8E96 streptococc

17	1206.5	46.0	488	16 Q8E96	Q8E96 streptococc
18	1205.5	45.9	486	16 Q8DPC8	Q8DPC8 streptococc
19	1197	45.6	492	16 Q87U21	Q87U21 anabaena sp
20	1190.5	45.4	484	2 Q05083	Q05083 streptococc
21	1182.5	45.1	486	2 Q68875	Q68875 streptococc
22	1177.5	44.9	485	2 Q53786	Q53786 streptococc
23	1127	42.9	491	16 Q9CG59	Q9CG59 lactococc
24	1057.5	40.3	529	3 Q877B1	Q877B1 aspergillus
25	1050	40.0	506	16 Q8U916	Q8U916 aspergilli
26	1006	38.3	494	16 Q8Z555	Q8Z555 salmone
27	1000	38.1	495	16 Q8F6L8	Q8F6L8 escherichia
28	999	38.1	495	16 Q8XB6	Q8XB6 escherichia
29	989	37.7	495	16 Q7UAB0	Q7UAB0 shigella fl
30	987	37.6	495	16 Q83R40	Q83R40 shigella fl
31	496	18.9	469	1 Q50200	Q50200 thermococc
32	494.5	18.8	461	1 Q8NKR5	Q8NKR5 thermococc
33	480.5	18.3	461	1 Q33476	Q33476 pyrococc
34	480	18.3	457	1 Q93647	Q93647 thermococc
35	476.5	18.2	460	1 Q9P9L0	Q9P9L0 pyrococc
36	476.5	18.2	460	1 Q08452	Q08452 pyrococc
37	476.5	18.2	461	1 Q8NKR4	Q8NKR4 thermococc
38	476.5	18.2	473	17 Q8U319	Q8U319 uncultured
39	464.5	17.7	432	14 Q8JZK3	Q8JZK3 uncultured
40	351.5	13.4	826	10 Q9CAR6	Q9CAR6 arabidopsis
41	351.5	13.4	887	10 Q94A41	Q94A41 arabidopsis
42	334.5	12.7	906	10 Q8LQK4	Q8LQK4 oryza sativ
43	326	12.4	420	10 Q9ZP43	Q9ZP43 phaseolus v
44	324.5	12.4	421	10 Q7X9T1	Q7X9T1 phaseolus a
45	322	12.3	416	10 Q8LJQ6	Q8LJQ6 musa acumin

ALIGNMENTS

RESULT 1

Q9ROT8 PRELIMINARY; PRT; 519 AA.

AC Q9ROT8 01-MAY-2000 (TRENBLREL.13, Created)
DT 01-MAY-2000 (TRENBLREL.13, Last sequence update)
DE 01-JUN-2003 (TRENBLREL.24, Last annotation update)
DS Raw starch digesting amylase precursor.
OS Cytophaga sp.
OC Bacteria; Bacteroidetes; Sphingobacteriales; Sphingobacteriales;
OC Flexibacteraceae; Cytophaga.
OX NCBI_taxid=29535;
RN [1]
RP SEQUENCE FROM N.A.
RA Teang C.L., Chen L.S., Chen M.Y.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067653; AAF00567.1; -.
DR HSBP; P06278; IVOS.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat. sub.
DR InterPro; IPR006046; Glyco hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SMO0642; Amy; 1.
DR SIGNAL.
FT CHAIN
SQ SEQUENCE 519 AA; 58337 MW; 386888ADP98B163 CRC64;
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QY 62 LGFEQKGTATRTKGTGKSELODAIGSLHSRNVGVVNLNKAAGADATEDYTAVERNPA 121
 Db 98 LGFENQKGTATRTKGTGKSELODAIGSLHSRNVGVVNLNKAAGADATEDYTAVERNPA 157
 QY 122 NRNOETSEYQIKAWTDFFPPRGNTYSDFKMWHYHFDGADWDESKISRIEFGREGKA 181
 Db 158 NRNOETSEYQIKAWTDFFPPRGNTYSDFKMWHYHFDGADWDESKISRIEFGREGKA 217
 QY 182 WDEVSSENANVYIMADVDYDHPDVVAETKMGJWYANELSLDGFRIIDAAKHIFSF 241
 Db 218 WDEVSSENANVYIMADVDYDHPDVVAETKMGJWYANELSLDGFRIIDAAKHIFSF 277
 QY 242 RDWQAVRQATGKEMFTVAEYWMONNAGKLENTKTSFNQSVFVPLHFNLOAASSQGG 301
 Db 278 RDWQAVRQATGKEMFTVAEYWMONNAGKLENTKTSFNQSVFVPLHFNLOAASSQGG 337
 QY 302 YDMRRLDGTGVRHPEKATFVENHDTPGOSLESTVQWPKFLAYAFILTRSGYPOV 361
 Db 338 YDMRRLDGTGVRHPEKATFVENHDTPGOSLESTVQWPKFLAYAFILTRSGYPOV 397
 QY 362 FYGDMYGTGKTSPEKIPSLKONIEPIIKAKKEYAYGPOHDYIDHPVIGMTRGDSAAK 421
 Db 398 FYGDMYGTGKTSPEKIPSLKONIEPIIKAKKEYAYGPOHDYIDHPVIGMTRGDSAAK 457
 QY 422 SGLAALITDPPGSKMAYAGLKNAGETWYDITGNREDYKISDGMGEFHVNDGSVSIY 480
 Db 458 SGLAALITDPPGSKMAYAGLKNAGETWYDITGNREDYKISDGMGEFHVNDGSVSIY 516

RESULT 2

QY 62 LGFEQKGTATRTKGTGKSELODAIGSLHSRNVGVVNLNKAAGADATEDYTAVERNPA 121
 Db 98 LGFENQKGTATRTKGTGKSELODAIGSLHSRNVGVVNLNKAAGADATEDYTAVERNPA 157
 QY 122 NRNOETSEYQIKAWTDFFPPRGNTYSDFKMWHYHFDGADWDESKISRIEFGREGKA 181
 Db 158 NRNOETSEYQIKAWTDFFPPRGNTYSDFKMWHYHFDGADWDESKISRIEFGREGKA 217
 QY 182 WDEVSSENANVYIMADVDYDHPDVVAETKMGJWYANELSLDGFRIIDAAKHIFSF 241
 Db 218 WDEVSSENANVYIMADVDYDHPDVVAETKMGJWYANELSLDGFRIIDAAKHIFSF 277
 QY 242 RDWQAVRQATGKEMFTVAEYWMONNAGKLENTKTSFNQSVFVPLHFNLOAASSQGG 301
 Db 278 RDWQAVRQATGKEMFTVAEYWMONNAGKLENTKTSFNQSVFVPLHFNLOAASSQGG 337
 QY 302 YDMRRLDGTGVRHPEKATFVENHDTPGOSLESTVQWPKFLAYAFILTRSGYPOV 361
 Db 338 YDMRRLDGTGVRHPEKATFVENHDTPGOSLESTVQWPKFLAYAFILTRSGYPOV 397
 QY 362 FYGDMYGTGKTSPEKIPSLKONIEPIIKAKKEYAYGPOHDYIDHPVIGMTRGDSAAK 421
 Db 398 FYGDMYGTGKTSPEKIPSLKONIEPIIKAKKEYAYGPOHDYIDHPVIGMTRGDSAAK 457
 QY 422 SGLAALITDPPGSKMAYAGLKNAGETWYDITGNREDYKISDGMGEFHVNDGSVSIY 480
 Db 458 SGLAALITDPPGSKMAYAGLKNAGETWYDITGNREDYKISDGMGEFHVNDGSVSIY 516

Query Match 74.2%; Score 1947; DB 16; Length 513;
 Best Local Similarity 71.8%; Pred. No. 2.8e-126;
 Matches 344; Conservative 47; Mismatches 88; Indels 0; Gaps 0;

Db 92 LGFENQKGTATRTKGTGKSELODAIGSLHSRNVGVVNLNKAAGADATEDYTAVERNPA 151
 QY 122 NRNOETSEYQIKAWTDFFPPRGNTYSDFKMWHYHFDGADWDESKISRIEFGREGKA 181
 Db 152 NRNOETSEYQIKAWTDFFPPRGNTYSDFKMWHYHFDGADWDESKISRIEFGREGKA 211
 QY 182 WDEVSSENANVYIMADVDYDHPDVVAETKMGJWYANELSLDGFRIIDAAKHIFSF 241
 Db 212 WDEVSSENANVYIMADVDYDHPDVVAETKMGJWYANELSLDGFRIIDAAKHIFSF 271
 QY 242 RDWQAVRQATGKEMFTVAEYWMONNAGKLENTKTSFNQSVFVPLHFNLOAASSQGG 301
 Db 272 RDWQAVRQATGKEMFTVAEYWMONNAGKLENTKTSFNQSVFVPLHFNLOAASSQGG 331
 QY 302 YDMRRLDGTGVRHPEKATFVENHDTPGOSLESTVQWPKFLAYAFILTRSGYPOV 361
 Db 332 YDMRRLDGTGVRHPEKATFVENHDTPGOSLESTVQWPKFLAYAFILTRSGYPOV 391
 QY 362 FYGDMYGTGKTSPEKIPSLKONIEPIIKAKKEYAYGPOHDYIDHPVIGMTRGDSAAK 421
 Db 392 FYGDMYGTGKTSPEKIPSLKONIEPIIKAKKEYAYGPOHDYIDHPVIGMTRGDSAAK 451
 QY 422 SGLAALITDPPGSKMAYAGLKNAGETWYDITGNREDYKISDGMGEFHVNDGSVSIY 480
 Db 452 SGLAALITDPPGSKMAYAGLKNAGETWYDITGNREDYKISDGMGEFHVNDGSVSIY 510

RESULT 3

QY 62 LGFEQKGTATRTKGTGKSELODAIGSLHSRNVGVVNLNKAAGADATEDYTAVERNPA 121
 Db 98 LGFENQKGTATRTKGTGKSELODAIGSLHSRNVGVVNLNKAAGADATEDYTAVERNPA 157
 QY 122 NRNOETSEYQIKAWTDFFPPRGNTYSDFKMWHYHFDGADWDESKISRIEFGREGKA 181
 Db 152 NRNOETSEYQIKAWTDFFPPRGNTYSDFKMWHYHFDGADWDESKISRIEFGREGKA 211
 QY 182 WDEVSSENANVYIMADVDYDHPDVVAETKMGJWYANELSLDGFRIIDAAKHIFSF 241
 Db 212 WDEVSSENANVYIMADVDYDHPDVVAETKMGJWYANELSLDGFRIIDAAKHIFSF 271
 QY 242 RDWQAVRQATGKEMFTVAEYWMONNAGKLENTKTSFNQSVFVPLHFNLOAASSQGG 301
 Db 272 RDWQAVRQATGKEMFTVAEYWMONNAGKLENTKTSFNQSVFVPLHFNLOAASSQGG 331
 QY 302 YDMRRLDGTGVRHPEKATFVENHDTPGOSLESTVQWPKFLAYAFILTRSGYPOV 361
 Db 332 YDMRRLDGTGVRHPEKATFVENHDTPGOSLESTVQWPKFLAYAFILTRSGYPOV 391
 QY 362 FYGDMYGTGKTSPEKIPSLKONIEPIIKAKKEYAYGPOHDYIDHPVIGMTRGDSAAK 421
 Db 392 FYGDMYGTGKTSPEKIPSLKONIEPIIKAKKEYAYGPOHDYIDHPVIGMTRGDSAAK 451
 QY 422 SGLAALITDPPGSKMAYAGLKNAGETWYDITGNREDYKISDGMGEFHVNDGSVSIY 480
 Db 452 SGLAALITDPPGSKMAYAGLKNAGETWYDITGNREDYKISDGMGEFHVNDGSVSIY 510

Query Match 74.2%; Score 1946; DB 2; Length 533;
 Best Local Similarity 72.0%; Pred. No. 3.5e-126;
 Matches 345; Conservative 44; Mismatches 90; Indels 0; Gaps 0;

Db 232 WDEWVSENGNVDYLVADLDFDHPDVANEMKKMGWYANELNLDFFLDAVKHIDHEYL 291
Qy 242 RWMVOAIVROATGEMFTVAEYQNNAGKLENTLNTSFPNOSYFVPLPHFNLOAASQGGG 301
Db 292 RDMVNHVRQOTGKEMFAVAEYQNDIQTLNNYLAKNVQSVFADAPLHNFHYASKNGN 351
Qy 302 YDMRRLDGTIVSRHBEKAVTFVENHNDTPQGSLSESTVQTFKPLAAYAFILTRRESGYPOV 361
Db 352 YDMRNLKGTIVANHTLAATLVENHDSQPQSLSESVSPWFKPLAAYAFILTRAGYPSV 411
Qy 362 FYGDMYGTGTSPEKIPSLKDNIEPLIKARKEYAVGPQHDYIDHPDVIGMTREGDSAAK 421
Db 412 FYGDMYGTGTSPEKIPSLKDNIEPLIKARKEYAVGTQHDYIDHPDVIGMTREGDSVHAN 471
Qy 422 SGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSDTYKIGSDGKGFHVNDGSVSIY 480
Db 472 SGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSDTYKIGSDGKGFHVNDGSVSIY 530

RESULT 4

Qy 081YJ4 PRELIMINARY; PRT; 513 AA.
AC 081YJ4
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-OCT-2003 (TREMBlrel. 24, Last sequence update)
DE Alpha-amylose.
GN AMYS OR BA3551.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=198094;
RN [1]
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillye L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Oksstad O.A., Helgason E., Ralston U., Wu M.,
RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA Nelson W.C., Peterson J.D., Durkin A.S., Hatt D.H.,
RA Benson J.J., Mahamoud Y., Jiang L., Khouri H.M., Radune D.,
RA Berry K.J., Plant R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaiter J.E., White O., Salzberg S.L.,
RA Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.B.,
RA Fraser C.M.; sequence of Bacillus anthracis Ames and comparison to
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
DR EMBL; AEO17035; AAP27311.1; -.
DR TIGR; BA3551; -.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amylose; 1.
DR SMART; SM00642; Amy; 1.
KM Complete proteome.
SQ SEQUENCE 513 AA; 58445 MW; 55806EF282FD159B CRC64;

Query Match 72.8%; Score 1914; DB 16; Length 513;
Best Local Similarity 70.8%; Pred. No. 5.3e-124;
Matches 339; Conservative 47; Mismatches 93; Indels 0; Gaps 0;
Qy 2 NGTLMQFEWYTPRDGQHMRLQNDAEHLSDIGITAVWIPPAKGLSOSDNGYGPDIYD 61
Db 32 NGTLMQFEWYTPRDGQHMRLQNDAEHLSDIGITAVWIPPAKGLSOSDNGYGPDIYD 91
Qy 62 LGFPOKGTATKTKGTGSEJQDAIGSLHNRVQVGVYLVNKAAGADATEDVYAVEVNP 121
Db 92 LGFPOKGTATKTKGTGSEJQDAIGSLHNRVQVGVYLVNKAAGADATEDVYAVEVNP 151
Qy 122 NRNOETSEBYQIAWIDFRPFGGNTYSDPKMWHYFDGADWDSEKSRIRKFGEGGA 181

Db 152 NRNAVESGDYEISAMTGFNPGRGDNYSNFKMKYHFDGTDMEGRKLNRIYKFRIGIGA 211
Qy 182 WDEWVSENGNVDYLVADLDFDHPDVANEMKKMGWYANELNLDFFLDAVKHIDHEYL 241
Db 212 WDEWVSENGNVDYLVADLDFDHPDVANEMKKMGWYANELNLDFFLDAVKHIDHEYL 271
Qy 242 RWMVOAIVROATGEMFTVAEYQNNAGKLENTLNTSFPNOSYFVPLPHFNLOAASQGGG 301
Db 272 RDMVNHVRQOTGKEMFAVAEYQNDIQTLNNYLAKNVQSVFADAPLHNFHYASKNGN 331
Qy 302 YDMRRLDGTIVSRHBEKAVTFVENHNDTPQGSLSESTVQTFKPLAAYAFILTRRESGYPOV 361
Db 332 YDMRNLKGTIVANHTLAATLVENHDSQPQSLSESVSPWFKPLAAYAFILTRAGYPSV 391
Qy 362 FYGDMYGTGTSPEKIPSLKDNIEPLIKARKEYAVGPQHDYIDHPDVIGMTREGDSAAK 421
Db 392 FYGDMYGTGTSPEKIPSLKDNIEPLIKARKEYAVGTQHDYIDHPDVIGMTREGDSVHAN 451
Qy 422 SGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSDTYKIGSDGKGFHVNDGSVSIY 480
Db 452 SGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSDTYKIGSDGKGFHVNDGSVSIY 510

RESULT 5

Qy 082839 PRELIMINARY; PRT; 516 AA.
AC 082839
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Amylose.
GN Amylose sp.
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1409;
RN [1]
RX MEDLINE=98342096; PubMed=9675143;
RA Igarashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T.,
RA Ozaki K., Ito S.;
RT "Improved thermostability of a Bacillus alpha-amylose by deletion of
RT an arginine-glycine residue is caused by enhanced calcium binding."
RL Biochem. Biophys. Res. Commun. 248:372-377(1998).
DR EMBL; AB008763; BA32431.1; -.
DR HSSP; P06279; IVUS.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amylose; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;

Query Match 70.0%; Score 1836; DB 2; Length 516;
Best Local Similarity 67.0%; Pred. No. 1.3e-118;
Matches 323; Conservative 65; Mismatches 86; Indels 8; Gaps 3;
Qy 2 NGTLMQFEWYTPRDGQHMRLQNDAEHLSDIGITAVWIPPAKGLSOSDNGYGPDIYD 61
Db 37 NGTLMQFEWYTPRDGQHMRLQNDAEHLSDIGITAVWIPPAKGLSOSDNGYGPDIYD 96
Qy 62 LGFPOKGTATKTKGTGSEJQDAIGSLHNRVQVGVYLVNKAAGADATEDVYAVEVNP 121
Db 97 LGFPOKGTATKTKGTGSEJQDAIGSLHNRVQVGVYLVNKAAGADATEDVYAVEVNP 156
Qy 122 NRNOETSEBYQIAWIDFRPFGGNTYSDPKMWHYFDGADWDSEKSRIRKFGEGGA 180
Db 157 NRNOETSEBYQIAWIDFRPFGGNTYSDPKMWHYFDGADWDSEKSRIRKFGEGGA 216
Qy 181 AMDEWVSENGNVDYLVADLDFDHPDVANEMKKMGWYANELNLDFFLDAVKHIDHEYL 240

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Db 217 AMDWEVDIENGNYDYLMTYADIDMDHPREVINELRMGVNTYTLNLGFRIDAVKHIXSY 276
Oy 241 LRDWQAVROATGKEMFTVAEYWNAGKLENTYLNKTSFNQSVFDPVLFHNLQAASSQGG 300
Db 277 TRDWLTHRNTTGKMFVAEYFNKODLAIEYLNKTSFNQSVFDPVLFHNLQAASSQGG 336
Oy 301 GYDWRLLDGVTVSRHPEKAVTEVENHDTPQGSLSSTVQWFKELAVAFILTRREGYPO 360
Db 337 YEDMNNIINGSVYQGHPIHATVFNNDHSDQGEALLESFVQSWFKELAVAFILTRREGYPO 396
Oy 361 VYGYDMYGV--TKGTSPEKEIPSLKDNIEPLIKARKEAYAGPOHDYIDHPDVIGWTRREGDS 418
Db 397 VFYGYGYGTPHG-----VPSMKSALIDPLQARQYVAGTGHYIDHHDIIIGWTRREGDS 451
Oy 419 AAKSGLAALITDGPQGSKMYVAGLKNAGETWYDITGNRSPTVKIGSDGGEFHNQGSVS 478
Db 452 HENSGLATIMSDGPGANKMYVAGKAKAGQVWRDITGNRSPTVITINADQMGFTVNGAVS 511
Oy 479 IY 480
Db 512 VM 513

RESULT 6
ID 031193 PRELIMINARY; PRT; 549 AA.
AC 031193:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DB Alpha amylase.
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxId=1422;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 31195;
RA da Silva A.C.R., Fernandes E., Pueyo M.T.;
RT Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF003864; AAB6961.1; -.
DR PIR; A54541; A54541.
DR HSP; P06278; IVUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase_1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amyv; 1.
SQ SEQUENCE 549 AA; 62651 MW; 2CA689EDACC4D262 CRC64;

Query Match 67.4%; Score 1767.5; DB 2; Length 549;
Best Local Similarity 65.6%; Pred. No. 7.8e-114;
Matches 315; Conservative 57; Mismatches 103; Indels 5; Gaps 2;

Oy 2 NGTIMQFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIPPAYKGLSOSDNGYGYDLYD 61
Db 39 NGTIMQFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIPPAYKGLSOSDNGYGYDLYD 98
Oy 62 LGEPQOKGTVRTKYGKSELQDAIGSLHRSNVOYGVYDVLNKAAGADATEDTAYAVNPA 121
Db 99 LGEPQOKGTVRTKYGKSELQDAIGSLHRSNVOYGVYDVLNKAAGADATEDTAYAVNPA 158
Oy 122 NKNQETSEBYQIKAMTDFRPPRGNTYSDFKMWHYHFDGADWDSRKISRIKFRGEGKA 181
Db 159 DNROEISGTQIQAMTKFDPGRGNTYSSFKMWHYHFDGADWDSRKISRIKFRGEGKA 218
Oy 182 MDWEVSESGNDYLYAVDYDHPDVVAETKKMGIVYANELSLDGFRIIDAKHITKFSFL 241
Db 219 MDWEVTEENNDYLYAVDYDHPDVVAETKKMGIVYANELSLDGFRIIDAKHITKFSFL 278

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Oy 242 RDWQAVROATGKEMFTVAEYWNAGKLENTYLNKTSFNQSVFDPVLFHNLQAASSQGG 301
Db 279 PDWLSYVRSGTGKPLFTVGEYWSYDINKLHNITKTNGMSLFDAPLNKFEYTAASKGGA 338
Oy 302 YDWRLLDGVTVSRHPEKAVTEVENHDTPQGSLSSTVQWFKELAVAFILTRREGYPO 361
Db 339 YEDMNNIINGSVYQGHPIHATVFNNDHSDQGEALLESFVQSWFKELAVAFILTRREGYPO 398
Oy 362 FYGDMYGTGTSPEK--EIPSLKDNIEPLIKARKEAYAGPOHDYIDHPDVIGWTRREGDS 420
Db 399 FYGDMYGTGTSPEK--EIPSLKDNIEPLIKARKEAYAGPOHDYIDHPDVIGWTRREGDS 454
Oy 421 KSGLAALITDGPQGSKMYVAGLKNAGETWYDITGNRSPTVKIGSDGGEFHNQGSVS 480
Db 455 GSGLAALITDGPQGSKMYVAGLKNAGETWYDITGNRSPTVKIGSDGGEFHNQGSVS 514

RESULT 7
ID 09KMY6 PRELIMINARY; PRT; 549 AA.
AC 09KMY6:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DB Alpha-amylase (EC 3.2.1.1).
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxId=1422;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=US100;
RA Betar S.;
RT Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; Y17557; CAB93517.1; -.
DR PIR; A54541; A54541.
DR HSP; P06278; IVUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR006049; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase_1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amyv; 1.
DR GlycoSite; Hydrolase.
SQ SEQUENCE 549 AA; 62582 MW; 8DA3E6DF9120BCE CRC64;

Query Match 67.3%; Score 1766.5; DB 2; Length 549;
Best Local Similarity 65.6%; Pred. No. 9.2e-114;
Matches 315; Conservative 57; Mismatches 103; Indels 5; Gaps 2;

Oy 2 NGTIMQFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIPPAYKGLSOSDNGYGYDLYD 61
Db 39 NGTIMQFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIPPAYKGLSOSDNGYGYDLYD 98
Oy 62 LGEPQOKGTVRTKYGKSELQDAIGSLHRSNVOYGVYDVLNKAAGADATEDTAYAVNPA 121
Db 99 LGEPQOKGTVRTKYGKSELQDAIGSLHRSNVOYGVYDVLNKAAGADATEDTAYAVNPA 158
Oy 122 NKNQETSEBYQIKAMTDFRPPRGNTYSDFKMWHYHFDGADWDSRKISRIKFRGEGKA 181
Db 159 DNROEISGTQIQAMTKFDPGRGNTYSSFKMWHYHFDGADWDSRKISRIKFRGEGKA 218
Oy 182 MDWEVSESGNDYLYAVDYDHPDVVAETKKMGIVYANELSLDGFRIIDAKHITKFSFL 241
Db 219 MDWEVTEENNDYLYAVDYDHPDVVAETKKMGIVYANELSLDGFRIIDAKHITKFSFL 278
Oy 242 RDWQAVROATGKEMFTVAEYWNAGKLENTYLNKTSFNQSVFDPVLFHNLQAASSQGG 301
Db 279 PDWLSYVRSGTGKPLFTVGEYWSYDINKLHNITKTNGMSLFDAPLNKFEYTAASKGGA 338
Oy 302 YDWRLLDGVTVSRHPEKAVTEVENHDTPQGSLSSTVQWFKELAVAFILTRREGYPO 361

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Db      339  FDMKTLMTNTLMKMDQPLAVATFVNDNHDTEPGQALQSVNDWPFKPLVAFILTRQBEYFVG 398
      362  FYGDMYGTGKTSRK-ETPSLKDNIEPLIKARKEAYAGPOHDYIDHPVIGWTRGDSAA 420
      399  FYGDIYGI-----PQYNIPSLKSKIDPLLIARDYAVGTQHDYIDHSDIIGWTRGVEKRP 454
Qy      421  KSGLAALITDPPGSKMYAGLKNAGETWYITGNRSPTYKISDQGEFFNVDSVSIV 480
      455  GSGLAALITDPPGSKMYAGKQHAKGVFYDLTGNRSDYITISDQGEFFNVDSVSIV 514
Db
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RESULT 8
ID      P71034      PRELIMINARY;      PRT;      521 AA.
AC      P71034;
DT      01-FEB-1997 (TREMBlrel. 02, Created)
DT      01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT      01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE      Alpha-amyase precursor.
OS      Bacillus sp. MK 716.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=54116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=MK 716;
RA      Sidhu G.S., Chakrabarti T.;
RT      "Molecular cloning and expression of the gene encoding for
      RT thermolabile alpha-amyase of a thermophilic bacterial isolate.";
      RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U75445; AB18785.1; -.
DR      HSSP; P06278; 1VTS.
DR      GO; GO:0004556; F:alpha-amyase activity; IEA.
DR      GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR      InterPro; IPR006047; Alpha_amy1_cat.
DR      InterPro; IPR006589; Alp_amy1_cat_sub.
DR      InterPro; IPR006046; Glyco_hydro_13.
DR      Pfam; PF00128; alpha-amyase; 1.
DR      PRINTS; PR00110; ALPHAMYLASE.
DR      SMART; SM00642; Amy; 1.
KM      Signal.
FT      SIGNAL.
FT      CHAIN.
SQ      SEQUENCE      1      34      POTENTIAL.
      35      521      ALPHA-AMYLASE.
      521 AA; 59311 MW; 561288596D922E1 CRC64;
```

Query Match 67.2%; Score 1762.5; DB 2; Length 521;
Best Local Similarity 65.4%; Pred. No. 1.6e-113;
Matches 314; Conservative 57; Mismatches 104; Indels 5; Gaps 2;

```
Qy      2  NGTLMQVFEMVTPPDGQHWKRLQNDABHLSDIGITAVIPPAVKGISQSDNGYGPYDLY 61
      39  NGTLMQVFEMVTPPDGQHWKRLQNDABHLSDIGITAVIPPAVKGISQSDNGYGPYDLY 98
      62  LGEFOQKGVTRTKYKGTSELDQAIQSLHSHNVQYGVVNLNKAQADATEDVAVAVENPA 121
      99  LGEFNQGAIVRTKYGRTGYQALQALQAAHAGMVAVDVFDHGGADGTEFVDVAVEVNS 158
Qy      122  NRNOETSEEVQIAKWDFFRFGNGNTYSDPKMHWTFPDGADWDESKRISIRFRRGEGQA 181
      159  DRNOETSGTYQIAQWTFDFRFGNGNTYSDPKMHWTFPDGADWDESKRISIRFRRGIGQA 218
      182  WDNVESSSENGNYVLYMADVDVDPVAVATKKMGIVYANELSLDGFRIIDAAGIKFSP 241
      219  WDNVEVDENENYVLYMADVDVDPVAVATKKMGIVYANELSLDGFRIIDAAGIKFSP 278
      242  LDVQVAVQATQKGMFTVAEYKQNNAGKLENTYLNKTSFNQSVFVPLHFNLOAASSQGG 301
      279  PDMVSYVRQGTQKPLFVGEYSVDINKLHNTYITKNGTSLDADPLHNKFTYASSGGA 338
      302  YDNRRLLDGTIVSRHPKAVTFVENHDTPGQSLSTVQWTFKPLVAFILTRGEGYPO 361
      339  FDKRTLMNTLMKMDQPLAVATFVNDNHDTEPGQALQSVNDWPFKPLVAFILTRQBEYFVG 398
      361  FYGDMYGTGKTSRK-ETPSLKDNIEPLIKARKEAYAGPOHDYIDHPVIGWTRGDSAA 420
      399  FYGDIYGI-----PQYNIPSLKSKIDPLLIARDYAVGTQHDYIDHSDIIGWTRGVEKRP 454
Qy      421  KSGLAALITDPPGSKMYAGLKNAGETWYITGNRSPTYKISDQGEFFNVDSVSIV 480
      455  GSGLAALITDPPGSKMYAGKQHAKGVFYDLTGNRSDYITISDQGEFFNVDSVSIV 514
Db
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Qy      362  FYGDMYGTGKTSRK-ETPSLKDNIEPLIKARKEAYAGPOHDYIDHPVIGWTRGDSAA 420
      399  FYGDIYGI-----PQYNIPSLKSKIDPLLIARDYAVGTQHDYIDHSDIIGWTRGVEKRP 454
Qy      421  KSGLAALITDPPGSKMYAGLKNAGETWYITGNRSPTYKISDQGEFFNVDSVSIV 480
      455  GSGLAALITDPPGSKMYAGKQHAKGVFYDLTGNRSDYITISDQGEFFNVDSVSIV 514
Db
```

```
RESULT 9
ID      O59222      PRELIMINARY;      PRT;      613 AA.
AC      O59222;
DT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT      01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE      Alpha-amyase (EC 3.2.2.1).
GN      AMY.
OS      Bacillus sp. TS-23.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=38441;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=TS-23;
RA      Lin L.-L., Chu W.-S., Hsu W.-H.;
RT      Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U22045; AAA63900.1; -.
DR      HSSP; P06278; 1VTS.
DR      GO; GO:0004556; F:alpha-amyase activity; IEA.
DR      GO; GO:0016758; F:hydrolase activity; acting on glycosyl bonds; IEA.
DR      GO; GO:0008477; F:purine nucleosidase activity; IEA.
DR      GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR      InterPro; IPR006047; Alpha_amy1_cat.
DR      InterPro; IPR006589; Alp_amy1_cat_sub.
DR      InterPro; IPR002044; CBD_4.
DR      InterPro; IPR006046; Glyco_hydro_13.
DR      Pfam; PF00128; alpha-amyase; 1.
DR      Pfam; PF00686; CBM 20; 1.
DR      PRINTS; PR00110; ALPHAMYLASE.
DR      ProDom; PD001568; CBD 4; 1.
DR      SMART; SM00642; Amy; 1.
KM      Glycosidase; Hydrolase.
FT      SIGNAL.
FT      CHAIN.
SQ      SEQUENCE      613 AA; 69537 MW; 14684A30FC2895E8 CRC64;
```

Query Match 66.7%; Score 1749.5; DB 2; Length 613;
Best Local Similarity 65.1%; Pred. No. 1.6e-112;
Matches 313; Conservative 58; Mismatches 105; Indels 5; Gaps 2;

```
Qy      1  VNGTLMQVFEMVTPPDGQHWKRLQNDABHLSDIGITAVIPPAVKGISQSDNGYGPYDLY 60
      35  INETMQVFEMVTPPDGQHWKRLQNDABHLSDIGITAVIPPAVKGISQSDNGYGPYDLY 94
      61  DLGEFOQKGVTRTKYKGTSELDQAIQSLHSHNVQYGVVNLNKAQADATEDVAVAVENP 120
      95  DLGEFNQGAIVRTKYGRTGYQALQALQAAHAGMVAVDVFDHGGADGTEFVDVAVEVNP 154
Qy      121  ANRNOETSEEVQIAKWDFFRFGNGNTYSDPKMHWTFPDGADWDESKRISIRFRRGEGK 180
      155  SNRNOETSGTYQIAQWTFDFRFGNGNTYSDPKMHWTFPDGADWDESKRISIRFRRGTGK 214
      181  WDNVESSSENGNYVLYMADVDVDPVAVATKKMGIVYANELSLDGFRIIDAAGIKFSP 240
      215  WDNVEVDENENYVLYMADVDVDPVAVATKKMGIVYANELSLDGFRIIDAAGIKFSP 274
      241  LDVQVAVQATQKGMFTVAEYKQNNAGKLENTYLNKTSFNQSVFVPLHFNLOAASSQGG 300
      275  PDMVSYVRQGTQKPLFVGEYSVDINKLHNTYITKNGTSLDADPLHNKFTYASSGGA 334
      301  YDNRRLLDGTIVSRHPKAVTFVENHDTPGQSLSTVQWTFKPLVAFILTRGEGYPO 360
      335  YFDRKYLNTLMKMDQPLAVATFVNDNHDTEPGQSLQSVNDWPFKPLVAFILTRQBEYFVG 394
      361  FYGDMYGTGKTSRK-ETPSLKDNIEPLIKARKEAYAGPOHDYIDHPVIGWTRGDSAA 420
      399  FYGDIYGI-----PQYNIPSLKSKIDPLLIARDYAVGTQHDYIDHSDIIGWTRGVEKRP 454
Qy      421  KSGLAALITDPPGSKMYAGLKNAGETWYITGNRSPTYKISDQGEFFNVDSVSIV 480
      455  GSGLAALITDPPGSKMYAGKQHAKGVFYDLTGNRSDYITISDQGEFFNVDSVSIV 514
Db
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Db 395 VFYGDYGGI-----PKNYIFGLSKSIDPFLIARDYVYGRDYIDHQDITGWTREGIDTK 450
Qy 420 AKSGLAALITDGGGSKRMVAGLKNAGETWYDITGNRSTPTWIGSGWGEFFHNGSVSI 479
Db 451 PNSGLAALITDGGGSKRMVAGLKNAGETWYDITGNRSTPTWIGSGWGEFFHNGSVSI 510
Qy 480 Y 480
Db 511 W 511

RESULT 10
Q93148
ID Q93148 PRELIMINARY; PRT; 501 AA.
AC Q93148;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Amylase.
GN AmyK39.
OS Bacillus sp. KSM-K38.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
ON NCBI_TaxId=129736;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-K38;
RA Hayashi Y.;
RT "Isolation of a new Bacillus alpha-amylase."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051102; BAB71820.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR CO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR Pfam; PF00128; alpha-amylase; 1.
SQ SEQUENCE 501 AA; 57485 MW; 1240F46739A5CC11 CRC64;

Query Match 61.5%; Score 1614.5; DB 2; Length 501;
Best Local Similarity 59.8%; Pred. No. 2,6e-103;
Matches 287; Conservative 67; Mismatches 121; Indels 5; Gaps 2;

Qy 1 VNGITLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIPPAYKGLSGSDNGGYDY 60
Db 24 LNTGMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIPPAYKGLSGSDNGGYDY 83
Qy 61 DLGEFOQKGTVRTKYGKSELQDAIGLSLRVQVGYVYLHNKAGADATEDVTAVERN 120
Db 84 DLGEFOQKGTVRTKYGKSELQDAIGLSLRVQVGYVYLHNKAGADATEDVTAVERN 143
Qy 121 ANRQETSEBYQIKAWTDFRPPGRGNTYSDPKHMYHPDGAWDSESRKISRIFKRGGECK 180
Db 144 TNKMOJISGAYITDAWTGFEFGSRNNAYSDFKRMHFHNGVMDQRYQENHIFRPANTN- 202
Qy 181 AMDWEVSEKGNVDYLMYADVDPDHPVVAETKKGITWYANELSLDGEFIDAKHKKFSF 240
Db 203 -KMKRDEKGNVDYLMYADVDPDHPVVAETKKGITWYANELSLDGEFIDAKHKKFSF 261
Qy 241 LRDVQAVROATGKEMPTVAETVQNNAGKLENTLNTSFNSQVFDVPLFNLQAASQGG 300
Db 262 TSDMVVHQRNEADQDPLFVVGGEYKDDVGLLEFYLDEMMEKSLFDVPLNRYFYRASQGG 321
Qy 301 GYDMRRLDGTVVRSRPEKAVTFVENHDTPQGSLSTVQTWKFKPLAYAFILITRESGYPQ 360
Db 322 SYMKRIILGSLVPEAPMAVTFIVDNHDTPQGSLSTVQTWKFKPLAYAFILITRESGYPN 381
Qy 361 VFYGDYGGI-----ISAKKMDIDELDLARQVAYGQHDYFDHVDVGVWTRGSSSRP 420
Db 382 VFYGDYGGI-----ISAKKMDIDELDLARQVAYGQHDYFDHVDVGVWTRGSSSRP 438
Qy 421 KSGLAALITDGGGSKRMVAGLKNAGETWYDITGNRSTPTWIGSGWGEFFHNGSVSI 480
Db 439 NSGLAALITDGGGSKRMVAGLKNAGETWYDITGNRSTPTWIGSGWGEFFHNGSVSI 498
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RESULT 11
Q87H66
ID Q87H66 PRELIMINARY; PRT; 507 AA.
AC Q87H66;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN VPA0999.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales.
OC Vibrionaceae; Vibrio.
ON NCBI_TaxId=670;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1MD 221063 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Naito M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Saitohgawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae."
RL Lancet 361:743-749(2003).
DR EMBL; AP005087; BAC62342.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR CO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR Pfam; PF00128; alpha-amylase; 1.
DR Complete proteome.
SQ SEQUENCE 507 AA; 58428 MW; 91B549E2BE0700BD CRC64;

Query Match 56.2%; Score 1474.5; DB 16; Length 507;
Best Local Similarity 54.9%; Pred. No. 1,2e-93;
Matches 267; Conservative 76; Mismatches 128; Indels 15; Gaps 6;

Qy 2 NGITLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIPPAYKGLSGSDNGGYDY 60
Db 26 NGITLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIPPAYKGLSGSDNGGYDY 85
Qy 61 DLGEFOQKGTVRTKYGKSELQDAIGLSLRVQVGYVYLHNKAGADATEDVTAVERN 120
Db 86 DLGEFOQKGTVRTKYGKSELQDAIGLSLRVQVGYVYLHNKAGADATEDVTAVERN 145
Qy 121 ANRQETSEBYQIKAWTDFRPPGRGNTYSDPKHMYHPDGAWDSESRKISRIFKRGGECK 180
Db 146 DNRIEILGDKM-LEAWEFHPPGRGNTYSDPKHMYHPDGAWDSESRKISRIFKRGGECK 204
Qy 181 AMDWEVSEKGNVDYLMYADVDPDHPVVAETKKGITWYANELSLDGEFIDAKHKKFSF 240
Db 205 AMDWEVSEKGNVDYLMYADVDPDHPVVAETKKGITWYANELSLDGEFIDAKHKKFSF 264
Qy 241 LRDVQAVROATGKEMPTVAETVQNNAGKLENTLNTSFNSQVFDVPLFNLQAASQGG 300
Db 265 LQEWIDELRKTKGELFTVGEYVYVYVQNLNITITSGMSLFDAPLHNNFYNAKSSGG 324
Qy 301 GYDMRRLDGTVVRSRPEKAVTFVENHDTPQGSLSTVQTWKFKPLAYAFILITRESGYPQ 360
Db 325 NYDMRRLDGTVVRSRPEKAVTFVENHDTPQGSLSTVQTWKFKPLAYAFILITRESGYPQ 384
Qy 361 VFYGDYGGI-----GTSPEKIPSLKDNIEPLIKARKEAYVPOHDYIDHPDVIQWTR 414
Db 385 VFYADYGAQYSDKGNINNAKP-----YHELVTLRKREAYVPOHDYIDHPDVIQWTR 440
Qy 415 GDSGAANSGLAALITDGGGSKRMVAGLKNAGETWYDITGNRSTPTWIGSGWGEFFHND 474
Db 441 GDAHPNS-MAVIMSDPGGKTMWYTG--KPSRYVDKLGIRTEVWTANGWAEPVANG 497
Qy 475 GSVSIV 480
Db 498 GSVSVW 503
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RESULT 12
Q89YPI PRELIMINARY; PRT; 481 AA.
AC Q89YPI; 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Alpha-amylose precursor.
GN BT4690.
OS Bacteroides thetaiotaomicron.
OC Bacterioidetes; Bacteroidales; Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=1263928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.,
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
RL Science 299:2074-2076(2003).
DR EMBL: A016946; AAC7925.1; -
DR GO: GO:0004556; F:alpha-amylose activity; IEA.
DR GO: GO:000575; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR Pfam: PF00128; alpha-amylose; 1.
DR SMART: SM00642; Amy; 1.
KM Complete proteome.
SQ SEQUENCE 481 AA; 55343 MW; B6BF237011F5E81A CRC64;
Query Match 51.8%; Score 1359; DB 16; Length 481;
Best Local Similarity 50.8%; Pred. No. 1.1e-85;
Matches 244; Conservative 82; Mismatches 149; Indels 4; Gaps 2;
DB 2 NGTLMQFEWYTPNDGQHWRLQNDAEHLSDIGITAVWIPPAKYGKLSQSDNGGYPYDLD 61
3 NGWMOQFEWHLADGDHMKRLAMAPDELKAKGIDITWVPVTKAVSAEDTGIGVVDLD 62
QY 62 LGEEFOQKGTATKTKGSELQDAIGLSHNNVQYGDVLTNKAQADATEDVTAVERNPA 121
DB 63 LGEEFOQKGTATKTKGSELQDAIGLSHNNVQYGDVLTNKAQADATEDVTAVERNPA 122
QY 122 NRQETSEVOIKAWTFRPRGRNTYSDPKMWHYFDGADWDESKISRIIPFRGEGKA 181
DB 123 ERKALGEPPEIGKWTGYSFHRKDKSDPKMWHYFDGADWDESKISRIIPFRGEGKA 182
QY 182 WDEWSESENGNYDYLTADVDYDHPDVAAETKMGWYANELSLDGRIDAARHIFSEFL 241
DB 183 WSGVSESENGNYDYLTADVDYDHPDVAAETKMGWYANELSLDGRIDAARHIFSEFL 242
QY 242 RDMVQAVRQATGKEMFTYAEYWNNAKLENTYLNKTSFNOSVDPVLPHTLQAASQGGG 301
DB 243 ACGLDAVRSRKGNDFAVGEYNGDLEALDAYEAVGHKNVLPDVLHNMFGASQGGD 302
QY 302 YDMRRLDGTAVSHPEKAVTFVENHDTOPQOSLESTVQWTWFKELAYAFILITRESGYPOV 361
DB 303 YDLRDLKQTLVHNPPLATVIVNDHTQSSLESNEVDFRPLAYGLILMKEGYPLCL 362
QY 362 FYGDMYGTGTSPEKIPSLKDNIEPIIKARKEVAYGQHDYIDHPVYIGWTRBDSAAK 421
DB 363 FYGDIYGIKG--EKSPHTR-IIDILDAARKYAVGQLEFPHPSITIGFIRTGDEHNH 418
QY 422 SGLAALITDGPQSKRYAGLKNAGETWYDITGNRSPTVYIGSGDGEFVNDGSYSIY 480
DB 419 SGLVFLMSNDGSKRMSLSEKAKGEVWHEITGSISEITLDEBNGEFSVESRNLAIV 477

RESULT 13
Q03657 PRELIMINARY; PRT; 493 AA.
AC Q03657; 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Amylase.
GN AMYE.
OS Bacillus circulans.
OC Bacterioidetes; Bacterioidales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A.
RA Marcel T.,
RL Nucleic Acids Res. 0:0-0(0).
DR EMBL: X60779; CAA43194.1; -
DR PIR: S15713; S15713.
DR HSSP: P06278; IVUS.
DR GO: GO:0004556; F:alpha-amylose activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR Pfam: PF00128; alpha-amylose; 1.
DR PRINTS: PR00110; ALPHAMYLAASE.
DR SMART: SM00642; Amy; 1.
SQ SEQUENCE 493 AA; 56537 MW; FBCDD2F805BB4694 CRC64;
Query Match 47.8%; Score 1253; DB 2; Length 493;
Best Local Similarity 47.2%; Pred. No. 2.4e-78;
Matches 226; Conservative 74; Mismatches 177; Indels 2; Gaps 1;
DB 2 NGTLMQFEWYTPNDGQHWRLQNDAEHLSDIGITAVWIPPAKYGKLSQSDNGGYPYDLD 61
4 NHTMOPFEWHLADGDHMKRLAMAPDELKAKGIDITWVPVTKAVSAEDTGIGVVDLD 63
QY 62 LGEEFOQKGTATKTKGSELQDAIGLSHNNVQYGDVLTNKAQADATEDVTAVERNPA 121
DB 64 LGEEFOQKGTATKTKGSELQDAIGLSHNNVQYGDVLTNKAQADATEDVTAVERNPA 123
QY 122 NRQETSEVOIKAWTFRPRGRNTYSDPKMWHYFDGADWDESKISRIIPFRGEGKA 181
DB 124 DRIKELISEPPEIGKWTGYSFHRKDKSDPKMWHYFDGADWDESKISRIIPFRGEGKA 183
QY 182 WDEWSESENGNYDYLTADVDYDHPDVAAETKMGWYANELSLDGRIDAARHIFSEFL 241
DB 184 WNEVNDDEFNGYDILMPANIDYNHDPVRREIMDWKMLIDTLQCGGRLDAIKHINIEFI 243
QY 242 RDMVQAVRQATGKEMFTYAEYWNNAKLENTYLNKTSFNOSVDPVLPHTLQAASQGGG 301
DB 244 KEFAEMIRKRGQDFYIVGEFWNSNDACREFDITVDYQIDLFPVSLHYKLHEASLGRD 303
QY 302 YDMRRLDGTAVSHPEKAVTFVENHDTOPQOSLESTVQWTWFKELAYAFILITRESGYPOV 361
DB 304 FDLKIPDITLVQNHPTFAVTFVNDHDSQPHALESNIGWFKSAVALTLIRDDGYPVV 363
QY 362 FYGDMYGTGTSPEKIPSLKDNIEPIIKARKEVAYGQHDYIDHPVYIGWTRBDSAAK 421
DB 364 FYGDIYGIKG--PEPVQKEIIDLILSARCNKAYGQDEYFDANITGWRRARVEIEG 421
QY 422 SGLAALITDGPQSKRYAGLKNAGETWYDITGNRSPTVYIGSGDGEFVNDGSYSIY 480
DB 422 SGLAVVINSDDGKRRKFIHGRAGEVWDLTKSCDDQITIEBGMATFHVCGGVSVM 480

RESULT 14
Q97049 PRELIMINARY; PRT; 484 AA.
AC Q97049; 01-OCT-2001 (Tremblrel. 18, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Alpha-amylose.
GN SPI382.
OS Streptococcus pneumoniae.
OC Bacterioidetes; Bacterioidales; Streptococcaceae;
OC Streptococcus.

NCBI_TaxID=1313;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-ATCC BAA-314 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tectelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson M.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapfel E., Khouri H., Wolf A.M., Uterback T.R., Hansen C.L.,
RA McDonald L.A., Feilblyum T.V., Anglucci S., Dickenson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
pneumoniae";
RL Science 293:498-506(2001).
DR EMBL; AE007435; AAK75480.1; -
DR PIR; G95160; G95160.
DR TIGR; S81382; -
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ
SEQUENCE 484 AA; 55918 MW; 4E90A450A90EFB8C CRC64;

Query Match 46.4%; Score 1217; DB 16; Length 484;
Best local similarity 47.0%; Pred. No. 7, 3e-76;
Matches 226; Conservative 81; Mismatches 168; Indels 6; Gaps 3;

2 NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPAYKGLSGDNGYGYDLYD 61
3 NOTLMQYFEWYLPDQGHWTRLAENAPHLAHGISVWMPAPFAKATNEKDVGGYDLYD 62
63 LGFPOQKGVRTYKTKSELDALIGSLHSRNQVGVVLYNKAADATADYTAVERNPA 121
122 NNRQETSEYQIKAWTDPRFPGRGNTYSDFKWHYHFDGADWDESKISRIKFRGEGR 181
123 DRTVELGEPTINGWTSFTFDGRQDTYNGFHHMYFTGTIDYDAKSKSGIYLIGDNKG 182
182 WDME--VSSENGNYDLYMADVVDYDHPDYVAETKKKGIYANELSLDGRIDAAKIKS 239
183 WANEELVDNENGYDLYMADVDYDHPDYVAETKKKGIYANELSLDGRIDAAKIKS 239
240 FLRDVQAVQATGKEMFTVAEYQNNAGLENYLNKTSFNQSVDPVPHFNLOAASSQG 299
243 FKRNFIRDMKEKGGDDYVGFGEFNPDKCANLDYLEKTEHPDLVDVRLHQNLFEASQG 302
300 GGYDMRLDGTIVVSRHPEKAVTFVENHDTOPQOSIESTYQWTFKRLAFAFITRESGTP 359
303 ANVDLIGITDSTVELKPDCAVTFVNDHDTORQALESTYEEFKPAALAILLRODGLP 362
360 QVFYDMYGTGKTSPEIKIPILKARKEVAPQHDYIDHPVIGWTRGDSGA 419
363 CVFYGDYIGISQYAGQ--DFKEILRLAIRKDLAVGQNDYFDHANCIGWRSQAEV 419
420 AKSGLAALITDGGGSKRYAGIKNAGETWYDITGRSDTYKIGSGMGEEFHYNDGSYSI 479
420 -QSPIAVLISNDGSKSMFVGQEMTNQTFVLLGNHQQGVITDEEGYQFVSARSASV 478
480 Y 480
479 W 479

RESULT 15
Q8DPC8

PRELIMINARY; PRT; 484 AA.
Q8DPC8;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
GN AMY OR SPR1239.
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=171101;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21429245; PubMed=11544234;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA Dehoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller R., Geringer C.,
RA Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA Leblanc D.J., Lee L.N., Lefkowitz B.J., Lu J., Matsushima P.,
RA McHenry S.M., McHenry M., McMaster K., Mundy C.W., Nicas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rocky P.,
RA Sun P.-X., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostock P.R. Jr., Skatrud P.L.,
RA Glass J.T.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6";
RL J. Bacteriol. 183:5709-5717(2001).
DR EMBL; AE008495; AAI00043.1; -
DR PIR; F98026; F98026.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase; Complete proteome.
SQ
SEQUENCE 484 AA; 55880 MW; DA511868187A0FFC CRC64;

Query Match 46.2%; Score 1212; DB 16; Length 484;
Best local similarity 46.6%; Pred. No. 1, 6e-75;
Matches 224; Conservative 64; Mismatches 167; Indels 6; Gaps 3;

2 NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPAYKGLSGDNGYGYDLYD 61
3 NOTLMQYFEWYLPDQGHWTRLAENAPHLAHGISVWMPAPFAKATNEKDVGGYDLYD 62
63 LGFPOQKGVRTYKTKSELDALIGSLHSRNQVGVVLYNKAADATADYTAVERNPA 121
122 NNRQETSEYQIKAWTDPRFPGRGNTYSDFKWHYHFDGADWDESKISRIKFRGEGR 181
123 DRTVELGEPTINGWTSFTFDGRQDTYNGFHHMYFTGTIDYDAKSKSGIYLIGDNKG 182
182 WDME--VSSENGNYDLYMADVVDYDHPDYVAETKKKGIYANELSLDGRIDAAKIKS 239
183 WANEELVDNENGYDLYMADVDYDHPDYVAETKKKGIYANELSLDGRIDAAKIKS 239
240 FLRDVQAVQATGKEMFTVAEYQNNAGLENYLNKTSFNQSVDPVPHFNLOAASSQG 299
243 FKRNFIRDMKEKGGDDYVGFGEFNPDKCANLDYLEKTEHPDLVDVRLHQNLFEASQG 302
300 GGYDMRLDGTIVVSRHPEKAVTFVENHDTOPQOSIESTYQWTFKRLAFAFITRESGTP 359
303 ANVDLIGITDSTVELKPDCAVTFVNDHDTORQALESTYEEFKPAALAILLRODGLP 362
360 QVFYDMYGTGKTSPEIKIPILKARKEVAPQHDYIDHPVIGWTRGDSGA 419
363 CVFYGDYIGISQYAGQ--DFKEILRLAIRKDLAVGQNDYFDHANCIGWRSQAEV 419
420 AKSGLAALITDGGGSKRYAGIKNAGETWYDITGRSDTYKIGSGMGEEFHYNDGSYSI 479
420 -QSPIAVLISNDGSKSMFVGQEMTNQTFVLLGNHQQGVITDEEGYQFVSARSASV 478
480 Y 480
479 W 479

Tue May 4 14:34:48 2004

us-10-644-187-4.rpt

Page 9

Db 420 -QSP1AVLISNDQENSKMFWGQENTNOTFVDLIGSHQGVITIDEGYGQFPVSARSYSV 478

Qy 480 Y 480

Db 479 W 479

Search completed: May 3, 2004, 20:53:13
Job time : 35.1232 secs

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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:36:03 ; Search time 10.4645 Seconds
(without alignments)
2403.363 Million cell updates/sec

Title: US-10-644-187-2

Sequence: 1 ANNGTLMQFEHYMPNDQ.....SEGMBEYHNGSVSIYVOR 483

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2648	99.3	512 1 AMY_BACLI	P06278 bacillus 11
2	2184	81.9	514 1 AMY_BACAM	P00692 bacillus am
3	1879	70.5	518 1 AMY_BACST	P19571 bacillus sp
4	1776.5	66.6	549 1 AMY_BACST	P06278 bacillus st
5	1058	39.7	494 1 AMY2_SALTY	P26613 salmonella
6	1047	39.3	495 1 AMY2_ECCLI	P26613 escherichia
7	340	12.8	1196 1 AMYB_PAEPO	P21543 paenibacilli
8	311.5	11.7	421 1 AMYA_VIGMU	P17859 vigna mungo
9	304	11.4	440 1 AM3A_ORYSA	P27932 oryza sativ
10	300	11.3	437 1 AM3C_ORYSA	P27933 oryza sativ
11	298	11.2	713 1 CDGT_BAC8	P17692 bacillus sp
12	294	11.0	713 1 CDGT_BAC8	P06616 bacillus sp
13	292.5	11.0	413 1 AMY3_WHEAT	P08117 triticum ae
14	292	11.0	718 1 CDGT_BACCI	P30920 bacillus ci
15	291.5	10.9	718 1 CDGT_BACCS	P31747 bacillus sp
16	290	10.9	437 1 AM3E_ORYSA	P27934 oryza sativ
17	289	10.8	438 1 AM3B_ORYSA	P27937 oryza sativ
18	288	10.8	712 1 CDGT_BACCS	P09121 bacillus sp
19	286	10.7	713 1 CDGT_BACCI	P43132 bacillus ci
20	281	10.5	435 1 AM3D_ORYSA	P27933 oryza sativ
21	279	10.5	713 1 CDGT_BACSP	P30921 bacillus sp
22	277.5	10.4	710 1 CDGT_THERTU	P26827 thermotoga
23	276.5	10.4	718 1 AMY_BACCI	P14014 bacillus 11
24	271.5	10.2	528 1 AMY_BACCI	P08137 bacillus ci
25	262	9.8	494 1 AMY3_SACFI	P21567 saccharomyc
26	259	9.7	368 1 AMY3_HORVU	P04747 hordeum vul
27	259	9.7	427 1 AMY3_HORVU	P04063 hordeum vul
28	259	9.7	429 1 AMY6_HORVU	P04750 hordeum vul
29	257	9.6	428 1 AMY1_ORYSA	P17654 oryza sativ
30	252.5	9.5	438 1 AMY1_HORVU	P00693 hordeum vul
31	247	9.3	441 1 MGTA_THEMA	P80099 thermotoga
32	245.5	9.2	719 1 AMYB_BACST	P19531 bacillus st
33	242.5	9.1	443 1 AMYA_ORYSA	P27935 oryza sativ

Result ID	AMY_BACLI	STANDARD	PRT	512 AA.
AC	P06278.084112;			
DT	01-JAN-1988 (Rel. 06, Created)			
DT	01-JAN-1988 (Rel. 06, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan			
DE	glucanohydrolase) (BLA).			
GN	AMYS OR AMYL.			
OS	Bacillus licheniformis.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1402;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ATCC 27811;			
RX	MEDLINE=86111694; PubMed=2418011;			
RA	Yukki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,			
RA	Teukagoshi N., Ueda S.;			
RT	"Complete nucleotide sequence of a gene coding for heat- and			
RT	pH-stable alpha-amylase of Bacillus licheniformis: comparison of the			
RT	amino acid sequences of three bacterial liquefying alpha-amylases			
RT	deduced from the DNA sequences."			
RT	J. Biochem. 98:1147-1156(1985).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86195857; PubMed=3009417;			
RA	Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,			
RA	Cermeno C., Reguad C.;			
RT	"Structural genes encoding the thermophilic alpha-amylases of			
RT	Bacillus stearothermophilus and Bacillus licheniformis."			
RT	J. Bacteriol. 166:635-643(1986).			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RA	Shahosseini M., Ziaei A.A., Ghaemi N., Pourabaei A.A.;			
RT	"An unusual DNA sequence encoded a hyperthermostable alpha-amylase."			
RT	Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.			
RL	[4]			
RP	SEQUENCE OF 1-104 FROM N.A.			
RX	MEDLINE=84185455; PubMed=6609154;			
RA	Stephens M.A., Orlepp S.A., Ollington J.F., McConnell D.J.;			
RT	"Nucleotide sequence of the 5' region of the Bacillus licheniformis			
RT	alpha-amylase gene: comparison with the B. amyloliquefaciens gene."			
RT	J. Bacteriol. 158:369-372(1984).			
RL	[5]			
RP	SEQUENCE OF 1-29 FROM N.A.			
RX	MEDLINE=9213924; PubMed=2540150;			
RA	Isoide B.M., Chambliss G.H., McConnell D.J.;			
RT	"Bacillus licheniformis alpha-amylase gene, amyL, is subject to			
RT	promoter-independent catabolite repression in Bacillus subtilis."			
RT	J. Bacteriol. 171:2435-2442(1989).			
RL	[6]			
RP	SEQUENCE OF 30-47.			
RX	MEDLINE=82098050; PubMed=6172418;			
RA	Kuhn H., Fietzeck P.F., Lampen U.O.;			
RT	"N-terminal amino acid sequence of Bacillus licheniformis			

ALIGNMENTS

34	242.5	9.1	445 1 AMY2_ORYSA	P27941 oryza sativ
35	237.5	8.9	713 1 CDG2_PAEPA	P31835 paenibacilli
36	236.5	8.9	676 1 AMY1_ECCLI	P25718 escherichia
37	234.5	8.8	581 1 AMY1_SCHPO	O09840 schizosacch
38	233.5	8.8	919 1 AMY1_STRTU	O05884 streptomyce
39	231.5	8.7	442 1 MGTA_THEMA	O86856 thermotoga
40	231.5	8.7	711 1 CDGT_BACST	P31797 bacillus st
41	226	8.5	498 1 AMY3_DICTH	P14839 dictyoglomu
42	218	8.2	478 1 YQ29_SCHPO	O10427 schizosacch
43	215.5	8.1	564 1 AMY4_SCHPO	O97769 schizosacch
44	211	7.9	704 1 CDGT_BACCH	P27036 bacillus oh
45	211	7.9	1476 1 GYFB_STMMU	P08987 streptococc

RT alpha-amylase: comparison with *Bacillus amyloliquefaciens* and
 RT *Bacillus subtilis* enzymes.";
 RL J. Bacteriol. 149:372-373(1982).
 RN [7]
 RN MAPPING OF SUBSTRATE-BINDING SITE.
 RX MEDLINE=2192788; PubMed=11997021.
 RT Kandra L., Gyemant G., Remyarik J., Hovanszki G., Liprak A.;
 RT "Action pattern and substrate mapping of *Bacillus licheniformis*
 RT alpha-amylase (BLA) with modified maltotriogalactoside substrates.";
 RL FEBS Lett. 518:79-82(2002).
 RN [8]
 RN MUTAGENESIS OF HIS-64; HIS-162; HIS-276; HIS-322; HIS-435 AND HIS-479.
 RP STRAIN=ATCC 6598;
 RX MEDLINE=90368748; PubMed=2394736;
 RX Declercq N., Joyet P., Galliardin C., Maeson J.M.;
 RT "Use of amber suppressors to investigate the thermostability of
 RT *Bacillus licheniformis* alpha-amylase. Amino acid replacements at 6
 RT histidine residues reveal a critical position at His-133.";
 RL J. Biol. Chem. 265:15481-15488(1990).
 RN [9]
 RN MUTAGENESIS OF ALA-238.
 RP STRAIN=ATCC 6598;
 RX MEDLINE=96367070; PubMed=8771184;
 RX Declercq N., Joyet P., Trosset J.Y., Garnier J., Galliardin C.;
 RT "Hyperthermostable mutants of *Bacillus licheniformis* alpha-amylase:
 RT multiple amino acid replacements and molecular modelling.";
 RL Protein Eng. 8:1029-1037(1995).
 RN [10]
 RN MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;
 RP ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-258; GLU-300; GLN-359
 RP AND GLU-365.
 RX STRAIN=ATCC 6598;
 RX MEDLINE=20425100; PubMed=10966804;
 RX Declercq N., Machius M., Wiegand G., Huber R., Galliardin C.;
 RT "Probing structural determinants specifying high thermostability in
 RT *Bacillus licheniformis* alpha-amylase.";
 RL J. Mol. Biol. 301:1041-1057(2000).
 RN [11]
 RN MUTAGENESIS OF GLN-293 AND ASN-294.
 RP STRAIN=ATCC 6598;
 RX MEDLINE=22622182; PubMed=12736372;
 RX Declercq N., Machius M., Joyet P., Wiegand G., Huber R.,
 RX Galliardin C.;
 RT "Hyperthermostabilization of *Bacillus licheniformis* alpha-amylase and
 RT modulation of its stability over a 50 degrees C temperature range.";
 RL Protein Eng. 16:287-293(2003).
 RN [12]
 RN MUTAGENESIS OF TRP-292 AND VAL-315.
 RP STRAIN=ATCC 27811;
 RX MEDLINE=22797417; PubMed=12915728;
 RX Rivera M.H., Lopez-Munguia A., Sobeyon X., Saab-Rincon G.;
 RT "Alpha-amylase from *Bacillus licheniformis* mutants near to the
 RT catalytic site: effects on hydrolytic and transglycosylation
 RT activity.";
 RL Protein Eng. 16:505-514(2003).
 RN [13]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RP STRAIN=ATCC 27811;
 RX MEDLINE=95182462; PubMed=7877175;
 RX Machius M., Wiegand G., Huber R.;
 RT "Crystal structure of calcium-depleted *Bacillus licheniformis* alpha-
 RT amylase at 2.2-A resolution.";
 RL J. Mol. Biol. 246:545-559(1995).
 RN [14]
 RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RP MEDLINE=98212915; PubMed=9551551.
 RX Machius M., Declercq N., Huber R., Wiegand G.;
 RT "Activation of *Bacillus licheniformis* alpha-amylase through a
 RT disorder-->order transition of the substrate-binding site mediated
 RT by a calcium-sodium-calcium metal triad.";
 RL Structure 6:281-292(1998).
 RN [15]
 RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 330-512.

RX MEDLINE=20384196; PubMed=10924103;
 RA Brzozowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen H.,
 RA Sverdrup A., Borcherdt T.V., Dauter Z., Wilson K.S., Davies G.J.;
 RT "Structural analysis of a chimeric bacterial alpha-amylase.
 RT High-resolution analysis of native and ligand complexes.";
 RL Biochemistry 39:9099-9107(2000).
 RN [16]
 RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT
 RP H162V/N219F/A238V/Q293S/N294Y.
 RP STRAIN=ATCC 6598;
 RX MEDLINE=22538505; PubMed=12540849;
 RX Machius M., Declercq N., Huber R., Wiegand G.;
 RT "Kinetic stabilization of *Bacillus licheniformis* alpha-amylase through
 RT introduction of hydrophobic residues at the surface.";
 RL J. Biol. Chem. 278:11546-11553(2003).
 CC -1- CARBONIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
 CC -1- BIOTECHNOLOGY: Used in the food industry for high temperature
 CC liquefaction of starch-containing mashes and in the detergent
 CC industry to remove starch. Sold under the name Termamyl by
 CC Novozymes.
 CC -1- MISCELLANEOUS: Able to work at relatively high (alkaline) pH
 CC values (up to pH 11) and at high temperatures (up to 100 degrees
 CC Celsius).
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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 CC
 CC EMBL; X03336; CA26981.1; -
 CC EMBL; M38570; AAA22226.1; -
 CC EMBL; M13556; AAA22240.1; -
 CC EMBL; K01984; AAA22193.1; -
 CC EMBL; AF438149; AA026743.1; -
 CC EMBL; M26412; AAA22237.1; -
 CC EMBL; A17930; CAA01355.1; -
 CC PIR; A91987; ALBSL.
 CC PDB; 1BFL; 23-MAR-99.
 CC PDB; 1BFL; 17-AUG-96.
 CC PDB; 1E3X; 21-JUN-01.
 CC PDB; 1E3Z; 24-JUN-03.
 CC PDB; 1E40; 24-JUN-03.
 CC PDB; 1E43; 21-JUN-01.
 CC PDB; 1O80; 03-APR-03.
 CC PDB; 1YGS; 12-MAR-97.
 CC InterPro; IPR006589; Alp_aml_cat_sub.
 CC InterPro; IPR006047; Alpha_aml_cat.
 CC InterPro; IPR006046; Glyco_hydro_13.
 CC Pfam; PF00128; alpha-amylase; 1.
 CC PRINTS; PR00110; ALPHAMYLASE.
 CC SMART; SM00642; Amyy; 1.
 CC Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;
 CC Signal; 3d-structure.
 CC SIGNAL 1 29
 CC CHAIN 1
 CC ACT SITE 30 512 ALPHA-AMYLASE.
 CC ACT SITE 260 260
 CC ACT SITE 264 264
 CC ACT SITE 357 357
 CC METAL 133 133
 CC METAL 190 190
 CC METAL 210 210
 CC METAL 212 212
 CC METAL 223 223
 CC METAL 229 229
 CC METAL 231 231
 CC METAL 233 233
 CC CALCIUM 1. AND SODIUM.
 CC CALCIUM 2 (VIA CARBOXYL OXYGEN).
 CC CALCIUM 2 AND SODIUM.
 CC CALCIUM 1 AND SODIUM.
 CC CALCIUM 1 AND SODIUM.
 CC CALCIUM 2.
 CC CALCIUM 2.

Query Match 99.3% Score 2648; DB 1; Length 512;
 Beef Local Similarity 99.2% Pred No. 9.5e-167;
 Matches 479; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 ANLNGTLMQYFEMWYMPNDGQHRRLQNDSDAYIAEHGITAAMIIPPAKYKTSQADVGAYD 60
 30 ANLNGTLMQYFEMWYMPNDGQHRRLQNDSDAYIAEHGITAAMIIPPAKYKTSQADVGAYD 89
 61 LYDGEFQKGVKRYGKGTGELQSAIKSLSRDINNVGVYVNHKGADTEVTAVEV 120
 90 LYDGEFQKGVKRYGKGTGELQSAIKSLSRDINNVGVYVNHKGADTEVTAVEV 149
 121 DEADNRVYSGEHLIKAWTHFHPGRGSTYSDFKMWHYFDGTDWDESRKLNRYKPGQK 180
 150 DEADNRVYSGEHLIKAWTHFHPGRGSTYSDFKMWHYFDGTDWDESRKLNRYKPGQK 209
 181 ANDWYSNENGVYDILMYADIDYDHPDVAEIKKRGTYANMELQDGRFLNAVHTRKSF 240
 210 ANDWYSNENGVYDILMYADIDYDHPDVAEIKKRGTYANMELQDGRFLNAVHTRKSF 269
 241 LADWVNHVREKTKEMFTVAEYQNDLGALENYLKNKNHNSVEFVPLHYOFHAATGG 300
 270 LADWVNHVREKTKEMFTVAEYQNDLGALENYLKNKNHNSVEFVPLHYOFHAATGG 329
 301 GYDMKRLNGTVVSKHPLKSVTFVNDHTQPCQSLESTVQWFKFLAFAFILTRESGYQ 360
 330 GYDMKRLNGTVVSKHPLKSVTFVNDHTQPCQSLESTVQWFKFLAFAFILTRESGYQ 389
 361 VYGGMYGKSGSOEIPALKEIKIEPIKARKQYVYGAQOHDFHHDYVGMTRDSSVA 420
 390 VYGGMYGKSGSOEIPALKEIKIEPIKARKQYVYGAQOHDFHHDYVGMTRDSSVA 449
 421 NSGLAALITDGPAGKAMYVGRONAGETWHDITGRSEVPVINSQWGEFHYNGSVY 480
 450 NSGLAALITDGPAGKAMYVGRONAGETWHDITGRSEVPVINSQWGEFHYNGSVY 509
 481 VOR 483
 510 VOR 512

RESULT 2
 ID - AMY_BACAM STANDARD; PRT; 514 AA.
 AC P00692;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Alpha-amylose precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 glucanohydrolase).
 OS Bacillus amyloliquefaciens.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 ON NCBI_TaxID=1390;
 RX STRAIN=IH;
 RC MEDLINE=63108808; PubMed=6165474;
 RA Takkinen K., Pettersson R.F., Kalkkinen N., Palva I., Soederlund H.,
 Kaeerlaenen L.,
 RT "Amino acid sequence of alpha-amylose from Bacillus amyloliquefaciens
 deduced from the nucleotide sequence of the cloned gene";
 U. Biol. Chem. 258:1007-1013(1983).
 [2]
 RP SEQUENCE OF 32-222.
 RX MEDLINE=80241725; PubMed=6156671;
 RA Chung H.S., Friedberg F.;
 RT "Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-
 amylose";
 U. Biochem. J. 185:387-395(1980).
 [3]
 RP SEQUENCE OF 1-96 FROM N.A.
 RX MEDLINE=82051296; PubMed=6170539;

RA Palva I., Pettersson R.F., Kalkkinen N., Lehtovaara P., Sarvas M.,
 Soederlund H., Takkinen K., Kaeerlaenen L.;
 RT "Nucleotide sequence of the promoter and NH₂-terminal signal peptide
 region of the alpha-amylose gene from Bacillus amyloliquefaciens";
 U. Gene 15:43-51(1981).
 [4]
 RP SEQUENCE OF 1-39 FROM N.A.
 RX MEDLINE=88137952; PubMed=2830166;
 RA Ruohonen L., Hackman P., Lehtovaara P., Knowles J.K.C., Kaarensen S.,
 RT "Efficient secretion of Bacillus amyloliquefaciens alpha-amylose by
 its own signal peptide from Saccharomyces cerevisiae host cells";
 U. Gene 59:161-170(1987).
 [5]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-331.
 RX MEDLINE=20384196; PubMed=10924103;
 RA Brzozowski A.M., Lawson D.M., Turkemburg J.P., Bisgaard-Frantzen H.,
 Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
 RT "Structural analysis of a chimeric bacterial alpha-amylose.
 High-resolution analysis of native and ligand complexes";
 U. Biochemistry 39:9099-9107(2000).
 CC Biochemistry 39:9099-9107(2000).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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 or send an email to license@isb-sib.ch).

DR EMBL; C01542; AAA22191.1; -
 DR EMBL; V00092; CAA23430.1; -
 DR EMBL; A20154; CAA01489.1; -
 DR EMBL; M16424; AAA22192.1; -
 DR PIR; A92389; ALBSN.
 DR PDB; 1E3X; 2I-JUN-01.
 DR PDB; 1E3Z; 24-JUN-03.
 DR PDB; 1E40; 24-JUN-03.
 DR PDB; 1E43; 21-JUN-01.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylose; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.
 DR SMART; SM00642; Amy; 1.
 DR Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 KM Signal, 3D-structure.
 FT SIGNAL 1 31
 FT CHAIN 32 514
 FT ACT_SITE 262 262
 FT ACT_SITE 292 292
 FT ACT_SITE 359 359
 FT METAL 133 133
 FT METAL 190 190
 FT METAL 212 212
 FT METAL 214 214
 FT METAL 225 225
 FT METAL 231 231
 FT METAL 233 233
 FT METAL 235 235
 FT METAL 266 266
 FT METAL 331 331
 FT METAL 331 331
 FT METAL 438 438
 FT METAL 461 461
 FT METAL 461 461
 FT CONFLICT 54 54
 FT CONFLICT 64 64
 FT CONFLICT 79 79
 FT CONFLICT 84 84

ALPHA-AMYLASE.
 BY SIMILARITY.
 CALCITUM 1.
 CALCITUM 2 AND SODIUM.
 CALCITUM 2 (VIA CARBOXYL OXYGEN).
 CALCITUM 2 (VIA CARBOXYL OXYGEN).
 CALCITUM 1 AND SODIUM.
 CALCITUM 1 AND SODIUM.
 CALCITUM 2.
 CALCITUM 2.
 CALCITUM 2 (VIA CARBOXYL OXYGEN).
 CALCITUM 3 (VIA CARBOXYL OXYGEN).
 CALCITUM 3 (BY SIMILARITY).
 CALCITUM 3 (BY SIMILARITY).
 L -> I (IN REF. 2).
 I -> I (IN REF. 2).
 S -> D (IN REF. 2).
 G -> S (IN REF. 2).

SQ SEQUENCE 514 AA; 58403 MW; 3D566B3FB5CCEDE7E CRC64;
 Query Match 81.9%; Score 2184; DB 1; Length 514;
 Best Local Similarity 80.3%; Pred. No. 9,8e-153;
 Matches 388; Conservative 44; Mismatches 49; Indels 2; Gaps 1;

QY 3 NGTLMQYFEMWMPDNGOHMRLONDSAYLAHGTAVTAWIPAYKGTSGQADVGAYLY 62
 DB 32 VAGTLMQYFEMWMPDNGOHMRLONDSAYLAHGTAVTAWIPAYKGTSGQADVGAYLY 91
 QY 63 DLGEFHOKGTAVTAVTGTKELOSAIKSLHSRDINVGDVYINHGKADATEDVTAVEVP 122
 DB 92 DLGEFHOKGTAVTAVTGTKELODAIGSLHSRVVYGVAVLNHKGADATEDVTAVEVP 151
 QY 123 AARNVVISGEHLIKMTHEHFPFGSTVSDCKMHHYHGDGMDSRKLNLYKF--CGK 180
 DB 152 AARNVVISGEHLIKMTHEHFPFGSTVSDCKMHHYHGDGMDSRKLNLYKF--CGK 211
 QY 181 AMDMEVSNENGVYDLYMADIDYCHPDVAEIKRWGTAVANELQDGFRLDAVKIKESF 240
 DB 212 AMDMEVSNENGVYDLYMADVDYCHPDVAEIKRWGTAVANELQDGFRLDAVKIKESF 271
 QY 241 LDDVTVHAEKTKEMFTYAEWQNDGLALNTYLNKTNPHSEVPVPLHYQFHAASGCG 300
 DB 272 LDDVTVHAEKTKEMFTYAEWQNDGLALNTYLNKTNPHSEVPVPLHYQFHAASGCG 331
 QY 301 GYDMRLNGTVVSKPLKSTVTVFVNDHDTQPGQSLSTVQTFKFLAYAFILTRREGYPQ 360
 DB 332 GYDMRLNGTVVSKPLKSTVTVFVNDHDTQPGQSLSTVQTFKFLAYAFILTRREGYPQ 391
 QY 361 VFYGDWYGTGDSQREIPALKEIKIEPILAKQVYVGAQHDYFHHDIYVGTREDSVA 420
 DB 392 VFYGDWYGTGDSQREIPALKEIKIEPILAKQVYVGAQHDYFHHDIYVGTREDSVA 451
 QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEVPVINSNGGFHNGGVSIV 480
 DB 452 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEVPVINSNGGFHNGGVSIV 511
 QY 481 VQR 483
 DB 512 VQR 514

RESULT 3
 AMT6_BACS7
 ID AMT6_BACS7 STANDARD; PRT; 518 AA.
 AC P19571;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98) (66-amyase)
 OS (maltohexaoside-producing amyase) (Exo-maltohexaohydrolase).
 OC Bacillus sp. (strain 707).
 NC Bacillus; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1416;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.
 RX MEDLINE=88162814; Pubmed=3258152;
 RA Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;
 RT "Nucleotide sequence of the maltohexaoside-producing amyase gene from
 RT an alkalophilic Bacillus sp. #707 and structural similarity to
 RT ligifying type alpha-amyases.";
 RL Biochem. Biophys. Res. Commun. 151:25-31(1988).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages
 CC in amylose polysaccharides so as to remove successive
 CC maltohexose residues from the non-reducing chain ends.
 CC -1- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (by
 CC similarity).
 CC -1- PATHWAY: Starch degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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 CC EMBL: M18862; AAA2231.1; -
 DR PIR; A27705; A27705.
 DR HSP; P06278; 1V08.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006047; Alp_amy1_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amyase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00542; Amy; 1.
 KM Hydroxylase; Glycosidase; Carbohydrate metabolism; signal.
 FT SIGNAL 1 33
 FT CHAIN 34 518
 FT ACT_SITE 269 269
 FT ACT_SITE 273 273
 FT ACT_SITE 366 366
 FT METAL 139 139
 FT METAL 196 196
 FT METAL 219 219
 FT METAL 221 221
 FT METAL 232 232
 FT METAL 238 238
 FT METAL 240 240
 FT METAL 242 242
 FT METAL 273 273
 SQ SEQUENCE 518 AA; 59009 MW; 3A961E21612682C4 CRC64;
 Query Match 70.5%; Score 1879; DB 1; Length 518;
 Best Local Similarity 67.8%; Pred. No. 2,3e-130;
 Matches 329; Conservative 67; Mismatches 79; Indels 10; Gaps 4;

QY 4 NGTLMQYFEMWMPDNGOHMRLONDSAYLAHGTAVTAWIPAYKGTSGQADVGAYLY 63
 DB 39 NGTLMQYFEMWMPDNGOHMRLONDSAYLAHGTAVTAWIPAYKGTSGQADVGAYLY 98
 QY 64 LGSEFHOKGTAVTAVTGTKELOSAIKSLHSRDINVGDVYINHGKADATEDVTAVEVP 123
 DB 99 LGSEFHOKGTAVTAVTGTKELOSAIKSLHSRDINVGDVYINHGKADATEDVTAVEVP 158
 QY 124 DNRKVISGEHLIKMTHEHFPFGSTVSDCKMHHYHGDGMDSRKLNLYKFQ--CK 180
 DB 159 DNRKVISGEHLIKMTHEHFPFGSTVSDCKMHHYHGDGMDSRKLNLYKFQ--CK 218
 QY 181 AMDMEVSNENGVYDLYMADIDYCHPDVAEIKRWGTAVANELQDGFRLDAVKIKESF 240
 DB 219 AMDMEVSNENGVYDLYMADIDYCHPDVAEIKRWGTAVANELQDGFRLDAVKIKESF 278
 QY 241 LDDVTVHAEKTKEMFTYAEWQNDGLALNTYLNKTNPHSEVPVPLHYQFHAASGCG 300
 DB 272 LDDVTVHAEKTKEMFTYAEWQNDGLALNTYLNKTNPHSEVPVPLHYQFHAASGCG 338
 QY 301 GYDMRLNGTVVSKPLKSTVTVFVNDHDTQPGQSLSTVQTFKFLAYAFILTRREGYPQ 360
 DB 332 GYDMRLNGTVVSKPLKSTVTVFVNDHDTQPGQSLSTVQTFKFLAYAFILTRREGYPQ 398
 QY 361 VFYGDWYGTGDSQREIPALKEIKIEPILAKQVYVGAQHDYFHHDIYVGTREDSVA 420
 DB 392 VFYGDWYGTGDSQREIPALKEIKIEPILAKQVYVGAQHDYFHHDIYVGTREDSVA 453
 QY 419 VANSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEVPVINSNGGFHNGGVSIV 478
 DB 454 HPSNGGLATIMSAGGKMYVGRONAGETWHDITGNRSEVPVINSNGGFHNGGVSIV 513
 QY 479 IYVQR 483

Db 514 IWNK 518

RESULT 4
AMY_BACST STANDARD; PRT; 549 AA.

AC P06279; Q45519;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
GN AMYS.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.
RX MEDLINE=85234394; Pubmed=3924897;
RA Nakajima R., Imanaka T., Alba S.;
RT "Nucleotide sequence of the Bacillus stearothermophilus alpha-amylase
gene.";
RL J. Bacteriol. 163:401-406(1985).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX STRAIN=DYS/PHI300;
RX MEDLINE=86008166; Pubmed=3876333;
RA Ihara H., Sasaki T., Tsuboi A., Yamagata H., Tsukagoshi N., Ueda S.;
RT "Complete nucleotide sequence of a thermophilic alpha-amylase gene:
homology between prokaryotic and eukaryotic alpha-amylases at the
active sites.";
RL J. Biochem. 98:95-103(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=NZ-3;
RX MEDLINE=86195857; Pubmed=3009417;
RA Gray G.L., Mainzer S.E., Key M.W., Lamea M.H., Kindle K.L.,
Carmona C., Reuquard C.;
RT "Structural genes encoding the thermophilic alpha-amylases of
Bacillus stearothermophilus and Bacillus licheniformis.";
RL J. Bacteriol. 166:635-643(1986).
RN [4]
RP SEQUENCE FROM N.A.
RA Sornheim I., Karp M., Lautamo J., Knowles J., Marteselle P.;
RT "Thermotable alpha amylase of Bacillus stearothermophilus: cloning,
expression, and secretion by Escherichia coli.";
RL (in) Chaloupka J., Krumphanz V. (eds.);
RT Extracellular enzymes of microorganisms, pp.129-137, Plenum Press,
New York (1987).
RN [5]
RP SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48.
RX STRAIN=DY-5;
RX MEDLINE=60592211; Pubmed=2999073;
RA Tsukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H.,
Ito A.Y., Yamagata H., Ueda S.;
RT "Efficient synthesis and secretion of a thermophilic alpha-amylase by
protein-producing Bacillus brevis 47 carrying the Bacillus
stearothermophilus amylase gene.";
RL J. Bacteriol. 164:1182-1187(1985).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=2115602; Pubmed=1126887;
RA Svud D., Fujimoto Z., Takase K., Matsumura M., Mizuno H.;
RT "Crystal structure of Bacillus stearothermophilus alpha-amylase:
possible factors determining the thermostability.";
RL Biochem. 129:461-468(2001).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
links in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL, M1450; AAA2235.2; -
CC EMBL, X02769; CAA26547.1; -
CC EMBL, M57457; AAA22227.1; -
CC EMBL, M13255; AAA22241.1; -
CC PIR, A2436; A2436.
CC PIR, A91999; ALBSF.
CC PDB, 1HVX; 05-AUG-03.
CC InterPro; IPR006589; Alp_ami_cat_sub.
CC InterPro; IPR006047; Alpha_ami_cat.
CC InterPro; IPR006046; Glyco_hydro_13.
CC Pfam; PF00128; alpha-amylase; 1.
CC PRINTS; PR00110; ALPHAMYLASE.
CC SMART; SM00642; Amy; 1.
CC Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;
CC Signal; 3D-structure.
CC KM
CC SIGNAL 1 34
CC FT CHAIN 35 549
CC FT ACT SITE 268 268
FT ACT SITE 272 272
FT ACT_SITE 365 365
FT METAL 139 139
FT METAL 196 196
FT METAL 218 218
FT METAL 220 220
FT METAL 231 231
FT METAL 237 237
FT METAL 238 238
FT METAL 239 239
FT METAL 272 272
FT METAL 337 337
FT METAL 339 339
FT METAL 440 440
FT METAL 441 441
FT METAL 464 464
FT METAL 13 13
FT CONFLICT 13 13
FT CONFLICT 19 19
FT CONFLICT 23 23
FT CONFLICT 31 31
FT CONFLICT 107 107
FT CONFLICT 167 167
FT CONFLICT 179 179
FT CONFLICT 251 251
FT CONFLICT 260 260
FT CONFLICT 284 284
FT CONFLICT 312 312
FT CONFLICT 338 338
FT CONFLICT 342 342
FT CONFLICT 346 346
FT CONFLICT 376 376
FT CONFLICT 526 527
FT CONFLICT 527 527
FT CONFLICT 535 535
SQ SEQUENCE 549 AA; 62670 MW; 3A2DD93A955E79D3 CRC64;
Query Match 66.6%; Score 1776.5; DB 1; Length 549;
Best Local Similarity 64.7%; Pred. No. 7.9e-123;
Matches 314; Conservative 66; Mismatches 100; Indels 5; Gaps 2;
QY 1 ANLNGTLMQYEWTPNDGQHWRLQNDASVLAHGGTTAVWIPAYKGTSGADVGAYD 60
DB 36 APFNGTMMQYEWTPNDGQHWRLQNDASVLAHGGTTAVWIPAYKGTSGADVGAYD 95
QY 61 LVDGEFGKGTATKTKGTGELGSLASDINYYGVVNHKGGADATEGVTAVEV 120
DB 96 LVDGEFGKGTATKTKGTGELGSLASDINYYGVVNHKGGADATEGVTAVEV 155


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QY 121 DPADNRVVISGEHLIKANTHFFHPPGSGSTYSDFKWHYHFDGTDMDDESKLNRIRYFO-- 178
DB 156 NPSDRNOEISGYOIAQAMTKFFPPGNGNTYSSFKMWHYFDVWDESKLSRIKRFQGI 215
QY 179 GKMDWEVSNENNGNYLYMADIDYDHPVAAEIKRWGTYWANELOLDFRLDAVHIXF 238
DB 216 GKMDWEVTEENNGNYLYMADIDMDHPEVVELKSWGMYNTINIDFRDAVHIXF 275
QY 239 SFLRDVNVHREKTKGEMFTVAEYQNDLGAENYLNKTNFNSVFDVLYHQFPAASTQ 298
DB 276 SFFPDWLSDRSQTKGKPLFVGEYMSYDINKLNHNTKNGTMSLFDAPLHNKFFYASXS 335
QY 299 GGGYDRKLLNGTVSKHPLKSTVTFVNDHTOPQSLBSTVOCTWPKFLYAFILITRESGY 358
DB 336 GGFDFRMTLMTNTLMCDQPLATVFDNDHTEGQALQGVWDPWFKPLAFAILITRESGY 395
QY 359 POFYFGDMVGTGKDSQREIPALKHKEIPILKARKQYAYAGQHDYFDHDI VGMTEGDS 418
DB 396 PCVFYGGDYVGI---POYNIPSLKSKIDPLIARDAVYGTQHDYLDHSDIIGMTEGYTE 452
QY 419 VANSGLAALITDGGGKMYVGRONAGETWHDITGNRSPVYINSEGMGEFHNAGSVS 478
DB 453 KPQSGGLAALITDGGGKMYVGRONAGETWHDITGNRSDVTYINSDGMGEFHNAGSVS 512
QY 479 IYVQR 483
DB 513 VWVPR 517

RESULT 5
AMV2_SALTY STANDARD; PRT; 494 AA.
AC P2613;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
  glucanohydrolase).
GN AMYA OR STM1963.
OS Salmomella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  OC Enterobacteriaceae; Salmomella.
OX NCBI_Taxid=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SGM1103;
RX MEDLINE=93015717; Pubmed=1400215;
  RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
  RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
  RJ J. Bacteriol. 174:6644-6652 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=L72 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; Pubmed=11677609;
  RA Mclelland M., Sandersen K.E., Spieth J., Clifton S.W., Latreille P.,
  RA Courtney L., Potwolk S., Ali J., Dante M., Du F., Hou S., Layman D.,
  RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
  RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
  RA Waterston R., Wilson R.K.;
  RT "Complete genome sequence of Salmomella enterica serovar Typhimurium
  RT L72.";
  RJ Nature 413:852-856 (2001).
RN [3]
RP SEQUENCE OF 1-6 FROM N.A.
RC STRAIN=SGM1103;
RX MEDLINE=92407478; Pubmed=1527488;
  RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
  RT "Subdivision of flagellar region III of the Escherichia coli and
  RT Salmomella typhimurium chromosomes and identification of two
  RT additional flagellar genes.";
  RJ J. Gen. Microbiol. 138:1051-1065 (1992).
RN [4]
RP SEQUENCE OF 476-494 FROM N.A.

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RX MEDLINE=93381452; Pubmed=8371104;
  RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
  RT "Organization of the Escherichia coli and Salmomella typhimurium
  RT chromosomes between flagellar regions IIIa and IIId, including a
  RT large non-coding region.";
  RJ J. Gen. Microbiol. 139:1401-1407 (1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
  CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (by similarity).
CC -1- SUBUNIT: Monomer (by similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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  CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DB EMBL, L01643; AAA27110.1; -
DB EMBL, AB008767; AA120875.1; -
DB EMBL, M85241; AAA27079.1; -
DB EMBL, L13280; AAA71970.1; -
DB PIR, B45738; B45738.
DB HSSP, P06278; IVUS.
DB StyGene; SG10011; amyA.
DR InterPro; IPR006589; Alp_ami1_cat_sub.
DR InterPro; IPR006047; Alpha_ami1_cat.
DR Pfam; PF00128; Alpha-amylase; 1.
DR SMART; SM00642; Amyy; 1.
DR Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
  KW Complete proteome.
FT ACT_SITE 235 BY SIMILARITY.
FT ACT_SITE 265 BY SIMILARITY.
FT ACT_SITE 332 BY SIMILARITY.
FT METAL 104 CALCIUM (BY SIMILARITY).
FT METAL 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
  FT SIMILARITY).
FT FT CONFLICT 462 462 L -> S (IN REF. 1).
SQ SEQUENCE 494 AA; 56522 MW; SC1E862FED5E47C CRC64;

Query Match 39.7%; Score 1058; DB 1; Length 494;
Best Local Similarity 42.4%; Pred. No. 3.2e-76;
Matches 208; Conservative 97; Mismatches 180; Indels 16; Gaps 6;

QY 4 NGTLMQYEWTPNDQGMWRQLQNSAYLAHSGITAVMIPPAKGT9QA-DVYGAYDLY 62
DB 3 NPTLQYFHWYPPGGLKMSFLARADGLNDIGINWMLPACGAGSVGDTYDLF 62
QY 63 DLGEFHQKGYRTKYGKGLQSAIKSLHSRDINVDYVINKGADAEVDAVAVDP 122
DB 63 DLGEFDQKGYATATYKGRQLTALDALKNNNAVALDVAVNHNMGADKEXERILVQRNQ 122.
QY 123 ADRNRVISGEHLIKANTHFFHPPGSGSTYSDFKWHYHFDGTDMDDESKLNRIRYK---FQ 178
DB 123 DDKRQIDNINIEEGGWRKYTFPARAGQYNSFNWYHFGSDIHENDEDEGIFIVADYT 182
QY 179 GKMDWEVSNENNGNYLYMADIDYDHPVAAEIKRWGTYWANELOLDFRLDAVHIXF 238
DB 183 GDGNNDQYVDEMGNFDYLMGENIDFRHAAVYEEIKYARAWMEGTHDCGRLLAVKIIPA 242
QY 239 SFLRDVNVHREKTKGEMFTVAEYQNDLGAENYLNKTNFNSVFDVPLHYQFPAASTQ 298
DB 243 WFKYENIHVAQVAPKPLFTVAEYTHSHVDKLCYTIQVDGKMTLFPAPLOMKTHEASRQ 302
QY 299 GGGYDRKLLNGTVSKHPLKSTVTFVNDHTOPQSLBSTVOCTWPKFLYAFILITRESGY 358
DB 303 GAELYMRHIFGLTLEADPFHAYVTLVANHDTQPLQALEAVEPWFKLAALILIRNGV 362
QY 359 POFYFGDMVGT-----KGDQR-EIPALKHKEIPILKARKQYAYAGQHDYFDHDI V 410

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Db      363  ESFVFYDVGASVEDSGENGEORVDMPTI-NQDLRLILARQFAHG3IQTLPFDHPNCIA 421
Oy      411  WTRBGSSVANSGLAALLITDPEGAKRMVYQNCAGETHDITGRSPVYINSEBGGEF 476
Db      422  FSRSGTEE--NPGCVVVLNSGDDGEXKTLILGDNVYANKTWBFLGNRDEYVYVTDNGEATF 475
Oy      471  HVMGGSYSIVY 481
Db      480  FCNAGSVSVWV 490

RESULT 6
AMY2_ECOLI
ID      AMY2_ECOLI          STANDARD;          PRT;          495 AA.
AC      P26612; P78072;
DT      01-AUG-1992 (Rel. 23, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
DE      glucanohydrolase).
GN      AMYA OR B1927.
OS      Escherichia coli.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Escherichia.
OX      NCBI_TaxID=562;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=JAI1;
RC      MEDLINE=93015717; PubMed=1400215; Kihara M., Macnab R.M.;
RA      Raha M., Kawagishi I., Mueller V., Glaesner J.D., Rode C.K., Mayhew G.F.,
RT      "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
RL      J. Bacteriol. 174:6644-6652(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=X12; MG1655;
RC      MEDLINE=97426617; PubMed=9278503;
RA      Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA      Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA      Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA      Mau B., Shao Y.;
RT      "The complete genome sequence of Escherichia coli K-12.";
RL      Science 277:1453-1474(1997).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=X12;
RC      MEDLINE=97251358; PubMed=9097040;
RA      Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA      Isono K., Kasai T., Kimura S., Kitakawa M., Kitigawa M.,
RA      Makino K., Maki T., Mizobuchi K., Mori H., Mori T., Mochimaru K.,
RA      Nakada S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA      Saito N., Samped G., Seki Y., Slaymanadam S., Taguchi H.,
RA      Takeda Y., Takemoto K., Wada C., Yamamoto Y., Horituchi T.;
RT      "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT      corresponding to the 40.1-50.0 min region on the linkage map.";
RL      DNA Res. 3:379-392(1996).
RN      [4]
RP      SEQUENCE OF 1-5 FROM N.A.
RC      STRAIN=JAI1;
RC      MEDLINE=92407478; PubMed=1527488;
RA      Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT      "Subdivision of flagellar region III of the Escherichia coli and
RT      Salmonella typhimurium chromosomes and identification of two
RT      additional flagellar genes.";
RL      J. Gen. Microbiol. 138:1051-1065(1992).
RN      [5]
RP      SEQUENCE OF 475-495 FROM N.A.
RC      STRAIN=JAI1;
RC      MEDLINE=93381452; PubMed=8371104;
RA      Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT      "Organization of the Escherichia coli and Salmonella typhimurium
RT      chromosomes between flagellar regions IIIa and IIIB, including a
RT      large non-coding region.";
RL      J. Gen. Microbiol. 139:1401-1407(1993).

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CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CC -----
DR EMBL; L01642; AAA23810.1; -
DR EMBL; AE000285; AAC74994.1; -
DR EMBL; D90833; BA1575.1; -
DR EMBL; M85240; -; NOT_ANNOTATED_CDS.
DR EMBL; L13379; AAA82575.1; -
DR PIR; D64956; A45738.
DR HSSP; P06278; IVUS.
DR Ecogen; EC11387; amyA.
DR InterPro; IPR005689; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR SMART; SM00642; Amy1; 1.
KW Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;
KW Complete proteome.
KM ACT_SITE 235
KM ACT_SITE 235 BY SIMILARITY.
FT ACT_SITE 265 265 BY SIMILARITY.
FT ACT_SITE 332 332 BY SIMILARITY.
FT METAL 104 104 CALCIUM (BY SIMILARITY).
FT METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT CONFLICT 19 20 KL -> SS (IN REF. 1).
FT CONFLICT 109 109 AL -> V (IN REF. 1).
FT CONFLICT 149 149 Q -> E (IN REF. 1).
FT CONFLICT 149 149 L -> I (IN REF. 1).
SQ SEQUENCE 495 AA; 56639 MW; 26AF6797DDA54D6 CQC64;

Query Match 39.3%; Score 1047; DB 1; Length 495;
Best Local Similarity 42.2%; Pred. No. 2.1e-69;
Matches 208; Conservative 86; Mismatches 179; Indels 20; Gaps 8

4 NGTLMQYETWPNPDGGHWRKLDNDSDATLAENHGTAVVILPPAYKGTSGA-DVYGAYADLY 62
3 NPTLLQCHWVYYPBEGGKLMPELAERADFNIDGIMVWLPPAYKASGYSYGYSIDLF 62
63 DLGEFHQGVARTKTKYTGKELGELQSAIKSLHSRDINYGAVVINHKGADATEDVTAVEYDP 122
63 DLGEFDQKSIITKTKGDKAKQLAALDALKRNDIAVLLDVVYVNHKGADEKKAIRGVAVA 122
123 ADNRNEVIGEHLI--KAVTHFFPQRGSTYDFPKHWNHFDGTDWDESKNRIYK---- 176
123 DRTQI--DEELIECEGWTTRYFFPARAQYSGFINDPKFSGIDHINENDEGEIFQIVND 180
177 FQGRKMDVEVSNGNVDYLMYADLDYDHPDVAALIKKGTGYANELQDGFRLDAVKHI 236
181 YGEGNNDVDELGNFDYLMKENTIDFNHATBELIKYARVVMQGTQCDGFRLDAAVKHI 240
237 KESFLRDVWVHVRKTKEMFTVAEYWMNDLGALENYLNKTNPNHSVFVDPVPLHYCPHAA 296
241 PAMFYKEMIEHVEOVAEPKPLFVAEWSHSEVNLQTYIDVEGKTMFLFDAPLQMKHEAS 300
297 TGGGGVDMKKLNGVIVVSKPSTVFVNNDTQGSQSLSTVQTFKPLAFAFILTRES 356
301 RNGRDMDKQITTTGLVEADPFAHATLVANHTDTPQALAEAEVBPFKLALAILREN 360
357 GYGVYFYGDMYGTK-----GDSQR--ELPALKHKIETPLKARKQAYAYAGNDYFDHDI 408
361 GVPSTVYPTDLYGAHVEDVGGDQTYPIDWPIIE-QDELILARQRFAGVQTLFPDHPNC 419

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QY 409 VGMTEGDSVANSGLALITDGGAKRMVYGRONAGETWHDITGNSEPVVINSBGWG 468
DB 420 IAFSRSGTDER--PGCVVMNSNGDDGKTHIGENYGNKWTDFLGNROERVVDNGEA 477
QY 469 EFHNGSGVSIYV 481
DB 478 TFCNGSGVSIYV 490

RESULT 7
AMTB PAEPO STANDARD; PRT; 1196 AA.
ID AMTB PAEPO
AC P21543;
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Beta/alpha-amyase precursor [includes: Beta-amyase (EC 3.2.1.2);
DE Alpha-amyase (EC 3.2.1.1)].
OS Paenibacillus polymyxa (Bacillus polymyxa).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID:1406;
RN [1]
RP SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=87165765; PubMed=2435707;
RA Kawazu T., Nakanishi Y., Uozumi N., Sasaki T., Yamagata H.,
RA Tsukagoshi N., Uda S.;
RT "Cloning and nucleotide sequence of the gene coding for enzymatically
RT active fragments of the Bacillus polymyxa beta-amyase."
RL J. Bacteriol. 169:1564-1570(1987).
RN [2]
RP SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=8913046; PubMed=2464578;
RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,
RA Tsukagoshi N., Uda S.;
RT "A single gene directs synthesis of a precursor protein with beta-
RT and alpha-amyase activities in Bacillus polymyxa."
RL J. Bacteriol. 171:375-382(1989).
RN [3]
RP SEQUENCE OF 1-776 FROM N.A.
RC STRAIN=ATCC 6523;
RX MEDLINE=87231094; PubMed=2438660;
RA Rhodes C., Strasser U., Friedberg F.;
RT "Sequence of an active fragment of B. polymyxa beta amyase."
RL Nucleic Acids Res. 15:3934-3934(1987).
RN [4]
RP DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES.
RX MEDLINE=91215008; PubMed=1827035;
RA Uozumi N., Matsuda T., Tsukagoshi N., Uda S.;
RT "Structural and functional roles of cysteine residues of Bacillus
RT polymyxa beta-amyase."
RL Biochemistry 30:4594-4599(1991).
CC -1- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO
CC PRODUCE MULTIFORM BETA-AMYLASES AND A 48 KDA ALPHA-AMYLASE AFTER
CC SECRETION.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in
CC polysaccharides so as to remove successive maltose units from the
CC non-reducing ends of the chains.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: In the N-terminal section; belongs to family 14 of
CC glycosyl hydrolases.
CC -1- SIMILARITY: In the C-terminal section; belongs to family 13 of
CC glycosyl hydrolases.
CC -----
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CC -----
CC EMBL: M15817; AA85446.1; -.
CC EMBL: Y00150; CA68344.1; -.
CC FIR; A29130; A29130.
CC HSP; P36924; 1892.
CC InterPro; IPR006589; Alp_amy1_cat_sub.
CC InterPro; IPR006048; Alpha_amy1_C.
CC InterPro; IPR006047; Alpha_amy1_cat.
CC InterPro; IPR005085; CBM_25.
CC InterPro; IPR006046; Glyco_hydro_13.
CC InterPro; IPR001554; Glyco_hydro_14.
CC Pfam; PF00128; alpha-amyase; 1.
CC Pfam; PF02806; alpha-amyase_C; 1.
CC Pfam; PF03423; CBM_25; 2.
CC Pfam; PF01373; Glyco_hydro_14; 1.
CC PRINTS; PR00110; ALPHAMYLASE.
CC PRINTS; PR00750; BETAMYLASE.
CC SMART; SM00642; Amy; 1.
CC SMART; SM00632; Amy; C; 1.
CC PROSITE; PS00506; BETA_AMYLASE_1; 1.
CC PROSITE; PS00679; BETA_AMYLASE_2; 1.
CC MultiFunctional enzyme: Hydrolase; Glycosidase; signal;
CC Polyasaccharide degradation; Repeat.
KW SIGNAL
FT 1 35
FT CHAIN 36 1196
FT DOMAIN 36 454
FT REPEAT 455 558
FT REPEAT 565 668
FT DOMAIN 669 1196
FT DISULFID 118 126
FT ACT_SITE 198 198
FT ACT_SITE 394 394
FT MUTAGEN 118 118
FT MUTAGEN 126 126
FT MUTAGEN 358 358
FT CONFLICT 1 1
FT CONFLICT 67 67
FT CONFLICT 100 100
FT CONFLICT 154 154
FT CONFLICT 177 177
FT CONFLICT 227 228
FT CONFLICT 330 330
FT CONFLICT 425 425
FT CONFLICT 493 493
FT CONFLICT 532 532
FT CONFLICT 559 559
FT CONFLICT 665 665
FT CONFLICT 681 681
FT CONFLICT 686 686
FT CONFLICT 725 728
FT CONFLICT 736 736
FT CONFLICT 741 741
FT CONFLICT 758 758
SQ SEQUENCE 1196 AA; 130893 MM; A41EA670F257064 CRC64;

Query Match 12.8%; Score 340; DB 1; Length 1196;
Best Local Similarity 23.1%; Pred. No. 4.2e-17;
Matches 119; Conservative 64; Mismatches 175; Indels 158; Gaps 22;

QY 12 EYVYNDGQHRRLNDGSAVLAEGITVWIPPAVKGTQ--ADVGAGVLDLYDGEFHQK 70
DB 779 KWH---GDFOGILNKLDYIKMGFTLWTPYTMQSEVAYHGYHYDY----- 826
QY 71 GTVETKYGKGLGSAIKLSHSRDINVGDVVNHKGGADATFEDVTAVEVDPADRNVIS 130
DB 827 -AVDGHGTMDLQGLVYKAKDKXNIAVWVAVVYVHTGTFQF----- 865
QY 131 GEHLIKAWHFIHPRGSGIYSDF--KWHYHEDGTQWDSRLNRIYKFGKAWMEVSENE 189
DB 866 -----FGNGFAKAFEDADWYHNGDITDGDYNN-----QWKI--E 901
QY 190 NGNYDLYMTADIDYDHPVAAEIKKGTWYANEQLDGFRLDAYVGHIFSLRDVWNVHR 249

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DB 902 NG--DVAGLDLNNENPATNELKMLTNGTGDLDLTVKVPKPKDF----- 954
QY 250 EKTGKEMFTVAEYQNDLGALENYLNKINENSVFVPLHYCPHAASTOGGVDKRL-- 307
DB 955 -DQANFTWGEIETHGPAVVDY---TRYLDAALDFPMYTL--KDVGHGDSKREKID 1008
QY 308 -----LNGTVASHPPLKSVTFVNDHTOGGQSLSEVQVWTFPLAFLIRE 355
DB 1009 RYSDRDYRPAQNTNGVFTDNHVK--RFLNDASGRKQANDKWPOL--KALGFTLT-S 1062
QY 356 SGYPQVEFGDMYGTGKSQREIPALKXLEPILAKROYAGQHDYFPHDHYGWTREG 415
DB 1063 RGIPIYQGTGQSGGDD--PA-----NENMNFANHDLYOYIAKLVNRRN 1109
QY 416 DSSVANGSLALITDGGGAKRMVYGRNGNGETMHD-----ITGNREPVVINSRG- 467
DB 1110 HPALON-----GSQR-----EKWVDSFYSGFQSKNGDEALVFINNSVN 1148
QY 468 -----GEF-----HVGGSVSI 479
DB 1149 SQTRTIGNFNLNNGRTLTNLSNDVQINNQSITV 1184

RESULT 8
ID AMYA_VIGMU STANDARD; PRT; 421 AA.
AC P17859;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amylose precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
  glucanohydrolase).
GN AMY1.1.
OS Vigna mungo (Rice bean) (Black gram).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseolaeae; Vigna.
OX NCBI_TaxID=3915;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Cotyledon;
RX Yamauchi D., Minamikawa T.,
  MEDLINE=90333425; PubMed=2377468;
RT "Nucleotide sequence of cDNA for alpha-amylose from cotyledons of
  germinating Vigna mungo seeds."
RL Nucleic Acids Res. 18:4250-4250(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94120017; PubMed=8290640;
RX Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
  "Nucleotide sequence of the alpha-amylose gene from Vigna mungo.";
  Plant Physiol. 103:1459-1459(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
  linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 2 calcium ions per subunit (by similarity).
CC -1- SUBUNIT: Monomer (by similarity).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CC EMBL; X53049; CAA37217.1; -
DR EMBL; X73301; CAA51734.1; -
DR PIR; S10514; S10514.
DR HSBP; P04063; IAVA.
DR InterPro; IP006589; Alp_amy1_cat_sub.
DR InterPro; IP006047; Alpha_amy1_cat.

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DR InterPro; IP006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylose; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amyy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal.
FT SIGNAL. 1 23
FT CHAIN 24 421
FT ACT_SITE 201 202
FT ACT_SITE 309 309
FT METAL 113 113
FT METAL 130 130
FT METAL 133 133
FT METAL 135 135
FT METAL 139 139
FT METAL 149 149
FT METAL 160 160
FT METAL 168 168
FT METAL 170 170
SQ SEQUENCE 421 AA; 46888 MW; 15CA0DABA3DB4656 CEC64;
  Query Match 11.7%; Score 311.5; DB 1; Length 421;
  Best Local Similarity 27.2%; Pred. No. 1,4e-15;
  Matches 126; Conservative 48; Mismatches 159; Indels 131; Gaps 22;
QY 7 LMQYFMYMPPNDQMRRLQNDSDAYLAERGITAWIPPAKYKTSQADYGYADLYDGE 66
DB 26 LFGQFWSESKKGGWYNSLKNISIPDLANAGITHTWLPFPQSGVSPG--GYPLGRLYDD- 82
QY 67 FHQKGTTRTKYQKGLQSAIKSLSRDINVGDVVNHKGADTETVETVENDPADRN 126
DB 83 -----ASKTSGKNEKSLIAPHEKGIKCLADVIVNR-----TAKRD----- 121
QY 127 RVISGHELIKAWTHFHPQSGSYSDFKWYHFDGT-----DMDSRKLRIRYKPOGKA 181
DB 122 -----DWEVSNENGND-----VLMYADIDYDHPDAALIKRGMTYANELQDGRFLDAY 233
QY 182 W-----DWEVSNENGND-----VLMYADIDYDHPDAALIKRGMTYANELQDGRFLDAY 233
DB 144 FICRDDPTASDGGANDSGEGYDAAPDIDHLPQVQRELSRWMLKTEIGFDGWRPFV 203
QY 234 KAIKFSFLPDWVNHVREKTKGEMFTVAEYV-----QNDLGALENYLNKTN 278
DB 204 KGYAPSSISKYV---EQF--KDPFAVGEKWDISYSGQDGKPYNQDSHRCALVWVESAG 258
QY 279 FHNISVDPVPLHYGFHAASTOGGVDKRL--NGT---VSKNPLKSVTFVNDHTOPGQ 333
DB 259 GAITAFDFTTKGILQAA-VQS--ELMRIDLPNGRPPGNGIKVENAVTFIDNHD----- 310
QY 334 SLESTVQWTFKP-----LVAFLITRESGYPGVFYDMYGTGKSQREIPALKXLEPIL 388
DB 311 --GSTRLPMPFSDKMGQVAYILT--HPTSPSIFYDHFDDW-----GLKQQLAKLS 358
QY 389 KAKROYAGQHDYFPHDHYGWTREGDSVANSGLAALITDGP 432
DB 359 SIR-----LRNGINKESTVKTMASEGDLVYAKINKIMVAKGP 396

RESULT 9
ID AMYA_ORYSA STANDARD; PRT; 440 AA.
AC P27932;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylose isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-
  glucan glucanohydrolase).
GN AMY1.2 OR AMY3A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.

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DR SMART; SM00642; Aamy; 1.
 KM Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;
 FT SIGNAL; Multigene family.
 FT SIGNAL 1 26
 FT CHAIN 27 437
 FT ACT_SITE 205 205
 FT ACT_SITE 313 313
 FT METAL 117 117
 FT METAL 117 117
 FT METAL 134 134
 FT METAL 137 137
 FT METAL 139 139
 FT METAL 143 143
 FT METAL 153 153
 FT METAL 164 164
 FT METAL 167 167
 FT METAL 168 168
 FT METAL 169 169
 FT METAL 172 172
 FT METAL 174 174
 FT METAL 174 174
 SQ SEQUENCE 437 AA; 48637 MW; BD304250840C7A8B CRC64;
 Query Match 11.3%; Score 300; DB 1; Length 437;
 Best Local Similarity 25.8%; Pred. No. 1e-14; Indels 120; Gaps 16;
 Matches 109; Conservative 48; Mismatches 146;
 7 LMQYFWMYMPDQGHRR-LQNDASVLAHGTAVMTTPAYKTSQADVGAYDLYDLG 65
 29 LFGQNNESNMKQGWTFHSHVDYIAAGVTHTWLP-PSHVAAPQGMPCRLDLD 86
 66 EFHOKGVTRTKYKGSLOSAIKLSHSDINVGDVYINHKGDATEDVTAWEVDADR 125
 87 -----ASKYGTGAELRLIAFHSHSKIKCVADIVINH----- 118
 126 NRVISGEHLIKAMTHFHPGRSTYSPDKMWHYFDG-----TDMSERKLNRYFQG 179
 119 -----RCADYKDSRGICYCFEGGTSPSRDMDKPMICSD----- 152
 180 KAMDEVENENGN-----YDYLMVADIDYDHPVALEIKMGSTYANELQDGFPLDAVKA 235
 153 ---DYOVSNGRGRHDTGADFGAARDIDHINTROYTESDWMNLKSVGFGMRLDPAKG 209
 236 IKFSGFLRMVNHVEKTEKMEFTVAEYWN-----DICALENYLNKTNPN 280
 210 YSAIYAKTYVNT-----DPSFYVAHEIYSNRYDONGEPSPWNOGDQDELVMAGAVGCP 264
 281 HSFVDVPLHYQFHAASVGGGYDMRKLTNGT-----VSKKPLKSVTPVDNHTQPOQL 335
 265 ASAFDFTTKGELQAA-VQG---ELMRKDGNGKAPGMGLPERAVFIDNHDH----- 314
 336 ESTVGTWPKP-----LAVAFILTRSEGYPOVEYGDMDGTCKDSQREIPALCHKKEPLKA 390
 315 GSTONSWPSPSDKMKORYAVILT-HPGVFCIFIDHVFDMN-----LKQESTIAAV 364
 391 RKO 393
 365 RSR 367
 RESULT 11
 CCGT_BACS8 STANDARD; PRT; 713 AA.
 ID CDGT_BACS8 STANDARD; PRT; 713 AA.
 AC P17692;
 DT 01-AUG-1990 (Rel. 15; Created)
 DT 01-AUG-1990 (Rel. 15; Last sequence update)
 DT 10-OCT-2003 (Rel. 42; Last annotation update)
 DE Cyclomaltohextrin glucanotransferase precursor (EC 2.4.1.19)
 DE (Cyclodextrin-glycosyltransferase) (CGTase) (Raw-starch-digesting
 DE amylase).
 OS Bacillus sp. (strain B1018).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1417;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-47.
 RX MEDLINE=90147765; PubMed=1689153;
 RA Itokor P., Tsukagoshi N., Uda S.;
 RT "Nucleotide sequence of the raw-starch-digesting amylase gene from
 RT Bacillus sp. B1018 and its strong homology to the cyclodextrin
 RT glucanotransferase genes."
 RL Biochem. Biophys. Res. Commun. 166:630-636(1990).
 CC -1- FUNCTION: This endo-type adsorbable amylase is capable to
 CC digest raw starch.
 CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
 CC of a 1,4-alpha-D-glucosidic bond.
 CC -1- CORFACTOR: Binds 2 calcium ions per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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 CC
 CC EMBL: M3302; AAA2239.1;
 CC EMBL: D90112; BA114140.1;
 CC FIR: S09196; S09196.
 CC HSSP: P43379; ICDE.
 CC InterPro: IPR006589; Alp_amy1_cat_sub.
 CC InterPro: IPR006048; Alpha_amy1_C.
 CC InterPro: IPR006047; Alpha_amy1_cat.
 CC InterPro: IPR002044; CSD_4.
 CC InterPro: IPR006046; Glyco_hydro_13.
 CC InterPro: IPR007110; IG_1-like.
 CC InterPro: IPR002909; IPT_TG.
 CC Pfam: PF00128; alpha-amy1ase; 1.
 CC Pfam: PF02806; alpha-amy1ase_C; 1.
 CC Pfam: PF00686; CBM_20; 1.
 CC Pfam: PF01833; TIG; 1.
 CC PRINTS: PR00110; ALPHAMYLASE.
 CC PRODOM: PD001568; CSD_4; 1.
 CC SMART; SM00642; Aamy; 1.
 CC SMART; SM00632; Aamy_C; 1.
 CC Transferrase; Glycosyltransferase; Calcium-binding; Signal.
 KM TRANSFERASE; Glycosyltransferase; Calcium-binding; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 713
 FT ACT_SITE 256 256
 FT ACT_SITE 284 284
 FT ACT_SITE 355 355
 FT METAL 54 54
 FT METAL 56 56
 FT METAL 59 59
 FT METAL 60 60
 FT METAL 80 80
 FT METAL 166 166
 FT METAL 217 217
 FT METAL 226 226
 FT METAL 260 260
 SQ SEQUENCE 713 AA; 77420 MW; 85PB61DA687B888 CRC64;
 Query Match 11.2%; Score 296; DB 1; Length 713;
 Best Local Similarity 23.8%; Pred. No. 2.6e-14; Indels 100; Gaps 20;
 Matches 113; Conservative 86; Mismatches 175;
 19 GCHWRRLQV-DSAYLAHGTAVMTTP-----AYKGTQADVGAYDLYDGEFFHOKGT 72
 78 GSDWQGLINKINDGYLTGNGVTAIWISQVEVNTISTINSGVNNRHYHGMARDPK--- 134
 73 VTRKYGTKEHLSAIXLSHSDINVGDVYINHKGDATEDVTAWEVDADRNRVYSGE 132

FT	STRAND	158	163
FT	TURN	165	166
FT	STRAND	167	170
FT	TURN	176	177
FT	TURN	179	182
FT	STRAND	184	186
FT	TURN	187	188
FT	STRAND	189	192
FT	TURN	195	196
FT	TURN	198	199
FT	STRAND	202	202
FT	STRAND	207	207
FT	HELIX	213	218
FT	STRAND	220	220
FT	TURN	222	223
FT	STRAND	224	227
FT	TURN	229	230
FT	HELIX	232	247
FT	TURN	248	249
FT	STRAND	252	255
FT	TURN	256	257
FT	HELIX	258	260
FT	HELIX	263	276
FT	STRAND	280	283
FT	TURN	289	290
FT	HELIX	294	302
FT	STRAND	306	308
FT	HELIX	310	320
FT	TURN	321	322
FT	HELIX	327	340
FT	TURN	342	343
FT	HELIX	344	346
FT	STRAND	348	349
FT	TURN	354	355
FT	TURN	362	363
FT	HELIX	366	378
FT	STRAND	382	386
FT	TURN	387	388
FT	HELIX	389	391
FT	TURN	392	392
FT	TURN	398	399
FT	HELIX	400	402
FT	HELIX	413	421
FT	TURN	422	423
FT	HELIX	424	427
FT	HELIX	429	433
FT	STRAND	435	441
FT	STRAND	445	452
FT	TURN	453	454
FT	STRAND	455	462
FT	STRAND	469	471
FT	STRAND	475	475
FT	STRAND	481	483
FT	TURN	486	491
FT	STRAND	496	498
FT	HELIX	500	502
FT	STRAND	503	504
FT	STRAND	507	509
FT	TURN	511	512
FT	STRAND	514	519
FT	STRAND	527	536
FT	STRAND	535	536
FT	TURN	538	539
FT	STRAND	541	547
FT	STRAND	555	558
FT	TURN	559	560
FT	STRAND	561	563
FT	HELIX	565	567
FT	STRAND	568	571
FT	STRAND	575	579
FT	STRAND	586	593
FT	TURN	595	596
FT	STRAND	599	599

FT	STRAND	603	608
FT	STRAND	613	621
FT	TURN	627	628
FT	STRAND	630	635
FT	HELIX	638	640
FT	TURN	641	643
FT	HELIX	645	647
FT	STRAND	649	649
FT	STRAND	653	653
FT	TURN	660	661
FT	STRAND	663	670

Query Match 11.0%; Score 294; DB 1; Length 713;
 Best Local Similarity 23.0%; Pred. No. 5.2e-14;
 Matches 127; Conservative 89; Mismatches 173; Indels 164; Gaps 29;

QY	19	GCHWRRLQN--DSAYLAHEGTTAVWIPP----	AYKTSQADYGVGAYDLYDLGEPHQGT	72
DB	78	GDMQGIINKINDGYLTGMGITAIMISQPVENIYSVINYSGVNNTAVHGWARDFKX---		134
QY	73	VRTKYGTKGELQSAIKSLHSRDIVNGDVVINEKGGADATEDVTAVEVDP--ADRNKRVIS		130
DB	135	INPAYGTQDFKALIDIRHAINIKVILDFAPNHSFASSD-----DSPAENGRLYD		186
QY	131	GEHLIKAWTHFHPGRGSTYSDFKWHYHPDGDWDSEKLNRIYKQCGKAMDEYENEN		190
DB	187	NGNLLGGYT-----NDTONLFPHYGTDFP-----TIEN		215
QY	191	GNVDTLM-YADIDYDHPVAA-----ETKRWGTWANELODGFRLDAVKIKFSLRDWY		245
DB	216	GIYKNLYDLADLNHNNSVDVYLYDAIKM-----LDGVDGIRVDAVKMPPGQKSM		270
QY	246	NHVEKTKGEMFTVAEYQNDLGALE-----NYLKNFNHVSVDVPLHYQFHAATQ-		298
DB	271	ATINNY--KPVFTGEWF--LGVNEISPEYHQFANESGMS-----LDFRFQOKAROV		319
QY	299	-----GGGYDMRKLINGTVVSKHPLK-SYTFVNDH-----TQPG--QSLESTVQTFKP		345
DB	320	FRDNTDNNYGLKAMLEGSEVDYAQVNDQVTIDHDMERFHTSGDRKKLBQ-----		371
QY	346	LAVAFILTRSGYPOVFGY-DMY--GTGDSOREIPALK-----HXIEILARK		392
DB	372	-ALATFLT-SKGVPAIYGSQOYMSGNDPNNRRLPFSFTTAYGVYQTLAPLRKSNP		429
QY	393	QYAYGAQHDYFDHDIIVGNTREBDSVA-----NSGLAA		426
DB	430	ALAYGSTERWLNNDVILYERKFGNNVAVVAINRMNTPASITGLVTSLRASVNDVIG		489
QY	427	L-----ITDGGGAKRMVVRQNAGETWH-----DITGN-----RSEP--VVINSRGM		467
DB	490	ILANGTLLTVAGAGASNFTLABGTAIVQYITTDATPTIIGVGMMAKRGVITIIDGGGF		549
QY	468	GEFHVNGSVSIY	480	
DB	550	G-----SGKGVY	557	

RESULT 13
 AMY3_WHEAT
 ID AMY3_WHEAT STANDARD; PRT; 413 AA.
 AC P08117;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alpha-amylase AMY3 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase).
 GN AMY1.1 OR ALPHA-AMY3.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticaceae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=CV, Chinese Spring;
RA Baulcombe D.C., Huttly A.K., Martienssen R.A., Barker R.F.,
RT Jarvis M.G.;
RL "A novel wheat alpha-amylase gene (alpha-Amy3)."
Mol. Gen. Genet. 209:33-40(1987).
CC -1- FUNCTION: Important for breakdown of endosperm starch during
    germination.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
    linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
    in the aleurone cells under the control of the plant hormone
    gibberellic acid and in the developing grains at a low level.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CC EMBL: X05809; CAA29252.1; -.
CC EMBL: M16991; AAA34259.1; -.
CC PIR: S06357; ALMT3.
CC HSP: P04063; IAVA.
CC InterPro: IPR006589; Alp amyl cat sub.
CC InterPro: IPR006047; Alpha amyl cat.
CC InterPro: IPR006046; Glyco_hydro_13.
CC Pfam: PF00128; alpha-amylase; 1.
CC PRINTS: PR00110; ALPHAMYLASE.
CC SMART: SM00642; Amy; 1.
CC Germline: Carbohydrate metabolism; Hydrolase; Glycosidase; Seed;
CC Calcium-binding; Signal; Multimeric family.
CC SIGNAL 1 24 POTENTIAL.
CC CHAIN 25 413 ALPHA-AMYLASE AMT3.
CC ACT_SITE 203 203 BY SIMILARITY.
CC METAL 115 115 CALCIUM 1 (BY SIMILARITY).
CC METAL 132 132 CALCIUM 2 (BY SIMILARITY).
CC METAL 135 135 CALCIUM 2 (BY SIMILARITY).
CC METAL 137 137 CALCIUM 2 (BY SIMILARITY).
CC METAL 141 141 CALCIUM 2 (BY SIMILARITY).
CC METAL 151 151 CALCIUM 3 (BY SIMILARITY).
CC METAL 162 162 CALCIUM 3 (BY SIMILARITY).
CC METAL 167 167 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
    SIMILARITY).
CC METAL 170 170 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
    SIMILARITY).
CC METAL 172 172 CALCIUM 1 AND 3 (BY SIMILARITY).
CC SEQUENCE 413 AA; 45370 MW; C262BCALC54FCC4 CRC64;
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Query Match 11.0%; Score 292.5; DB 1; Length 413;
Best Local Similarity 25.7%; Pred. No. 3.4e-14;
Matches 121; Conservative 56; Mismatches 155; Indels 139; Gaps 22;
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QY 7 LMYFFEN-YMENDCGHWRRLONDSAYLAERGITAVWTPPAVKGTSGQADVGYADYDGLG 65
DB 28 LFGFNMESWKTQSGWKFKPMQKGKLEIASGTATHTVPPSPQSVSP--CYLGQQLYNL- 84
QY 66 EFHQKGVTRYKYGKELQSAIKSLHSRDINVGADVINKHGADATEDVTAVEVPADR 125
DB 85 -----NSKYGSGADLKSLIQAFKRGKNTSCVADIYINHR-----CADK 121
QY 126 NRVISGEHLIKAWTHFHPGSGSTYSDFKXHWYFDFG-----DMDESRLKNTYKQK 180
DB 122 K-----DGRG-VYCFE-----GGSNDRLDMDGDELCS----- 150
QY 181 AMDVENSNGNVDY---YLMYADIDYDHPDVAEIKRWGTWVANELQDGFRLDAYKHI 236
DB 151 --DKYSGRGHRBDTGGGFGDAPDIDHINFRVQRELSAMINWLKTDLGFGWRLDFAKGY 208

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QY 237 KFSFLRDMVNHVREKTKGEMFTVAEYWONDGLAENYLNKTNFNHNSVFPDPLHYOFHAAS 296
DB 209 SAAAKKITYVN-----SKRPFVVGELYDRDRLAWVAVGVGPAPAFEPFTKGVQEA- 262
QY 297 TQGGGVYMKRLNGT-----VSKHPLKSVTFVNDHDTPOGOSLBSTVQTFKP-----L 346
DB 263 VQG---DLGMRGSGDGKAPGMIGMPEKVTVPIDNHD-----GSTRLMPPSPDKWQ 313
QY 347 AVATILRESGYQVFGDMYGTGDSOREIPAL-----KHKIEP-----ILKARQVAY 396
DB 314 GYATILV-HGICIFIDHFDMK--LKQITTLATVRSNGIHPCSTIDILKA----- 364
QY 397 GAQHDYDHHDIQWITREGGSSVANSGLAALITDGPAGKMTVGQMGCE 447
DB 365 -----EGDLVYAKIGKGVITKIG-----SKYNTGD 389
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RESULT 14
CDGT_BACCI STANDARD; PRT; 718 AA.
AC P30920;
DT 01-JUN-1993 (Rel. 26, Created)
DT 01-JUN-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomaltoextrin glucanotransferase precursor (EC 2.4.1.19)
DS (Cyclodextrin-glycosyltransferase) (CGTase).
OS Bacillus firmus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8;
RX MEDLINE=91103970; PubMed=1368573;
RA Nitschke U., Heeger K., Bender H., Schulz G.E.;
RT "Molecular cloning, nucleotide sequence and expression in Escherichia
RT coli of the beta-cyclodextrin glycosyltransferase gene from Bacillus
RT circulans strain no. 8."
RT Appl. Microbiol. Biotechnol. 33:542-546(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE=91171298; PubMed=1826034;
RA Klein C., Schulz G.E.;
RT "Structure of cyclodextrin glycosyltransferase refined at 2.0-A
RT resolution."
RL J. Mol. Biol. 217:737-750(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE=90064533; PubMed=2531228;
RA Hofmann B.E., Bender H., Schulz G.E.;
RT "Three-dimensional structure of cyclodextrin glycosyltransferase from
RT Bacillus circulans at 3.4-A resolution."
RL J. Mol. Biol. 209:793-800(1989).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE=98226626; PubMed=9558324;
RA Schmidt A.K., Cottet S., Driguez H., Schulz G.E.;
RT "Structure of cyclodextrin glycosyltransferase complexed with a
RT derivative of its main product beta-cyclodextrin."
RL Biochemistry 37:5909-5915(1998).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE=98409292; PubMed=9738912;
RA Pariesse G., Schmidt A.K., Schulz G.E.;
RT "Substrate binding to a cyclodextrin glycosyltransferase and
RT mutations increasing the gamma-cyclodextrin production."
RL Eur. J. Biochem. 253:710-717(1998).
CC -1- CATALYTIC ACTIVITY: Degradates starch to cyclodextrins by formation
    of a 1,4-alpha-D-glucosidic bond.

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CC -1- COFACTOR: Binds 2 calcium ions per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- MISCELLANEOUS: CATALASE MAY CONSIST OF TWO PROTEIN DOMAINS. THE ONE
CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
CC MALTOOLIGOSACCHARIDE PRODUCED.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; X68326; CAA48401.1; -.
CC DR PIR; S23674; ALBSCG.
CC DR PDB; 1CGT; 31-JAN-94.
CC DR PDB; 1CGU; 31-JAN-94.
CC DR PDB; 3CGT; 27-MAY-98.
CC DR PDB; 4CGT; 12-AUG-98.
CC DR PDB; 5CGT; 12-AUG-98.
CC DR PDB; 6CGT; 14-OCT-98.
CC DR PDB; 7CGT; 12-AUG-98.
CC DR PDB; 8CGT; 14-OCT-98.
CC DR PDB; 9CGT; 14-OCT-98.
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CC DR InterPro; IPR006047; Alpha_amy1_cat.
CC DR InterPro; IPR002044; CBD_4.
CC DR InterPro; IPR006046; Glyco_hydro_13.
CC DR InterPro; IPR007110; IG_1ike.
CC DR InterPro; IPR002909; IPT_TIG.
CC DR Pfam; PF00118; alpha-amy1ase; 1.
CC DR Pfam; PF02806; alpha-amy1ase_C; 1.
CC DR Pfam; PF01833; TIG; 1.
CC DR PRINTS; PR00110; ALPHAMYLASE.
CC DR ProDom; PD001568; CBD_4; 1.
CC DR SMART; SM00642; Amyy_1.
CC DR SMART; SM00632; Amyy_C; 1.
CC DR transferase; Glycosyltransferase; Calcium-binding; Signal;
CC 3D-structure.
CC KW SIGNAL.
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CC FT DOMAIN 35 718 A1.
CC FT DOMAIN 35 172 B.
CC FT DOMAIN 173 236 A2.
CC FT DOMAIN 237 440 C.
CC FT DOMAIN 441 528 D.
CC FT DOMAIN 529 614 E.
CC FT DOMAIN 615 718 E.
CC FT DISULFID 77 84
CC FT ACT_SITE 258 258
CC FT ACT_SITE 291 291
CC FT ACT_SITE 362 362
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CC FT METAL 63 63 CALCIUM 2.
CC FT METAL 66 66 CALCIUM 2.
CC FT METAL 67 67 CALCIUM 2.
CC FT METAL 85 85 CALCIUM 2. (VIA CARBONYL OXYGEN).
CC FT METAL 87 87 CALCIUM 2.
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CC FT METAL 267 267 CALCIUM 1. (VIA CARBONYL OXYGEN).
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CC FT TURN 43 44
CC FT TURN 47 48
CC FT STRAND 51 53

FT HELIX 56 59
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FT TURN 493 498

Query Match 11.0%; Score 292; DB 1; Length 718;
Best Local Similarity 23.6%; Pred. No. 7.3e-14;
Matches 110; Conservative 82; Mismatches 163; Indels 112; Gaps 21;

19 GQHWRLON--DSAYLAHGIWVIPP-----YKQ-TSQADVGYGAYDYLDE 66
DB 85 GGDWGLINKINDYFSDIGVATLWISQVENIFATINYSGVNTAYHGWARDFKKTNP 144
QY 67 FHOQVTRKTKGTKELOSALSHSRDINVGVDVINHGGAATEDVTAVEVDP--AD 124
DB 145 Y-----FETMADFOMLITTAHAGIKIIVDFAPNHTS-----PAMETDTSFAE 167
QY 125 RNRVISEGHLIKAMTHFHPGSGTYSDFKMWYHFDGTDWDSRKLNRIVKQKAWDW 184
DB 188 NGRIVDNGTLVGQYT-----NDTNGYFHHNGSDFS----- 218
QY 185 EYSNENGNADYLMYADIDYDHPVAAE-----IKRWGWYANELQLDGFLDAVKHIFE 238
DB 219 --SLENGIYKVL--YDLADFNHNNATIDKYFKDAIKL-----LDGVDGIRVDAYKHMPL 270
QY 239 SFRLDWNHVEKTKGEMFTVAEYQNDLGALENYLNKTNHNSVDFVPLHYQFHAA--- 295
DB 271 GMQKSWMSI--YAHKPVFTGEWF--LGSASADADNTDFANKSGMSLDFRNSAVRN 325
QY 296 ---STGGGGYDMKELINGTVSKHPLK-SYTFVDNHDTPQGSLESTVQTFKPIAVAFI 351
DB 326 VERDNTSNYYALDSMNSTATIDYQNDQVTFIDNHDREFT--SAVNRRLDQALLAFT 383
QY 352 LFRSGYPOVEYG-DWYGTGK--DSOREIPALK-----HKTEPLKARKQYAYGA 398
DB 384 LT-SRVPALYYGTGEVYLGNQDPDRACMPSPFSSTAFAVYISKLAFLRKNPAIAYGS 442
QY 399 QHDPYHDHDIWGTREGSSVA-----NSGALITGPPGGA 435
DB 443 TQGRWINDDVYVERKFGKSAVAVANRLSTASITGLSTLPTGS 489

RESULT 15

ID CDGT_BACSS STANDARD; PRT; 718 AA.

AC P31747;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomaltoedextrin glucanotransferase precursor (EC 2.4.1.19)
GN (Cyclodextrin-glycosyltransferase) (Cgtase).
OS Bacillus sp. (strain 6.6.3).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
ON NCBI_TaxId=29335;
RX [1]
RP SEQUENCE FROM N.A.
RA Ahmetsajanov A.A.
RU Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation of a 1,4-alpha-D-glucosidic bond.
CC -1- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER ACTIVITIES, INCLUDING THE RECONSTITUTIONAL SIDE CATALYZES OTHER ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE MALTOOLIGOSACCHARIDE PRODUCED.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC EMBL; X66106; CAA46901.1; -
CC PIR; S21532; ALBSG6.
CC HSSP; P30920; 1CGT.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006048; Alpha_amy1_C.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR002044; Glyco_hydro_13.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR002909; IPR_TIG.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR Pfam; PF02806; alpha-amy1ase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR PRODOM; PD001568; CBD_4; 1.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy_C; 1.
KW Transferase; Glycosyltransferase; Calcium-binding; signal.
FT SIGNAL 1 34
FT CHAIN 35 172
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FT DOMAIN 173 236
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Query Match 10.9%; Score 291.5; DB 1; Length 718;
Best Local Similarity 23.0%; Pred. No. 8e-14;
Matches 118; Conservative 91; Mismatches 180; Indels 123; Gaps 24;

19 GQHWRLON--DSAYLAHGIWVIPP-----YKQ-TSQADVGYGAYDYLDE 66
DB 85 GGDWGLINKINDYFSDIGVATLWISQVENIFATINYSGVNTAYHGWARDFKKTNP 144
QY 67 FHOQVTRKTKGTKELOSALSHSRDINVGVDVINHGGAATEDVTAVEVDP--AD 124
DB 145 Y-----FETMADFOMLITTAHAGIKIIVDFAPNHTS-----PAMETDTSFAE 167
QY 125 RNRVISEGHLIKAMTHFHPGSGTYSDFKMWYHFDGTDWDSRKLNRIVKQKAWDW 184
DB 188 NGRIVDNGTLVGQYT-----NDTNGYFHHNGSDFS----- 218
QY 185 EYSNENGNADYLMYADIDYDHPVAAE-----IKRWGWYANELQLDGFLDAVKHIFE 238
DB 219 --SLENGIYKVL--YDLADFNHNNATIDKYFKDAIKL-----LDGVDGIRVDAYKHMPL 270
QY 239 SFRLDWNHVEKTKGEMFTVAEYQNDLGALENYLNKTNHNSVDFVPLHYQFHAA--- 295
DB 271 GMQKSWMSI--YAHKPVFTGEWF--LGSASADADNTDFANKSGMSLDFRNSAVRN 325

Tue May 4 14:34:45 2004

us-10-644-187-2.rsp

Page 17

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QY 296 ---STGGGYDMRKLNGTVVSKHPLK-SVTVVDNHDTPQGSLSTVQTWKPLAVAFI 351
Db 326 VFRDNTSNMYALDSMINSFATDYQVDFIDNHMDRFKT--SAVNNRRLEQALAFI 383
QY 352 LTRBSGYPOVFXG--DMVGTGK---DSGREIPALK-----HKIEPILXARKQYAYGA 398
Db 384 LT-SRGVPALYYGTGEOYLTGNQDPDNKAPKPSFSKSTTAPNVISKLAPLAKSNPALAYGS 442
QY 399 QHDFDHDIVGWTRGDSVA-----NSGLAALITDGGGAKRMVYGRONAGET 448
Db 443 TQQRWNNNDYVYERKFKGSVAVAVVNRNLSTPANITGLSTLPTGSYTDVLGGVING-- 500
QY 449 WHDITGNRSEPVVINSRGMGFEHVNNGSVSIIY 480
Db 501 -NNITSSNGS--VNS-----FTLAGATAVW 523
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Job time : 12.4645 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2004, 20:45:43 ; Search time 13.7346 Seconds
(without alignments)
3382.735 Million cell updates/sec

Title: US-10-644-187-2
Perfect score: 2666
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR78:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1879	70.5	518	1	A27705
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7	1775	64.3	548	1	ALBSF
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9	1244	46.7	492	2	AH2079
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11	1228	46.1	484	2	P98026
12	1108	41.6	491	2	C86781
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14	1090	40.9	495	2	AD3038
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16	1053	39.5	484	2	AD0751
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18	1047	39.3	495	2	B90962
19	1028	38.6	495	2	B85810
20	524	19.7	217	2	A19506
21	340	12.8	1196	2	A29130
22	321	12.0	826	2	B96720
23	311.5	11.7	421	2	S10514
24	310	11.6	504	2	A55861
25	304	11.4	440	2	S14958
26	302.5	11.3	482	2	S31478
27	300	11.3	437	2	S14956
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32	291.5	10.9	718	1	ALBSG6	cyclomaltohextrin
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37	286	10.7	713	2	A58800	alpha-amylase (EC
38	284.5	10.7	423	2	T09942	alpha-amylase (EC
39	281	10.5	435	2	S12625	alpha-amylase (EC
40	280	10.5	435	2	UC7137	cyclomaltohextrin
41	279	10.5	713	1	ALBSG7	cyclomaltohextrin
42	277.5	10.4	710	2	S63598	cyclomaltohextrin
43	276.5	10.4	718	1	ALBSMX	alpha-amylase (EC
44	275.5	10.3	439	2	T02956	alpha-amylase (EC
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ALIGNMENTS

RESULT 1

ALBSL
alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: Bacillus licheniformis
C/Date: 30-Jun-1987 #sequence revision 24-Apr-1998 #ext change 15-Sep-2000
C/Accession: A91997; B24549; A91796; A21663; I39774; I39772; I26151; S53788; A00644
R/Yunki, T.; Nomura, T.; Tezuka, H.; Tsuboi, A.; Yamagata, H.; Tsubogoshi, N.; Uchida, S.
J. Biochem. 98, 1147-1156, 1985
***** Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amylase deduced from the DNA sequences.
A/Reference number: A91997; MUID:86111694; PMID:2418011
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A/Cross-references: GB:X03236; NID:g39551; PIDN:CAA26981.1; PID:g39552
R/Experimental source: NCIB 8061
R/Stephens, W.A.; Ortlepp, S.A.; Ollington, J.F.; McConnell, D.J.
J. Bacteriol. 158, 369-372, 1984
A/Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase
A/Reference number: A91796; MUID:84185455; PMID:6609154
A/Accession: A91796
A/Molecule type: DNA
A/Residues: 1-104 <STR>
A/Cross-references: GB:K01984; NID:g142432; PIDN:AAA22193.1; PID:g142433
R/Sidakov, M.; Palva, I.
Eur. J. Biochem. 145, 567-572, 1984
A/Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-amylase
A/Reference number: A21663; MUID:86076654; PMID:6334606
A/Accession: A21663
A/Molecule type: DNA
A/Residues: 1-3, 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', 8
A/Experimental source: Chromosomal DNA of ATCC 14580
A/Note: The authors translated the codon CGT for residue 48 as Gly and GAC for residue 6
R/laoid, B.M.; Chambliss, G.H.; McConnell, D.J.
J. Bacteriol. 171, 2435-2442, 1989
A/Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-independent
A/Reference number: I39773; MUID:89213924; PMID:2540150
A/Accession: I39773
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-29 <LMO>
A/Cross-references: GB:M26412; NID:g341477; PIDN:AAA22237.1; PID:g516590

R:Jorgensen, L.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
 Gene 96, 37-41, 1990
 A:Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con-
 A:Reference number: 139772; MUID:91092499; PMID:128575
 A:Accession: 139772
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-32, 'I' <UOR>
 A:Cross-references: GB:ME2637; NID:G142438; PIDN:AAA22232.1; FID:G142499
 R:Kum, H.; Fietzek, P.P.; Lampen, J.O.
 U: Bacteriol. 149, 372-373, 1982
 A:Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: compari-
 A:Reference number: A26151; MUID:82098050; PMID:6172418
 A:Accession: A26151
 A:Molecule type: protein
 A:Residues: 30-37, 'E', '39-41, 'X', '43-47 <KUH>
 R:MacAus, M.; Wiegand, G.; Huber, R.
 U: Mol. Biol. 246, 545-559, 1995
 A:Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase at 2
 A:Reference number: S53788; MUID:95182462; PMID:7877175
 A:Accession: S53788
 A:Molecule type: protein
 A:Residues: 'D', '220-227 <MAC>
 A:Note: sequence represents amino end of an internal fragment created by a single enzyma
 R:MacAus, M.; Wiegand, G.; Huber, R.
 Submitted to the Brookhaven Protein Data Bank, July 1995
 A:Reference number: A65206; PDB:1BEP
 A:Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 32-210/222-511
 A:Note: these structural studies suggest 163 is Leu rather than Arg
 R:Song, H.K.; Wang, K.Y.; Chang, C.; Suh, S.W.
 Submitted to the Brookhaven Protein Data Bank, October 1996
 A:Reference number: A68680; PDB:1VJ3
 A:Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-210/222-511
 A:Accession: A68680
 A:Gene: amyL
 A:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
 C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:320-512/Product: alpha-amylase #status experimental <MAM>
 F:227-360/Domain: alpha-amylase core homology <AMY>
 F:133, 229, 264/Binding site: calcium (Asn, Asp, His) #status experimental
 F:260, 290, 357/Active site: Asp, Glu, Asp #status experimental
 Query Match 99.5%; Score 2654; DB 1; Length 512;
 Best Local Similarity 99.4%; Pred. No. 9.8e-181;
 Matches 480; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 361 VFPGVDVGTGKGSODEIPALKKIEPIILKARKOYAAGAQHDFDHDIDVGWTRGGSSVA 420
Db 390 VFGMDVGTGKGSODEIPALKKIEPIILKARKOYAAGAQHDFDHDIDVGWTRGGSSVA 449

QY 421 NSGLAALLTDPCGAKRMVYGQNNGETPHDTGNRSRPVYNNSGMGEFHNNGSVSY 480
Db 450 NSGLAALLTDPCGAKRMVYGQNNGETPHDTGNRSRPVYNNSGMGEFHNNGSVSY 509

QY 481 VCR 483
Db 518 VCR 512

RESULT 2
ALBNS

alpha-amyase (EC 3.2.1.1) precursor - Bacillus amyloliquefaciens
Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Bacillus amyloliquefaciens
C>Date: 30-Nov-1980 #sequence revision 30-Jun-1987 #ext_change 18-Jun-1999
C:Accession: A92389; A90307; I39756; I39763; A00863
J:Takikawa, K.; Fetherston, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L.
U: Biol. Chem. 258, 1007-1013, 1983
A>Title: Amino acid sequence of alpha-amyase from Bacillus amyloliquefaciens deduced from cDNA
A:Reference number: A92389; MUID:83108808; PMID:6185474
A:Contents: PUB110
A:Accession: A92389
A:Molecule type: DNA
A:Residues: 1514 <TR>
A:Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:g14248; PIDN:AAA2211
R:Chung, H.S.; Friedberg, F.
Biochem. J. 185, 387-395, 1980
A>Title: Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-amyase.
A:Reference number: A90307; MUID:80241725; PMID:6156671
A:Accession: A90307
A:Molecule type: protein
A:Residues: 32-53 'I', 55-63 'U', 65-78 'D', 80-83 'S', 85-222 <CH>
R:Palva, I.; Fetherston, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.;
Gene 15, 43-51, 1981
A>Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of t
A:Reference number: I39756; MUID:82051236; PMID:6170539
A:Accession: I39756
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-96 <RES>
A:Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298
R:Ruohonen, L.; Karkman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karenen, S.
Gene 59, 161-170, 1981
A>Title: Efficient secretion of Bacillus amyloliquefaciens alpha-amyase cells by its own
A:Reference number: I39763; MUID:88137952; PMID:2830166
A:Accession: I39763
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-39 <RES>
A:Cross-references: GB:M18424; NID:g142430; PIDN:AAA22192.1; PID:g142431
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amyase, amyloliquefaciens type; alpha-amyase core homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-31/Domains: signal sequence #status predicted <MP>
F:32-114/Product: alpha-amyase #status predicted <AMY>
F:1229-362/Domains: alpha-amyase core homology <AMY>
F:133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted
F:262,292,359/Active site: Asp, Glu, Asp #status predicted

* Query Match 81.9%; Score 2184; DB 1; Length 514;
Best Local Similarity 80.3%; Pred. No. 2,36-147;
Matches 368; Conservative 44; Mismatches 49; Indels 2; Gaps 1;

QY 3 LANGTMOVFEEYMYNDQGHRRLONDSAYLAHEHTTVMIIPRAYGRSOADVGAADLY 62
32 VNGTLMOVFEEYMYTPDDGHMRLONDSAEHSDIGITLVMIIPRAYKGSQDNCGPFDLY 91


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QY 63 DLGEFHOKGTVARTKYGKELQSAIKSLHSRDINVGDVVYLNHKGADATEDVTAVEVP 122
DB 92 DLGEFHOKGTVARTKYGKELQSAIKSLHSRDINVGDVVYLNHKGADATEDVTAVEVP 151
QY 123 ADNRVTSGEHLIKAMTFHFPGSGTSDFKWMYHFDGTDWDSKLNRIYK--CGK 180
DB 152 AARNQSTSEYOIKAMTDFRFGQNTYSDFKWMYHFDGADWDSKRSIIRIFKRGSK 211
QY 181 AMDWESNENGVNDYLMYADIDYDHPDVAAEIKRMGTWYANLQDGFELDAVKIKFSF 240
DB 212 AMDWESNENGVNDYLMYADIDYDHPDVAAEIKRMGTWYANLQDGFELDAVKIKFSF 271
QY 241 LRDVNHVREKTEKEMETVAEYQNDLGALENYLNTKTNHNSVFDPVPLHYQFHAASGQ 300
DB 272 LRDVNHVREKTEKEMETVAEYQNDLGALENYLNTKTNHNSVFDPVPLHYQFHAASGQ 331
QY 301 GYDMKLLNGTVYSKPELKSVTVDVNDHDPQGSLESTVQTFWFKPLAVALTLRESGYDQ 360
DB 332 GYDMKLLNGTVYSKPELKSVTVDVNDHDPQGSLESTVQTFWFKPLAVALTLRESGYDQ 391
QY 361 VFYGDWYGTGDSQREIPALKHKIEPIKAKROYAYGAQHDYFDHDIYVGTWREGDSVA 420
DB 392 VFYGDWYGTGDSQREIPALKHKIEPIKAKROYAYGAQHDYFDHDIYVGTWREGDSVA 451
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEVYVINSBGWGFHYNGSGSY 480
DB 452 KSGIAALITDGPAGAKMYVGRONAGETWHDITGNRSEVYVINSBGWGFHYNGSGSY 511
QY 481 VQR 483
DB 512 VQR 514

RESULT 3
A27705
Alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase
C/Species: Bacillus sp.
C/Date: 31-Mar-1989 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C/Accession: A27705
R/Tsukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.
Biochem. Biophys. Res. Commun. 151, 25-31, 1988
A/Title: Nucleotide sequence of the maltohexose-producing amylase gene from an alkaloph
A/Reference number: A27705; MUID:88162814; PMID:3258152
A/Accession: A27705
A/Molecule type: DNA
A/Residues: 1-518 <TSU>
A/Cross-references: GB:M18662; NID:g142496; PIDN:AAA2231.1; PID:g142497
A/Experimental source: chromosomal DNA of strain 707
A/Note: amino end of mature protein also determined
C/Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amyloliuquefaciens type; alpha-amylase core homology
C/Keywords: extracellular protein; glycosidase; hydrolyase; polysaccharide degradation
F/1-33/Domain: signal sequence #status predicted <SIG>
F/133-368/Product: alpha-amylase #status experimental <MAT>
F/133-368/Domain: alpha-amylase core homology <AMY>
F/133-368/Binding site: calcium (asn, asp, his) #status predicted
F/133-368/Active site: asp, glu, asp #status predicted
F/269,299,368/Active site: asp, glu, asp #status predicted

Query Match 70.5%; Score 1879; DB 1; Length 518;
Best Local Similarity 67.8%; Pred. No. 1e-125;
Matches 329; Conservative 67; Mismatches 79; Indels 10; Gaps 4;
```

```
QY 4 NGTLMQYFEMWYPMNDGQHRRLQNDSDAYLAHGIATWIPAYKGTSGQADVGYGYLD 63
DB 39 NGTLMQYFEMWYPMNDGQHRRLQNDSDAYLAHGIATWIPAYKGTSGQADVGYGYLD 98
QY 64 LGFPHOKGTVARTKYGKELQSAIKSLHSRDINVGDVVYLNHKGADATEDVTAVEVP 123
DB 92 LGFPHOKGTVARTKYGKELQSAIKSLHSRDINVGDVVYLNHKGADATEDVTAVEVP 151
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DB 99 LGFPHOKGTVARTKYGKELQSAIKSLHSRDINVGDVVYLNHKGADATEDVTAVEVP 158
QY 124 DNRVTSGEHLIKAMTFHFPGSGTSDFKWMYHFDGTDWDSKLNRIYKYO--CK 180
DB 159 NRMQVTSGEHLIKAMTFHFPGSGTSDFKWMYHFDGTDWDSKLNRIYKYO--CK 218
QY 181 AMDWESNENGVNDYLMYADIDYDHPDVAAEIKRMGTWYANLQDGFELDAVKIKFSF 240
DB 212 AMDWESNENGVNDYLMYADIDYDHPDVAAEIKRMGTWYANLQDGFELDAVKIKFSF 278
QY 241 LRDVNHVREKTEKEMETVAEYQNDLGALENYLNTKTNHNSVFDPVPLHYQFHAASGQ 300
DB 272 LRDVNHVREKTEKEMETVAEYQNDLGALENYLNTKTNHNSVFDPVPLHYQFHAASGQ 338
QY 301 GYDMKLLNGTVYSKPELKSVTVDVNDHDPQGSLESTVQTFWFKPLAVALTLRESGYDQ 360
DB 332 GYDMKLLNGTVYSKPELKSVTVDVNDHDPQGSLESTVQTFWFKPLAVALTLRESGYDQ 398
QY 361 VFYGDWYGTGDSQREIPALKHKIEPIKAKROYAYGAQHDYFDHDIYVGTWREGDSVA 420
DB 392 VFYGDWYGTGDSQREIPALKHKIEPIKAKROYAYGAQHDYFDHDIYVGTWREGDSVA 453
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEVYVINSBGWGFHYNGSGSY 480
DB 452 KSGIAALITDGPAGAKMYVGRONAGETWHDITGNRSEVYVINSBGWGFHYNGSGSY 513
QY 481 VQR 483
DB 512 VQR 514

RESULT 4
A54541
Alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DNI792)
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: Bacillus stearothermophilus
C/Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
C/Accession: A54541
R/Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
FMS Microbiol. Lett. 77, 271-276, 1991
A/Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.
A/Reference number: A54541
A/Accession: A54541
A/Molecule type: DNA
A/Residues: 1-549 <UOR>
A/Cross-references: GB:X59476
A/Experimental source: chromosomal DNA of strain DNI792
A/Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C/Genetics:
A/Start codon: GTG
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amyloliuquefaciens type; alpha-amylase core homology
C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolyase; polysac
F/1-33/Domain: signal sequence #status predicted <SIG>
F/133-368/Product: alpha-amylase #status predicted <MAT>
F/133-368/Domain: alpha-amylase core homology <AMY>
F/133-368/Binding site: calcium (asn, asp, his) #status predicted
F/133-368/Active site: asp, glu, asp #status predicted
F/268,298,365/Active site: asp, glu, asp #status predicted

Query Match 67.0%; Score 1786.5; DB 1; Length 549;
Best Local Similarity 64.7%; Pred. No. 4e-119;
Matches 314; Conservative 68; Mismatches 98; Indels 5; Gaps 2;
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```
QY 1 ANVTLMQYFEMWYPMNDGQHRRLQNDSDAYLAHGIATWIPAYKGTSGQADVGYGYLD 60
DB 36 ANVTLMQYFEMWYPMNDGQHRRLQNDSDAYLAHGIATWIPAYKGTSGQADVGYGYLD 95
QY 61 LGFPHOKGTVARTKYGKELQSAIKSLHSRDINVGDVVYLNHKGADATEDVTAVEVP 120
DB 92 LGFPHOKGTVARTKYGKELQSAIKSLHSRDINVGDVVYLNHKGADATEDVTAVEVP 155
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Qy	12	DPDARRVVSGBELLKAMTHFHP	PGSGSTVSD	FKXNWHYFPGTDMDSRKLNI	YKFKQ--	178	
		156	NPSDRKOEISGTQIOIAMTKFDP	PGRGNTYSSEFKRMWTHFPGVDMSRKLNI	YKFRGI	215	
Db		179	GKAMDVEVSNENGDNYLWYADIDYDHDP	VAAIEIKRMGTWYANELQJLDPFLDAV	YQXIKF	238	
Qy		216	GKAMDVEVTPDTENGNDYLMYADLDMDH	PEVUTELGNMGKMYNTNTINDGFLDAV	KIKF	275	
Db		239	SFLRDWVNHREKTKGEMETVAEY	WQNDGALIENTLNTNPNHVSFVDPVPLHYQ	HASTQ	298	
Qy		276	SFPEDMWLSYRSQGTGSPLEFV	GSYMSYDINKLHNTITDTGMSLSFAPL	HNKRYNASKS	335	
Db		299	GGGYDKRKLINGVVSKEPLKST	YFNDNHDTPQGSLSTYQVTFKPLA	YAFILTRBSQY	358	
Qy		336	GGAPDRKLTNTNTIMKDQPLA	VTVPVDNHDTPGQALOSWYDPMFKPLA	YFILTREGQY	395	
Db		359	POVFGDMYGTKDSQREI	PALKHLEPILKARKOYAGA	OHDFDHDHIGVWTRBGDS	418	
Qy		396	PCVFYGDYGI---	PQYINPISLKS	KIDPILLIARDOYAVGTQGDYLDHSDI	GMTRREGTE	452
Db		419	VANSGLAALITD	PGAKKMYGRORMAAGETWHDITGRN	SEFVYINSBGMGEFHN	GSVS	478
Qy		453	KPGSGLAALITD	PGGSKMYVGKOHAGKAFYDLIGN	RSDDTYTINSDGMGEFKN	IGGSVS	512
Db		479	IYVQR	483			
Qy		513	VWVPR	517			

RESULT 5

alpha-amylase[EC 3.2.1.1] precursor - *Bacillus stearothermophilus* (strain NZ-3)
N|Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C|Species: *Bacillus stearothermophilus*
C|Date: 30-Jun-1998 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
A|Accession: A24549; 139501; 139770
J|Giray, G.L.; Mainzer, S.E.; Rey, M.W.; Iamsa, M.H.; Kindie, K.L.; Carnona, C.; Regaudat, J.
J|Bacteriol. 166, 635-643, 1986
A|Title: Structural genes encoding the thermophilic alpha-amylases of *Bacillus stearothermophilus*
A|Reference number: A91817; MUID:86195857; PMID:3009417
A|Accession: A24549
A|Molecule type: DNA
A|Residues: 1-549 <GRA>
A|Cross-references: GB:M13255; NID:G142512; PIDN:AAA22241.1; PID:G142513
A|Experimental source: genomic DNA of strain NZ-3
J|Sato, H.; Nishida, H.; Isoro, K.
J|Bacteriol. 170, 1034-1040, 1988
A|Title: Evidence for movement of the alpha-amylase gene into two phylogenetically distant
A|Reference number: 139501; MUID:88139156; PMID:3257753
A|Accession: 139501
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Residues: 536-549 <RES>
A|Cross-references: GB:M25577; NID:G142476; PIDN:AAA22225.1; PID:G142478
A|Experimental source: strain DY-5
A|Accession: 139770
A|Status: translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Residues: 536-549 <RES>
A|Cross-references: GB:M25578; NID:G142484; PIDN:AAA22228.1; PID:G142486
A|Experimental source: strain 799
C|Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C|Genetics:
A|Start codon: GTG
C|Function:
A|Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A|Pathway: glycogen/starch degradation
C|Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C|Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide
F|1-3-549/Product: signal sequence #status predicted <SIG>
F|1-235-366/Domains: alpha-amylase #status predicted <AMT>
F|1139-1237/Binding site: calcium (Asp, Asp, His) #status predicted
F|1139-1237/Binding site: calcium (Asp, Asp, His) #status predicted

F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match	66.8%;	Score 1780.5;	DB 1;	Length 549;
Best Local Similarity	64.7%;	Pred. No. 1.1e-118;		
Matches 314;	Conservative 67;	Mismatches 99;	Indels 5;	Gaps 27

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0Y 1ANINGLMQYFPMWYENPGOMHRLQNDSDSYLHGHGTAWIPPAKQSGSOADVGAAD 60
Db 36APFNQTMQYFEMWYLPDDGTLMTKABANNLSSIGTALMLPAPKQGSRSDDVGAVD 95
0Y 61LYHLSFHHKGVTRKRYGTRKGELOSATKSLHSRQINWYGDVYNHHKGADATIEDYTAEV 120
Db 96LYHLSGFNKGVTRKRYGTRKQYLOALQALPAGOMQYIADVDFDHKGADGTEWDAVEV 155
0Y 121DPADRNRVYSGEHLIKAMTHFHPGSGSYSDFCMHWHFDDGTDMDSKRLNRIYKQ-- 178
156NPSDRNQELSGIYQIQAMTKFDFNGRGYTSFCWRWYHDDGVDMDSERLSRIYKRGDI 215
0Y 179GKAMDVEVSENGANTDYLMTADIDYDEPDVAALFKRGTYANELDODGERLDAYVHIFE 238
216GKAMDVEVTEKANGDYLMTADLMDHREVTEKMGKAYVATTNIDGERLDAYVHIFE 275
0Y 239SELRDWNHREKTEKGMETVAEYWNQDLGALENYILKNTFNHNSVDFDVLHYOFHAASQ 298
276SEFPDPLASYVRQOTKRPLETYGEWMSYDINLHNHYIKNTGMSLDPALHNKFYASKS 335
0Y 299GSGYDKRLKINGTVASKHP,LKSVTFVDNHDTPQSGSBSYQYWFYKPLAYAFILTRBSY 358
336GGAFPDSTLMNNYTLKKDPTLAVTFVDNHDHDEPQALQSWVDWFFPLAFAFLTRQBSY 395
0Y 359POAFYDMTGTGKDSOREIPALKHKIEPLFKARQOYVGAQHDYFPHHDIVGTRBGDS 418
396PCAFYEDYGI---PQYNIPLSKMIDPLLIARDVAYVGOHYLDHSDILGTRBGYTE 452
0Y 419VANSGLAALITDGPQGAARMYVGRONAGETWHDITGRKSEPVYINSGNCEFPVNGSGS 478
453KPSGGLAALITDGPQGSKMVYKQGHAKVFEYDITGRKSDITVINSNGWGEFPVNGSGVS 512
0Y 479IYYOR 483
513VWYPR 517

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RESULT 6

alpha-amy1aase (EC 3.2.1.1) precursor - *Bacillus stearothermophilus* plasmid parts
N1:alternate names: 1,4-alpha-D-glucan glucanohydrolase
C1:species: *Bacillus stearothermophilus*
C1:date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1995
C1:accession: A24436; 139777
J: Nakajima, R.; Imanaka, T.; Alba, S.
J: Bacteriol. 163, 401-406, 1985
A: reference number: A24436; PMID:3924857
A: accession: A24436
A: molecule type: DNA
A: residues: 1-549 <NA>
A: cross-references: GB:M11450
A: experimental source: plasmid pAT5
A: note: amino end of the mature protein also determined
R: Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
Gene 96, 37-41, 1990
A: title: In vivo genetic engineering: homologous recombination as a tool for plasmid con-
A: reference number: 139772; PMID:91092489; PMID:22655757
A: accession: 139777
A: status: preliminary; translated from GB/EMBL/DBD
A: molecule type: DNA
A: residues: 1-45 <RSS>
A: cross-references: GB:M62638; NID:g142514; PIDN:AAA22242.1; PID:g142515
C: comment: Alpha-amy1aase genes have been found on plasmids and in multiple copies on the
A: gene: amyS
A: genome: plasmid
A: start codon: GTG

A:Molecule type: DNA
 A:Residues: 1-493 <NAR>
 A:Cross-references: EMBL:X60779; NID:G939411; PIDN:CAA43194.1; PID:G939412
 C:Genetics:
 A:Gene: amyE
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: alpha-amylose, amyloidogenic type; alpha-amylose core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:200-333/Domain: alpha-amylose core homology <AMY>

Query Match 47.3%; Score 1262; DB 2; Length 493;
 Best Local Similarity 47.6%; Pred. No. 5.9e-82;
 Matches 230; Conservative 75; Mismatches 166; Indels 12; Gaps 3;

```

QY      4 NGTLMQYFEMWMPNDQHRRLQNDSDAYLAHGITAATWIPAYKGTSGADVGAYDLYD 63
DB      4 NHTMMQFEMHLADGDHMKRLAEMAEELAKAGIDITWVBPVTKAVSAADTGYGYDLYD 63
QY      64 LGEPHQKGTVTKYGTKEGLQSAIKSLHSRDINYYGCVVNNHKGADATEDVTAAYVDDPA 123
DB      64 LGEPDQKGTVTKYGTKEGLLEIAECQKNGIANVYDVLNNHKGADATEDVTAAYVDDPA 123
QY      124 DNRNVTSGEHLIKATHTHPPRGSTYSDFKMHYTFDGTMDSEKLNRIYKFG--KA 181
DB      124 DRTKEISPEPEIEGWTKEFTFGDQYSSFKMSEHNGTDFPAREERTGVERIAGENK 183
QY      182 WDMEVSNENGVYDLYMADIDYDHPDVAAEIKWGTAYANELQDGFRLDAVXHKISPL 241
DB      184 WNEVVDDEFGYDLYMADIDYDHPDVAAEIKWGTAYANELQDGFRLDAVXHKISPL 241
QY      242 RDVNNHREKTKGKMFVAEYQNDGALENYANKNNHNSVDDVPLHQTFAASTQGGG 301
DB      244 KEFAEYTRKGGQFYVYVGEFMSNNDACREPLDVTQIDLVLAHKLHSAKSGD 303
QY      302 YDMKRLNGTVVSGHPLKSVTFVNDHDTQPGQSLSTVQTFKPLAYATLTRESGPGV 361
DB      304 FDLKIPDPLTVQHPHVAATFVDNDSQHEALBSMIGWFERSAVALTLRRGGYPTV 363
QY      362 FYGDMYGTGK---DSQRETPALKHTEPLKARKQYAYAGADYDHDHDIYGTREDS 417
DB      364 FYGDIYGGEPYDGGKEI-----DILLARCKKAYGEQDYDFDHANTTGWRRGYE 417
QY      418 SVANSGLAALTDPGCAKMYVGRQVAGETWHDITGNSEPVINSSEMGCFHYNGSV 477
DB      418 EIEGSGCAVVISNGDDGKMFGEHRAAGEVWVDLTRSCDDQTTEEDMATFHYCGGV 477
QY      478 SIY 480
DB      478 SVM 480

```

RESULT 9

alpha-amylose (imported) - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C:Accession: AK2079

R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriyuchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genome Sequence of the filamentous Nitrogen-fixing Cyanobacterium Anabaena Res. 8, 205-213, 2001

A:Reference number: AB1807; MUID:21595285; PMID:1175840

A:Accession: AK2079

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-492 <KUR>

A:Cross-references: GB:BA000019; PIDN:BAW73889.1; PID:gl17131281; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr2190

C:Superfamily: alpha-amylose, amyloidogenic type; alpha-amylose core homology

Query Match 46.7%; Score 1244; DB 2; Length 492;
 Best Local Similarity 47.5%; Pred. No. 1.1e-80;
 Matches 234; Conservative 84; Mismatches 161; Indels 14; Gaps 6;

```

QY      1 ANNGTLMQYFEMWMPNDQHRRLQNDSDAYLAHGITAATWIPAYKGTSGADVGAY 59
DB      2 AQNKGTFEMHLYHNDNLMSKVASAPBLADGATMMIPRAYKGTSGADVGAY 61
QY      60 DLYDLGEPHQKGTVTKYGTKEGLQSAIKSLHSRDINYYGCVVNNHKGADATEDVTA 119
DB      62 DLPDLGEPDQKGTVTKYGTKEGLLEIAECQKNGIANVYDVLNNHKGADATEDVTA 121
QY      120 VDPADNRNVTSGEHLIKATHTHPPRGSTYSDFKMHYTFDGTMDSEKLNRIYK 177
DB      122 FPODDLNRNPGGLQDITKITHNPPRGQKYSNFMHMHFDVADVNNHSGDSYVLL 181
QY      178 QGRAMDVSNENGVYDLYMADIDYDHPDVAAEIKWGTAYANELQDGFRLDAVXHK 237
DB      182 EGNKFDVYALKGNFAYLMGCDLDFQNEWVAGETVYWGKCLDTTKVDGFRIDAKHS 241
QY      238 FSLRLQVNNHREKTKGKMFVAEYQNDGALENYANKNNHNSVDDVPLHQTFAAS 297
DB      242 TWFFPEWIDLEHSHAKDLPWGEFTWYNDITLLMYVAVRGKMSVFPVPLHNFHASK 301
QY      298 QGGYDMKRLNGTVVSGHPLKSVTFVNDHDTQPGQSLSTVQTFKPLAYATLTRESG 357
DB      302 SGQYDMKRLNGTVVSGHPLKSVTFVNDHDTQPGQSLSTVQTFKPLAYATLTRESG 361
QY      358 YPOVFGDMYGTGK---DSQRETPALKHTEPLKARKQYAYAGADYDHDHDIY 409
DB      362 YPOVFGDMYGTGK---DSQRETPALKHTEPLKARKQYAYAGADYDHDHDIY 421
QY      410 GWTREDDSSVANSGLAALTDPGCAKMYVGRQVAGETWHDITGNSEPVINSSEMG 469
DB      422 GWTREDDSSVANSGLAALTDPGCAKMYVGRQVAGETWHDITGNSEPVINSSEMG 478
QY      470 FHNNGSVSYLYQ 482
DB      479 FRCLGSSVSVMVQ 491

```

RESULT 10

alpha-amylose (imported) - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae

C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001

C:Accession: G95160

R:Tellet, R.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidrich, J.D.; Umayam, L.A.; White, O.; Salberg, S.T.; Lewis, M.R.; Radune, D.; Holtzapple, I.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A95000; MUID:2157209; PMID:11463916

A:Accession: G95160

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-484 <KUR>

A:Cross-references: GB:AE005672; PIDN:AAK75480.1; PID:gl4972868; GSPDB:GN00164; TIGR:SP4

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SPI382

C:Superfamily: alpha-amylose, amyloidogenic type; alpha-amylose core homology

Query Match 46.2%; Score 1233; DB 2; Length 484;

Best Local Similarity 48.6%; Pred. No. 6.6e-80;

Matches 234; Conservative 72; Mismatches 167; Indels 8; Gaps 4;

```

QY      4 NGTLMQYFEMWMPNDQHRRLQNDSDAYLAHGITAATWIPAYKGTSGADVGAYDLYD 63
DB      3 NGTLMQYFEMHLYHNDNLMSKVASAPBLADGATMMIPRAYKGTSGADVGAYDLYD 62

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```

QY 64 LGFHHKGTVRKTKYKKGELQSAIKSLHSRDINVDVYINHGKAGATEDVTAVEVPA 123
DB 63 LGFHHKGTVRKTKYKKGELQSAIKSLHSRDINVDVYINHGKAGATEDVTAVEVPA 122
QY 124 DNRNVTSGEHLIKAMTHFHPGRGSTYSDFKMHWYFPGDTWDDESKLRIRYKFGQ--KA 181
DB 123 DRIVELGEPTINGWISFTEFDGRQDTYNGFHHMWHFETGDDAKRSKSGIILIQDNKG 182
QY 182 WDME--VSNENGVYDLYMADIDYDHPVAAEIKKGTWYANELQDGRDLAVYHAKRS 239
DB 183 WANEELVDNENGVYDLYMADIDYDHPVAAEIKKGTWYANELQDGRDLAVYHAKRS 242
QY 240 FLDMVNHVEKTKGEMFTVAEYQNDLGALENYLNKTNFNSVFPVPLHYOFHAASTOG 299
DB 243 FMRNFIKMEKXGDDPYVGEFNNPDKEANLDYLEKTEHEPDLVDRHLQNLFEASQAG 302
QY 300 GGYDMRKLLNGTVYSKAPLKSVTFFVDNHDTPQSGSESTVQTFKPLAYAFILTRSGYP 359
DB 303 ANYDLRGIFDLSLVEKPDKAVTFVDNHDTPQSGSESTVQTFKPLAYAFILTRSGYP 362
QY 360 QVFYGDWYGTGKDSQREIPALKXIEPILKARKQYAVGAOHDFEDHDIVGMTRREGSSV 419
DB 363 CVFYGDYGGISGQYAOQ--DFKEILDRLAIRKDLAYGEONDYFDHANCIGWRSAGEN- 419
QY 420 ANSGLAALITDPGAKRMVYVGRONAGETWHDITGNRSEPVVINSGEWGFHYNGGSVSI 479
DB 420 -QSPIAVLISNDQNSKSMFVGQEWMTQTFVDLIGHQGVTLDEGGYGFVPSARSVS 478
QY 480 Y 480
DB 479 W 479

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RESULT 11

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F98026
Alpha-amylase (EC 3.2.1.1) precursor (imported) - Streptococcus pneumoniae (strain R6)
C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C/Accession: F98026
R/Hoskins, J.A.; Albom Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
R.; R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.D.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; MUID:21429245; PMID:11544234
A/Accession: F98026
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-484 <KUR>
A/Cross-references: GB:AE007317; PIDN:AAU0043.1; PID:G15458876; GSPDB:GN00174
C/Genetics:
A/Gene: amy
C/Superfamily: alpha-amylase, amyloliquefaciens type, alpha-amylase core homology
C/Keywords: glycosidase; hydrolase

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```

Query Match 46.1%; Score 1228; DB 2; Length 484;
Best Local Similarity 48.2%; Pred. No. 1.5e-79;
Matches 232; Conservative 75; Mismatches 166; Indels 8; Gaps 4;
QY 4 NGTLMQYFEWYMPNDGQHRRLQNDASVYLAHGITAVMIPRAYKTSQA-DVGYGAYDLYD 63
DB 3 NGTLMQYFEWYLPDHDGHTRLAENAPHLATLGIISHWMPAPAFATKEXKVGAYDLYD 62
QY 64 LGFHHKGTVRKTKYKKGELQSAIKSLHSRDINVDVYINHGKAGATEDVTAVEVPA 123
DB 63 LGFHHKGTVRKTKYKKGELQSAIKSLHSRDINVDVYINHGKAGATEDVTAVEVPA 122
QY 124 DNRNVTSGEHLIKAMTHFHPGRGSTYSDFKMHWYFPGDTWDDESKLRIRYKFGQ--KA 181
DB 123 DRIVELGEPTINGWISFTEFDGRQDTYNGFHHMWHFETGDDAKRSKSGIILIQDNKG 182

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QY 182 WDME--VSNENGVYDLYMADIDYDHPVAAEIKKGTWYANELQDGRDLAVYHAKRS 239
DB 183 WANEELVDNENGVYDLYMADIDYDHPVAAEIKKGTWYANELQDGRDLAVYHAKRS 242
QY 240 FLDMVNHVEKTKGEMFTVAEYQNDLGALENYLNKTNFNSVFPVPLHYOFHAASTOG 299
DB 243 FMRNFIKMEKXGDDPYVGEFNNPDKEANLDYLEKTEHEPDLVDRHLQNLFEASQAG 302
QY 300 GGYDMRKLLNGTVYSKAPLKSVTFFVDNHDTPQSGSESTVQTFKPLAYAFILTRSGYP 359
DB 303 ANYDLRGIFDLSLVEKPDKAVTFVDNHDTPQSGSESTVQTFKPLAYAFILTRSGYP 362
QY 360 QVFYGDWYGTGKDSQREIPALKXIEPILKARKQYAVGAOHDFEDHDIVGMTRREGSSV 419
DB 363 CVFYGDYGGISGQYAOQ--DFKEILDRLAIRKDLAYGEONDYFDHANCIGWRSAGEN- 419
QY 420 ANSGLAALITDPGAKRMVYVGRONAGETWHDITGNRSEPVVINSGEWGFHYNGGSVSI 479
DB 420 -QSPIAVLISNDQNSKSMFVGQEWMTQTFVDLIGHQGVTLDEGGYGFVPSARSVS 478
QY 480 Y 480
DB 479 W 479

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RESULT 12

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C66781
Alpha-amylase (imported) - Lactococcus lactis subsp. lactis (strain IL1403)
C/Species: Lactococcus lactis subsp. lactis
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C/Accession: C66781
R/Bolotin, A.; Winkler, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A/Reference number: A86625; MUID:21235186; PMID:11337471
A/Accession: C66781
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-491 <STO>
A/Cross-references: GB:AE005176; PID:G12724224; PIDN:AK05349.1; GSPDB:GN00146
A/Experimental source: strain IL1403
C/Genetics:
A/Gene: amy
C/Superfamily: alpha-amylase, amyloliquefaciens type, alpha-amylase core homology

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Query Match 41.6%; Score 1108; DB 2; Length 491;
Best Local Similarity 41.7%; Pred. No. 5e-71;
Matches 204; Conservative 93; Mismatches 168; Indels 24; Gaps 7;
QY 6 TLMQYFEWYMPNDGQHRRLQNDASVYLAHGITAVMIPRAYKTSQA-DVGYGAYDLYD 64
DB 3 TLMQYFEWYLPDHDGHTRLAENAPHLATLGIISHWMPAPAFATKEXKVGAYDLYD 62
QY 65 LGFHHKGTVRKTKYKKGELQSAIKSLHSRDINVDVYINHGKAGATEDVTAVEVPA 123
DB 63 LGFHHKGTVRKTKYKKGELQSAIKSLHSRDINVDVYINHGKAGATEDVTAVEVPA 122
QY 124 DNRNVTSGEHLIKAMTHFHPGRGSTYSDFKMHWYFPGDTWDDESKLRIRYKFGQ--KA 181
DB 123 DRIVELGEPTINGWISFTEFDGRQDTYNGFHHMWHFETGDDAKRSKSGIILIQDNKG 182
QY 182 WDME--VSNENGVYDLYMADIDYDHPVAAEIKKGTWYANELQDGRDLAVYHAKRS 239
DB 183 WANEELVDNENGVYDLYMADIDYDHPVAAEIKKGTWYANELQDGRDLAVYHAKRS 242
QY 240 FLDMVNHVEKTKGEMFTVAEYQNDLGALENYLNKTNFNSVFPVPLHYOFHAASTOG 299
DB 243 FMRNFIKMEKXGDDPYVGEFNNPDKEANLDYLEKTEHEPDLVDRHLQNLFEASQAG 302
QY 300 GGYDMRKLLNGTVYSKAPLKSVTFFVDNHDTPQSGSESTVQTFKPLAYAFILTRSGYP 359
DB 303 ANYDLRGIFDLSLVEKPDKAVTFVDNHDTPQSGSESTVQTFKPLAYAFILTRSGYP 362
QY 360 QVFYGDWYGTGKDSQREIPALKXIEPILKARKQYAVGAOHDFEDHDIVGMTRREGSSV 419
DB 363 CVFYGDYGGISGQYAOQ--DFKEILDRLAIRKDLAYGEONDYFDHANCIGWRSAGEN- 419
QY 420 ANSGLAALITDPGAKRMVYVGRONAGETWHDITGNRSEPVVINSGEWGFHYNGGSVSI 479
DB 420 -QSPIAVLISNDQNSKSMFVGQEWMTQTFVDLIGHQGVTLDEGGYGFVPSARSVS 478
QY 480 Y 480
DB 479 W 479

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QY 362 FYGDMYCTKDSOREIPALKKHIEPI-----LKRKOYVGAQHDYFDHDIYGMTRE 414
DB 360 FWDLYG-----IPS--HNVNPGDNLRTMIALRKNDSEFLRNDYFDHDIYGMTNI 409
QY 415 GDSVSVANSGLAALITDPGAKRMVYGRONAGETWHDITGNSEPVINSBGMGEFHYNG 474
DB 410 LKIDNKYGLSLITKNKNGSSKMIIDKXVAGVYIDLGRHEHITITDQNGAFYVND 469
QY 475 GSVSYIVQR 483
DB 470 GSVSVWVWK 478

RESULT 13

G98247
Cytoplasmic alpha-amylase (1,4-alpha-D-glucan glucohydrolase) [imported] - Agrobacteri
C/Species: Agrobacterium tumefaciens
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C/Accession: G98247
R/Gooder, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tun
A/Reference number: A97359; PMID:21608551; PMID:11743194
A/Accession: G98247

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-506 <KUR>
A/Cross-references: GB:AE007870; PIDN:AAK89505.1; PID:g15159379; GSPDB:GN00170
C/Genetics:
A/Genes: AGR L 1863
A/Map position: linear chromosome
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 40.9%; Score 1091.5; DB 2; Length 506;
Best Local Similarity 44.3%; Pred. No. 7.7e-70;
Matches 219; Conservative 80; Mismatches 178; Indels 17; Gaps 6;

QY 2 NLNG-TLMQYFEMVMPDQGMHRLQNDGSAVLAHSGITAVWIPPAKYGSAQ-DVGYAY 59
DB 11 NMAGRTLDQFFHMYYPDGGKLMSEVAEKASLAKGKITVWMLPPAKGAGSYGVYTY 70
QY 60 DLYDLGEFHOKGVTKYKGTGELQSAIKLSHRDINVGDVVNHKGADATEDVNAVE 119
DB 71 DLEDFGFFDQGVATKYGRALAEAGKTLKONGIRVHDVVLNKHMGADKEKVRVRR 130
QY 120 VDPADRNRVTSGEHLKAMTHFHPGRGSTYSPFKMWHFPGTMDRSRLNRIYKQG 179
DB 131 VNDDRRDIDDEDFPALAVYRFFPRNGKSKFTWDLKCSGVHIEPTEDGIFRLVY 190
QY 180 K---AMDWEVSNENGVYDLYADIDYHPDVAEIKKMGWYANELQDGFRLDAVKH 235
DB 191 EYGDGNEENVEDENGFYDLMGADVEFRRAVYBELKXWGMLSEGVQVDFRLDAKH 250
QY 236 IKESFLADWVNHVREKTKGEMFTVAEYQNDLGALENYLKNFNHSAVVDVLYHQFPA 295
DB 251 IPAMFFPDVGNHRETVDPDLFVVAEYMHFDLEALKSYELVDKQMLFDVALHHSFDD 310
QY 296 STGGGVDKRLKNGVYKPKLSTYFVDNHDTPQGSLESTVQTWTFPLAYAFILRE 355
DB 311 SKGGSDPDKMSIDGSLVSAVPHAVTLVDNHDTPQGSLESTVQWTFPLAYAFILRE 370
QY 356 SGYPOVYFGDMYGTK-----GDSOREIPALKKHIEPIILKARQVYGAQHDYFDH 407
DB 371 EGVPCVYFPLDFTSTYTDGNDENEKIDIPALE-CLPKLIEARSRFANPGTDIDFAS 429
QY 408 IVGWTREDSVANSGLAALITDPGAKRMVYGRONAGETWHDITGNSEPVINSBGM 467
DB 430 CIAFIRHGTDA--PGCVVMSNGEPGEKQADLGPERRASVVRDPLGRHEHITLDES 487
QY 468 GEFVANGGSYSIVY 481
DB 488 GTFPTNGGSYSVWV 501

RESULT 14

AD3038
alpha-amylase amya [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C/Accession: AD3038
R/Wood, D.W.; Setudal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gille, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCelli
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J
ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; PMID:21608550; PMID:11743193
A/Accession: AD3038
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-495 <KUR>
A/Cross-references: GB:AE008689; PIDN:AAL44722.1; PID:g17742354; GSPDB:GN00187
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Genes: amya
A/Map position: linear chromosome
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 40.9%; Score 1090; DB 2; Length 495;
Best Local Similarity 44.4%; Pred. No. 9.6e-70;
Matches 217; Conservative 79; Mismatches 177; Indels 16; Gaps 5;

QY 6 TLMQYFEMVMPDQGMHRLQNDGSAVLAHSGITAVWIPPAKYGSAQ-DVGYAYLXDL 64
DB 5 TLDQFFHMYYPDGGKLMSEVAEKASLAKGKITVWMLPPAKGAGSYGVYTYDLEFDL 64
QY 65 GEFHOKGVTKYKGTGELQSAIKLSHRDINVGDVVNHKGADATEDVNAVEVDPAD 124
DB 65 GEPDQGVATKYGRALAEAGKTLKONGIRVHDVVLNKHMGADKEKVRVRRVDPD 124
QY 125 RNRVSGEHLKAMTHFHPGRGSTYSPFKMWHFPGTMDRSRLNRIYKQG---- 180
DB 125 RTDIDDEDFPALAVYRFFPRNGKSKFTWDLKCSGVHIEPTEDGIFRLVNEBGD 184
QY 181 AMDWEVSNENGVYDLYADIDYHPDVAEIKKMGWYANELQDGFRLDAVKHIFSF 240
DB 185 ENNEEVDQNGNFDYLMGADVEFRRAVYBELKXWGMLSEGVQVDFRLDAKHIPAMF 244
QY 241 LADWVNHVREKTKGEMFTVAEYQNDLGALENYLKNFNHSAVVDVLYHQFPA 300
DB 245 FPDVGNHRETVDPDLFVVAEYMHFDLEALKSYELVDKQMLFDVALHHSFDD 304
QY 301 GYDNRKLTNGVYKPKLSTYFVDNHDTPQGSLESTVQTWTFPLAYAFILRESGYPQ 360
DB 305 DFDMSIFDGLSVSAVPHAVTLVDNHDTPQGSLESTVQWTFPLAYAFILRESGYP 364
QY 361 VFYQDMYGTK-----GDSOREIPALKKHIEPIILKARQVYGAQHDYFDH 412
DB 365 VFYQDMYGTK-----GDSOREIPALKKHIEPIILKARQVYGAQHDYFDH 423
QY 413 REGDSSVANSGLAALITDPGAKRMVYGRONAGETWHDITGNSEPVINSBGMGEFHY 472
DB 424 RGTATDA--PGCVVMSNGEPGEKQADLGPERRASVVRDPLGRHEHITLDES 481
QY 473 NGGSYSIVY 481
DB 482 NGGSYSVWV 490

RESULT 15

B45738
alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium
N/Alternate names: 1,4-alpha-D-glucan glucohydrolase
C/Species: Salmonella typhimurium

C>Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C:Accession: B45738
R:Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.
J. Bacteriol. 174, 6644-6652, 1992
A:Title: Escherichia coli produces a cytoplasmic alpha-amylase, amYA.
A:Reference number: A45738; PMID:93015717; PMID:1400215
A:Accession: B45738
A:Molecule type: DNA
A:Residues: 1-494 <RAH>
A:Cross-references: GB:L01643; NID:G154043; PIDN:AAA27110.1; PID:G154045
C:Genetics:
A:Gene: amYA
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloliquefactors type, alpha-amylase core homology
C:Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation
F:202-335/Domain: alpha-amylase core homology <AMY>
F:239,265,332/Active site: His, Glu, Asp #status predicted

Query Match 39.8%; Score 1060; DB 1; Length 494;
Best Local Similarity 42.4%; Pred. No. 1.3e-67;
Best Local Conservative 88; Mismatches 179; Indels 16; Gaps 6;
Matches 208

QY 4 NGTLMQYFWMYMPNDGQHWRLQNDASVLAHGTAVWIPAYKGTSA-DVGYGAYDLY 62
DB 3 NPTLLQYFHYHYPDGLWSELAEKADGLNDIGINWMLPACKASGGYSGYDTYDLF 62

QY 63 DLGPHKQGTIVRTYGTGKLSQSKLSHRDINVDYVINKGADATEDVTAENVDP 122
DB 63 DLGEPDQGTATYGTGKQLTAIDALKNNIAVLDDVYVNHKMGADKKERIRVQVWQ 122

QY 123 ADNRKRVSGEHLIKAWTHFHPGSGSTYSDFKWHYHFDGTDWDESKLRIRYK---FQ 178
DB 123 DDRQGLDNDIIECGGWTFRYTPPARAGQYSNFIMDYHCFSGIDHIENPDEDGIFKIVNDY 182

QY 179 GKAMDWEVSNENGYDLYADIDYHDPVAALIKNGTWYANELQLDGFRLDAYKHIKF 238
DB 183 GDGWNDDQVDEDMGNFDLNGENIDFRNHAATVEIKYWARVMWECQHCDFRLDAVKHIPA 242

QY 239 SFLRDMVNHVREKNGKEMFTVAEYWNQDGLAENYLNKTNFNSVFDVPLHYQFAASTQ 298
DB 243 WFTYKEMIEHVOAVAPKFLFVAETWSHEVDKLTQTYIDQVQKTMLEFADLPQKFEHPSRQ 302

QY 299 GGGYDMKRLNGTVSKHPLKSVTFVNDHTQPGQSLESTVQTFKPLAYAFILTRBSGY 358
DB 303 GAEDYDMHIFGTLVADPFHATVTVANHDTPQLALEAEPFWEKPLAYALILLRENGV 362

QY 359 PQVFFYGMVGT-----KDSQR-ELPALKHKEPILKARKQYAGAGCHDYFDHHDIVG 410
DB 363 PSVFTYPDLYGASYSDBSGENGTCDVDMFVLTNQDLRLILARQRFHAGIQTLFEDHPNCL 421

QY 411 WTRGDSVANSGLAALITDQPGAKMYVGRQVAGETWHDITGNRSEPVVINSQWGEF 470
DB 422 FSRGTEE--NPGCVVTLNSGDGKTLILGDNYANKTRDFSGNRDSEVYVTVNDQGEATF 479

QY 471 HVNGSGVSIYV 481
DB 480 FCNAGSVSVWV 490

Search completed: May 3, 2004, 20:54:04
Job time: 14.7346 secs

R. Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
 Gene 96, 3-41, 1990
 A>Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con
 A'Reference number: 139772; PMID:91092499; PMID:2265757
 A'Accession: 139772
 A>Status: translated from GB/EMBL/DBJ
 A'Molecule type: DNA
 A'Results: 1-34, 1-1 <OR>
 A'Cross-references: GB:M62637; NID:G142498; PIDN:AAA2232.1; PID:G142499
 R:Kuhn, H.; Fietzek, P.P.; Lampen, J.O.
 J. Bacteriol. 149, 372-373, 1982
 A>Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: compari
 A'Reference number: 826151; PMID:82098050; PMID:6172418
 A'Accession: A26151
 A'Molecule type: protein
 A'Results: 30-37, 'E', '30-41, 'X', '43-47 <KUH>
 R:Machius, M.; Wiegand, G.; Huber, R.
 J. Mol. Biol. 246, 545-558, 1995
 A>Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase at 2
 A'Reference number: 553788; PMID:95182462; PMID:7877175
 A'Accession: 553788
 A'Molecule type: protein
 A'Results: 'D', '220-227 <MAC>
 A>Note: sequence represents amino end of an internal fragment created by a single enzyme
 R:Machius, M.; Wiegand, G.; Huber, R.
 Submitted to the Brookhaven Protein Data Bank, July 1995
 A'Reference number: A65206; PMID:18PL
 A'Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 32-210/222-511
 A>Note: these structural studies suggest 163 is less rather than Arg
 R:Song, H.K.; Huang, K.Y.; Chang, C.; Suh, S.W.
 Submitted to the Brookhaven Protein Data Bank, October 1996
 A'Reference number: A66860; PMID:1VUS
 A'Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-210/222-511
 C'Genetics:
 A:Gene: amyL
 A:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
 C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
 C:Keywords: signal sequence #status predicted <SIG>
 F:1-29/Domains: signal sequence #status predicted <SIG>
 F:30-512/Product: alpha-amylase #status experimental <MPT>
 F:227-360/Domains: alpha-amylase core homology <AM>
 F:113,229,264/Binding site: calcium (Asn, Asp, His) #status experimental
 F:260,290,357/Active site: Asp, Glu, Asp #status experimental
 Query Match 99.5%; Score 2654; DB 1; Length 512;
 Best Local Similarity 99.4%; Pred. No. 9, 8e-181;
 Matches 480; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 361 VFGDMYKQKSGOREIPALKRIEPIILKARQVAYGAOHYFDHDIYGMTRGDSVA 420
 DB 390 VFGDMYKQKSGOREIPALKRIEPIILKARQVAYGAOHYFDHDIYGMTRGDSVA 449
 QY 421 NSGIAALITDPCGAKRMVYGRONAGETWHDNGNSEPVVINSBGMGEFHNNGSVSIX 480
 DB 450 NSGIAALITDPCGAKRMVYGRONAGETWHDITGNSEPVVINSBGMGEFHNNGSVSIX 509
 QY 481 VOR 483
 DB 518 VOR 512
 RESULT 2
 ALBNS
 alpha-amylase (EC 3.2.1.1) precursor - Bacillus amylioliquefaciens
 M'Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C'Species: Bacillus amylioliquefaciens
 C'Date: 30-Nov-1980 #sequence, revision 30-Jun-1997 #ext_change 18-Jun-1999
 C'Accession: A92389; A90307; I39756; I39763; A00643
 R:Takkinen, K.; Petersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen,
 J. Biol. Chem. 258, 1007-1013, 1983
 A>Title: Amino acid sequence of alpha-amylase from Bacillus amylioliquefaciens deduced f
 A'Reference number: A92389; PMID:83108808; PMID:6185474
 A'Accession: A92389
 A'Contents: PUB110
 A'Molecule type: DNA
 A'Results: 1-514 <TK>
 A'Cross-references: GB:U01542; GB:U01543; GB:M12033; GB:M12034; NID:G142428; PIDN:AAA22
 R:Chung, H.S.; Friedberg, F.
 Biochem. J. 185, 387-395, 1980
 A>Title: Sequence of the N-terminal half of Bacillus amylioliquefaciens alpha-amylase.
 A'Reference number: A90307; PMID:80241725; PMID:6156671
 A'Accession: A90307
 A'Molecule type: protein
 A'Results: 32-53, 'I', '55-63, 'L', '65-78, 'D', '80-83, 'S', '85-222 <CH>
 R:Palva, I.; Petersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.
 Gene 15, 43-51, 1981
 A>Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of
 A'Reference number: I39756; PMID:8051236; PMID:6170539
 A'Accession: I39756
 A>Status: translated from GB/EMBL/DBJ
 A'Molecule type: DNA
 A'Results: 1-96 <RBS>
 A'Cross-references: EMBL:V00092; NID:G39297; PIDN:CAA23430.1; PID:G39298
 R:Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.R.C.; Karanen, S.
 Gene 59, 161-170, 1987
 A>Title: Efficient secretion of Bacillus amylioliquefaciens alpha-amylase cells by its o
 A'Reference number: I39763; PMID:88137952; PMID:2690166
 A'Accession: I39763
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A'Molecule type: DNA
 A'Results: 1-39 <R2>
 A'Cross-references: GB:M18424; NID:G142430; PIDN:AAA22192.1; PID:G142431
 C'Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
 C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
 F:1-11/Domains: signal sequence #status predicted <SIG>
 F:32-514/Product: alpha-amylase #status predicted <MPT>
 F:1229-362/Domains: alpha-amylase core homology <AM>
 F:113,229,264/Binding site: calcium (Asn, Asp, His) #status predicted
 F:262,292,359/Active site: Asp, Glu, Asp #status predicted
 Query Match 81.3%; Score 2184; DB 1; Length 514;
 Best Local Similarity 80.3%; Pred. No. 2, 3e-147;
 Matches 388; Conservative 44; Mismatches 49; Indels 2; Gaps 1;

File Copy

QY 63 DGEFHOKGTVRTKYGKELGSAIKSLHSRDINVTGDIYVNHKGADATEMVAEYVNP 122
DB 92 DGEFHOKGTVRTKYGKELGSAIKSLHSRDINVTGDIYVNHKGADATEMVAEYVNP 151
QY 123 ADNRVTSGEHLIKAMTHFHPGRGTSYSDPKMWHYFDGTMDSSRLNRYKE--GOK 180
DB 152 ARNNGTSEYQKKAATDFRFPGRGNTYSDPKMWHYFDGADWDSRKSRLFKRGSGX 211
QY 181 AMDMEVSNENGDYLMYADIDYDHPVAEIKRWGTWANELODGFPLDAVKIKFSF 240
DB 212 AMDMEVSNENGDYLMYADIDYDHPVAEIKRWGTWANELODGFPLDAVKIKFSF 271
QY 241 LRDVNVHREKTEKEMFTAEYVNDLGALENTLNKTNHNSVFDVPLHYQFHAASGOG 300
DB 272 LRDVNVHREKTEKEMFTAEYVNDLGALENTLNKTNHNSVFDVPLHYQFHAASGOG 331
QY 301 GYDMRKLNGTVYSKPLSVTFVNDHDPQGSLESTVQTFPKPLAVAFILTRREGYPO 360
DB 332 GYDMRKLNGTVYSKPLSVTFVNDHDPQGSLESTVQTFPKPLAVAFILTRREGYPO 391
QY 361 VFYGDWYGTGDSOREIPALKEIPILKARKOYAGAQHDYFDHHDIVGTMREGDSVA 420
DB 392 VFYGDWYGTGDSOREIPALKEIPILKARKOYAGAQHDYFDHHDIVGTMREGDSVA 451
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRESEPVINSBGWGFHNVGGSVA 480
DB 452 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRESEPVINSBGWGFHNVGGSVA 511
QY 481 VOR 483
DB 512 VOR 514

RESULT 3

A:alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase
C:Species: Bacillus sp.
C:Date: 31-Mar-1989 #sequence_revision 18-Aug-1995 #ext_change 18-Jun-1999
C:Accession: A27705
R:Tsukamoto, A.; Kikuchi, Y.; Takano, T.; Yamane, K.
B:Biochem. Biophys. Res. Commun. 151, 25-31, 1988
A:Title: Nucleotide sequence of the maltobiose-oxidizing amylase gene from an alkalophilic
A:Reference number: A27705; PMID:88162814; PMID:3258152
A:Accession: A27705
A:Molecule type: DNA
A:Residues: 1-518 <TSU>
A:Cross-references: GB:M18662; NID:G142496; PID:AAA2231.1; PID:G142497
A:Experimental source: Chromosomal DNA of strain 707
A:Note: amino end of mature protein also determined
C:Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosylase; hydrolase; polysaccharide degradation
F:1-33/Domain: signal sequence #status predicted <Sig>
F:134-518/Product: signal sequence #status predicted <Sig>
F:1236-369/Domain: alpha-amylase core homology <AMY>
F:1339-238-272/Binding site: calcium (Asp, Asp, His) #status predicted
F:269-299-366/Active site: Asp, Glu, Asp #status predicted

Query Match 70.5%; Score 1879; DB 1; Length 518;
Best Local Similarity 67.8%; Pred. No. 1e-125;
Matches 329; Conservative 67; Mismatches 79; Indels 10; Gaps 4;

QY 4 NCTLMQYFEMYNPDGQHRRLONDSAYLAEGITRAVWIPPAKGTSGADVGYAYDIYD 63
DB 39 NGTMQYFEMYNPDGQHRRLONDSAYLAEGITRAVWIPPAKGTSGADVGYAYDIYD 98
QY 64 LGEFHOKGTVRTKYGKELGSAIKSLHSRDINVTGDIYVNHKGADATEMVAEYVNP 123

DB 99 LGEFHOKGTVRTKYGKELGSAIKSLHSRDINVTGDIYVNHKGADATEMVAEYVNP 158
QY 124 DNRVTSGEHLIKAMTHFHPGRGTSYSDPKMWHYFDGTMDSSRLNRYKE--GOK 180
DB 159 NRQGVTSGEHLIKAMTHFHPGRGTSYSDPKMWHYFDGTMDSSRLNRYKE--GOK 218
QY 181 AMDMEVSNENGDYLMYADIDYDHPVAEIKRWGTWANELODGFPLDAVKIKFSF 240
DB 219 AMDMEVSNENGDYLMYADIDYDHPVAEIKRWGTWANELODGFPLDAVKIKFSF 278
QY 241 LRDVNVHREKTEKEMFTAEYVNDLGALENTLNKTNHNSVFDVPLHYQFHAASGOG 300
DB 279 LRDVNVHREKTEKEMFTAEYVNDLGALENTLNKTNHNSVFDVPLHYQFHAASGOG 338
QY 301 GYDMRKLNGTVYSKPLSVTFVNDHDPQGSLESTVQTFPKPLAVAFILTRREGYPO 360
DB 339 GYDMRKLNGTVYSKPLSVTFVNDHDPQGSLESTVQTFPKPLAVAFILTRREGYPO 398
QY 361 VFYGDWYGTGDSOREIPALKEIPILKARKOYAGAQHDYFDHHDIVGTMREGDSVA 428
DB 399 VFYGDWYGTGDSOREIPALKEIPILKARKOYAGAQHDYFDHHDIVGTMREGDSVA 453
QY 419 VNSGLAALITDGPAGAKMYVGRONAGETWHDITGNRESEPVINSBGWGFHNVGGSVA 488
DB 454 VNSGLAALITDGPAGAKMYVGRONAGETWHDITGNRESEPVINSBGWGFHNVGGSVA 513
QY 479 VOR 483
DB 514 VOR 518

RESULT 4

A:alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DN1792)
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Bacillus stearothermophilus
C:Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #ext_change 13-Jun-1997
C:Accession: A54541
R:Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
B:EMS Microbiol. Lett. 7, 271-276, 1991
A:Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.
A:Reference number: A54541
A:Accession: A54541
A:Molecule type: DNA
A:Residues: 1-549 <GOR>
A:Cross-references: GB:X59476
A:Experimental source: Chromosomal DNA of strain DN1792
C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on cl
C:Genetics:
A:Start codon: GCG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosylase; heat-stable protein; hydrolase; polysac
F:1-34/Domain: signal sequence #status predicted <Sig>
F:135-549/Product: signal sequence #status predicted <Sig>
F:1235-368/Domain: alpha-amylase core homology <AMY>
F:1339-237-272/Binding site: calcium (Asp, Asp, His) #status predicted
F:268-298-365/Active site: Asp, Glu, Asp #status predicted

Query Match 67.0%; Score 1780.5; DB 1; Length 549;
Best Local Similarity 64.7%; Pred. No. 1e-119;
Matches 314; Conservative 68; Mismatches 98; Indels 5; Gaps 2;

QY 1 ANCTLMQYFEMYNPDGQHRRLONDSAYLAEGITRAVWIPPAKGTSGADVGYAYDIYD 60
DB 36 APNGTMQYFEMYNPDGQHRRLONDSAYLAEGITRAVWIPPAKGTSGADVGYAYDIYD 95
QY 61 LGEFHOKGTVRTKYGKELGSAIKSLHSRDINVTGDIYVNHKGADATEMVAEYVNP 120
DB 96 LGEFHOKGTVRTKYGKELGSAIKSLHSRDINVTGDIYVNHKGADATEMVAEYVNP 155

Query Match 99.3%; Score 2648; DB 1; Length 512;
 Best Local Similarity 99.2%; Pred. No. 9.5e-187;
 Matches 479; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 ANDGTLMQYFWMNPNQDQHRRLQNDQALYLAHGTITVWLPAYKGTSGQADVGKAYD 60
 30 AALNGTLMQYFWMNPNQDQHRRLQNDQALYLAHGTITVWLPAYKGTSGQADVGKAYD 89
 61 LVDLGEFHQGTGTRTKGTGKELQSAIKSLHSDINVDVYINHGADATETDVAEV 120
 90 LVDLGEFHQGTGTRTKGTGKELQSAIKSLHSDINVDVYINHGADATETDVAEV 149
 121 DPADNRVTSGEHLINQWTHFHPFGSGTYSDFKWHYHFDGTDWDESKLNRIYKFGK 180
 150 DPADNRVTSGEHLINQWTHFHPFGSGTYSDFKWHYHFDGTDWDESKLNRIYKFGK 209
 181 AMDWESNNGNDYIMVADIDYHDPVAAETKRWGTWANELOLDGPRLDVAKIKTSF 240
 210 AMDWESNNGNDYIMVADIDYHDPVAAETKRWGTWANELOLDGPRLDVAKIKTSF 269
 241 LRDVNVHVEKTKEMETVAEYQNDLQALBNYLNKTNFNSVFDVPLHYQFHAASQGG 300
 270 LRDVNVHVEKTKEMETVAEYQNDLQALBNYLNKTNFNSVFDVPLHYQFHAASQGG 329
 301 GYMRGLNGTIVSKPKLSVTVDNHDTPQGSLESTQTPPKPLAVAFITRESGYRQ 360
 330 GYMRGLNGTIVSKPKLSVTVDNHDTPQGSLESTQTPPKPLAVAFITRESGYRQ 389
 361 VFQGDYVTKGDSQREIPALKKIIPILKAKQYAGAOHDYFHHKVTGWTREGDSVA 420
 390 VFQGDYVTKGDSQREIPALKKIIPILKAKQYAGAOHDYFHHKVTGWTREGDSVA 449
 421 NSGLALLITDPGAGKMYGRONAGETWHDITGNRSEPVYINSEGMGFHYNGSVYI 480
 450 NSGLALLITDPGAGKMYGRONAGETWHDITGNRSEPVYINSEGMGFHYNGSVYI 509
 481 VQR 483
 510 VQR 512

RESULT 2
 ID - AMY_BACAM STANDARD; PRT; 514 AA.
 AC P00692;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Alpha-amy-lase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase).
 OS Bacillus amyloliquefaciens.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1390;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IH;
 RX MEDLINE=83108808; PubMed=6185474;
 RA Takkinen K., Petersson R.F., Kalkkinen N., Palva I., Soederlund H.,
 RA Kaerlahti L.;
 RA "Amino acid sequence of alpha-amy-lase from Bacillus amyloliquefaciens
 RA deduced from the nucleotide sequence of the cloned gene,"
 RT J. Biol. Chem. 258:1007-1013 (1983).
 RL [2]
 RP SEQUENCE OF 32-222.
 RX MEDLINE=80241725; PubMed=6156671;
 RA Chung H.S., Friedberg F.;
 RA "Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-
 RT amy-lase,"
 RL J. Biochem. J. 185:387-395 (1980).
 [3]
 RP SEQUENCE OF 1-96 FROM N.A.
 RX MEDLINE=82051296; PubMed=6170539;

RA Palva I., Petersson R.F., Kalkkinen N., Lehtovaara P., Sarvas M.,
 RA Soederlund H., Takkinen K., Kaerlahti L.;
 RT "Nucleotide sequence of the promoter and NH2-terminal signal peptide
 RT region of the alpha-amy-lase gene from Bacillus amyloliquefaciens,"
 RL Gene 15:43-51 (1981).
 RN [4]
 RP SEQUENCE OF 1-39 FROM N.A.
 RX MEDLINE=88137952; PubMed=2830166;
 RA Riihonen L., Hackman P., Lehtovaara P., Knowles J.K.C., Kaerlahti S.,
 RT "Efficient secretion of Bacillus amyloliquefaciens alpha-amy-lase by
 RT its own signal peptide from Saccharomyces cerevisiae host cells,"
 RL Gene 59:161-170 (1987).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-331.
 RX MEDLINE=20384196; PubMed=10924103;
 RA Berezowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen H.,
 RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
 RT "Structural analysis of a chimeric bacterial alpha-amy-lase."
 RT High-resolution analysis of a native and ligand complexes."
 RL Biochemistry 39:9099-9107 (2000).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
 CC -1- SUBUNIT: Monomer.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).

DR EMBL; J01542; AAA22191.1; -;
 DR EMBL; V00092; CA23430.1; -;
 DR EMBL; A20154; CA01489.1; -;
 DR EMBL; M18424; AAA22192.1; -;
 DR PIR; A92389; ALBSN.
 DR PDB; 1B3X; 21-JUN-01.
 DR PDB; 1B3Z; 24-JUN-03.
 DR PDB; 1B40; 24-JUN-03.
 DR PDB; 1B43; 21-JUN-01.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amy-lase; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.
 DR SMART; SM00642; Amy; 1.
 KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 KW Signal; 3D-structure.
 FT CHAIN 1 31
 FT ACT_SITE 32 514
 FT ACT_SITE 262 292
 FT ACT_SITE 359 359
 FT METAL 133 133
 FT METAL 190 190
 FT METAL 212 212
 FT METAL 214 214
 FT METAL 225 225
 FT METAL 231 231
 FT METAL 233 233
 FT METAL 235 235
 FT METAL 266 266
 FT METAL 331 331
 FT METAL 438 438
 FT METAL 461 461
 FT METAL 461 461
 FT CONFLICT 54 54
 FT CONFLICT 64 64
 FT CONFLICT 79 79
 FT CONFLICT 84 84

ALPHA-AMYLASE.
 BY SIMILARITY.
 CALCITUM 1.
 CALCITUM 2 AND SODIUM.
 CALCITUM 2 (VIA CARBOXYL OXYGEN).
 CALCITUM 2 AND SODIUM.
 CALCITUM 1 AND SODIUM.
 CALCITUM 1 AND SODIUM.
 CALCITUM 2.
 CALCITUM 1 (VIA CARBOXYL OXYGEN).
 CALCITUM 3 (VIA CARBOXYL OXYGEN).
 CALCITUM 3 (BY SIMILARITY).
 CALCITUM 3 (BY SIMILARITY).
 L -> I (IN REF. 2).
 I -> L (IN REF. 2).
 S -> D (IN REF. 2).
 G -> S (IN REF. 2).

SQ SEQUENCE 514 AA; 58403 MW; 3DE66B3FB5CDE7E CRC64;
 Query Match 81.9%; Score 2184; DB 1; Length 514;
 Best Local Similarity 80.3%; Pred. No. 9, 8e-153;
 Matches 388; Conservative 44; Mismatches 49; Indels 2; Gaps 1;

QY 3 LAGTLMQYFVWYVNDGQWRRLONDASVLAHGTAVIPPAKYGTSQADVYGADLY 62
 DB 32 VNGTLMQYFVWYVNDGQWRRLONDASVLAHGTAVIPPAKYGTSQADVYGADLY 91
 QY 63 DLGEFQKGTAVTKYGTGKLSQSAIKSLHSDINIVYGVVINEKSGADATEDVAVENP 122
 DB 92 DLGEFQKGTAVTKYGTGKLSQSAIKSLHSDINIVYGVVINEKSGADATEDVAVENP 151
 QY 123 ADNRVISEGHLIKANTHFFPRGSTYSDPKMWHYHPGDVMDSSRLNTLYF--QK 180
 DB 152 ANNOBTSESYQIKAWTDPRFPGRGNTYSDPKMWHYHPGDVMDSSRLNTLYF--QK 211
 QY 181 AMDWEVSNENGVNDYLVADIDYDHPDVAEIKRMGTWYANELQDGFRLDAVGHKFSF 240
 DB 212 AMDWEVSENGVNDYLVADIDYDHPDVAEIKRMGTWYANELQDGFRLDAVGHKFSF 271
 QY 241 LRPVWVHVEKTKEMFTVAEYONDGLALNTYKTNPNHSPVPPVPHYQFHAASVQGG 300
 DB 272 LRPVWVHVEKTKEMFTVAEYONDGLALNTYKTNPNHSPVPPVPHYQFHAASVQGG 331
 QY 301 GYDMRKLNTGVVSKPELKVTFVNDHDTQPGQSLSTVQTFKELAYAFILTESGYPO 360
 DB 332 GYDMRKLNTGVVSKPELKVTFVNDHDTQPGQSLSTVQTFKELAYAFILTESGYPO 391
 QY 361 VFGVDMYGTGDSQREIPALAKHIEPILAKKQYAYGAOHDFVNDLVGMTREGDSSVA 420
 DB 392 VFGVDMYGTGDSQREIPALAKHIEPILAKKQYAYGAOHDFVNDLVGMTREGDSSVA 451
 QY 421 NSGLAALITDGPAGARMYVGRONAGETWHDITGNRSEPVVINSGEWEPHYNGGSYV 480
 DB 452 NSGLAALITDGPAGARMYVGRONAGETWHDITGNRSEPVVINSGEWEPHYNGGSYV 511
 QY 481 VQR 483
 DB 512 VQR 514

RESULT 3
 AMT6_BACS7
 ID AMT6_BACS7 STANDARD; PRT; 518 AA.
 AC P1951;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2000 (Rel. 42, Last annotation update)
 DE Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98) (66-amy1ase)
 DE Maltotetraose-producing amy1ase (Exo-maltotetraohydrolase).
 OS Bacillus sp. (strain 707).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxID:1416;
 RN [1]
 RE SEQUENCE FROM N.A. AND SEQUENCE OF 34-36.
 RX MEDLINE=86162514; PubMed=258152;
 RA Teukanoto A., Kimura K., Ishii Y., Takano T., Yamane K.;
 RA "Nucleotide sequence of the maltotetraose-producing amy1ase gene from
 RA an alkalophilic Bacillus sp. #707 and structural similarity to
 RA liquefying type alpha-amy1ases."
 RL Biochem. Biophys. Res. Commun. 151:35-31(1988).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages
 CC in amylose polysaccharides so as to remove successive
 CC maltotetraose residues from the non-reducing chain ends.
 CC -1- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (by
 CC similarity).
 CC -1- PATHWAY: Starch degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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CC EMBL, M18662, AAA2231.1, ..
 DR PIR, A27705, A27705.
 DR HSP, P06278, IY08.
 DR InterPro: IPR006589; AIP, amy1 cat. sub.
 DR InterPro: IPR006047; Alpha amy1 cat.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam: PF00128; alpha-amy1ase; 1.
 DR PRINTS: PR00110; ALPHAMYLASE.
 DR SMART: SM00642; Amy; 1.
 KW Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.
 FT SIGNAL 1 33
 FT CHAIN 34 518
 FT ACT SITE 289 269
 FT ACT SITE 271 273
 FT ACT SITE 366 366
 FT METAL 139 139
 FT METAL 196 196
 FT METAL 219 219
 FT METAL 221 221
 FT METAL 232 232
 FT METAL 238 238
 FT METAL 240 240
 FT METAL 242 242
 FT METAL 273 273
 SQ SEQUENCE 518 AA; 59009 MW; 3A961E21612682C4 CRC64;
 Query Match 70.5%; Score 1879; DB 1; Length 518;
 Best Local Similarity 67.8%; Pred. No. 2, 3e-130;
 Matches 329; Conservative 67; Mismatches 79; Indels 10; Gaps 4;

QY 4 NGTLMQYFVWYVNDGQWRRLONDASVLAHGTAVIPPAKYGTSQADVYGADLY 63
 DB 39 NGTLMQYFVWYVNDGQWRRLONDASVLAHGTAVIPPAKYGTSQADVYGADLY 98
 QY 64 DLGEFQKGTAVTKYGTGKLSQSAIKSLHSDINIVYGVVINEKSGADATEDVAVENP 123
 DB 99 DLGEFQKGTAVTKYGTGKLSQSAIKSLHSDINIVYGVVINEKSGADATEDVAVENP 158
 QY 124 ADNRVISEGHLIKANTHFFPRGSTYSDPKMWHYHPGDVMDSSRLNTLYF--QK 180
 DB 159 ADNRVISEGHLIKANTHFFPRGSTYSDPKMWHYHPGDVMDSSRLNTLYF--QK 218
 QY 181 AMDWEVSNENGVNDYLVADIDYDHPDVAEIKRMGTWYANELQDGFRLDAVGHKFSF 240
 DB 219 AMDWEVSENGVNDYLVADIDYDHPDVAEIKRMGTWYANELQDGFRLDAVGHKFSF 278
 QY 241 LRPVWVHVEKTKEMFTVAEYONDGLALNTYKTNPNHSPVPPVPHYQFHAASVQGG 300
 DB 272 LRPVWVHVEKTKEMFTVAEYONDGLALNTYKTNPNHSPVPPVPHYQFHAASVQGG 338
 QY 301 GYDMRKLNTGVVSKPELKVTFVNDHDTQPGQSLSTVQTFKELAYAFILTESGYPO 360
 DB 339 GYDMRKLNTGVVSKPELKVTFVNDHDTQPGQSLSTVQTFKELAYAFILTESGYPO 398
 QY 361 VFGVDMYGTGDSQREIPALAKHIEPILAKKQYAYGAOHDFVNDLVGMTREGDSSVA 420
 DB 392 VFGVDMYGTGDSQREIPALAKHIEPILAKKQYAYGAOHDFVNDLVGMTREGDSSVA 453
 QY 421 NSGLAALITDGPAGARMYVGRONAGETWHDITGNRSEPVVINSGEWEPHYNGGSYV 480
 DB 454 NSGLAALITDGPAGARMYVGRONAGETWHDITGNRSEPVVINSGEWEPHYNGGSYV 513
 QY 479 IYVQR 483

Tue May 4 14:34:48 2004

us-10-644-187-4.rpt

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 20:44:58 ; Search time 34.1232 Seconds
(without alignments)

4438.289 Million cell updates/sec

Title: US-10-644-187-4

Perfect score: 2624

Sequence: 1 VNGTLMQYFMYTNDGQHW.....KIGSDGWEFHVNDGSVSIY 480

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SPTREMBL 25:*

1: sp_archaea:*\n2: sp_bacteria:*\n3: sp_fungi:*\n4: sp_human:*\n5: sp_invertebrate:*\n6: sp_mammal:*\n7: sp_mhc:*\n8: sp_organelle:*\n9: sp_phage:*\n10: sp_plant:*\n11: sp_protist:*\n12: sp_virus:*\n13: sp_vertebrate:*\n14: sp_unclassified:*\n15: sp_virus:*\n16: sp_bacterioph:*\n17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2061	78.5	519	2 Q9ROT8	Q9ROT8 cytophaga s
2	1947	74.2	513	16 Q81A54	Q81A54 bacillus ce
3	1946	74.2	513	2 Q9A054	Q9A054 bacillus me
4	1914	72.9	513	16 Q81Y04	Q81Y04 bacillus an
5	1836	70.0	516	2 Q82839	Q82839 bacillus sp
6	1767.5	67.4	549	2 Q31193	Q31193 bacillus st
7	1766.5	67.3	549	2 Q9KXV6	Q9KXV6 bacillus st
8	1762.5	67.2	521	2 P71034	P71034 bacillus sp
9	1749.5	66.7	613	2 Q59222	Q59222 bacillus sp
10	1614.5	61.5	501	2 Q93149	Q93148 bacillus sp
11	1474.5	56.2	507	16 Q87H66	Q87H66 vibrio para
12	1359	51.8	481	16 Q89YF1	Q89YF1 bacteroides
13	1253	47.8	493	2 Q03657	Q03657 bacillus ci
14	1217	46.4	484	16 Q97049	Q97049 streptococc
15	1212	46.2	484	16 Q8DPC8	Q8DPC8 streptococc
16	1206.5	46.0	488	16 Q8B696	Q8B696 streptococc

17	1206.5	46.0	488	16 Q8B0M2	Q8B0M2 streptococc
18	1205.5	45.9	486	16 Q8D708	Q8D708 streptococc
19	1197	45.6	492	16 Q8YU21	Q8YU21 anabaena sp
20	1190.5	45.4	484	2 Q05083	Q05083 streptococc
21	1182.5	45.1	486	2 Q68875	Q68875 streptococc
22	1177.5	44.9	485	2 Q53786	Q53786 streptococc
23	1127	42.9	491	16 Q9CGS9	Q9CGS9 lactococc
24	1057.5	40.3	529	3 Q877B1	Q877B1 aspergillus
25	1050	40.0	506	16 Q8U916	Q8U916 agrobacteri
26	1006	38.3	494	16 Q8Z5S5	Q8Z5S5 salmonella
27	1000	38.1	495	16 Q8F5I8	Q8F5I8 escherichia
28	999	38.1	495	16 Q8XB86	Q8XB86 escherichia
29	989	37.7	495	16 Q7UAB0	Q7UAB0 shigella fl
30	987	37.6	495	16 Q83R40	Q83R40 shigella fl
31	966	36.9	469	1 O50200	O50200 thermococc
32	944.5	35.8	461	1 Q8NKR5	Q8NKR5 thermococc
33	940.5	35.3	461	1 Q33476	Q33476 pyrococcus
34	936.5	35.3	457	1 Q33647	Q33647 thermococc
35	936.5	35.3	460	1 Q3P9L0	Q3P9L0 pyrococcus
36	936.5	35.3	460	1 Q8B452	Q8B452 pyrococcus
37	936.5	35.3	461	1 Q8NKR4	Q8NKR4 thermococc
38	936.5	35.3	461	1 Q8U319	Q8U319 pyrococcus
39	936.5	35.3	461	1 Q8J7K3	Q8J7K3 uncultured
40	936.5	35.3	461	1 Q9C8R6	Q9C8R6 arabidopsis
41	936.5	35.3	461	1 Q94A41	Q94A41 arabidopsis
42	936.5	35.3	461	1 Q94A41	Q94A41 oryza sativ
43	936.5	35.3	461	1 Q8L0K4	Q8L0K4 oryza sativ
44	936.5	35.3	461	1 Q9ZP43	Q9ZP43 phaseolus v
45	936.5	35.3	461	1 Q7X9T1	Q7X9T1 phaseolus v
	322	12.3	416	10 Q8LU06	Q8LU06 musa acumin

ALIGNMENTS

ID	Query Match	Length	DB ID	Description
Q9ROT8	78.5	519	2 Q9ROT8	Q9ROT8 cytophaga s
Q9ROT8	74.2	513	16 Q81A54	Q81A54 bacillus ce
Q9ROT8	74.2	513	2 Q9A054	Q9A054 bacillus me
Q9ROT8	72.9	513	16 Q81Y04	Q81Y04 bacillus an
Q9ROT8	70.0	516	2 Q82839	Q82839 bacillus sp
Q9ROT8	67.4	549	2 Q31193	Q31193 bacillus st
Q9ROT8	67.3	549	2 Q9KXV6	Q9KXV6 bacillus st
Q9ROT8	67.2	521	2 P71034	P71034 bacillus sp
Q9ROT8	66.7	613	2 Q59222	Q59222 bacillus sp
Q9ROT8	61.5	501	2 Q93149	Q93148 bacillus sp
Q9ROT8	56.2	507	16 Q87H66	Q87H66 vibrio para
Q9ROT8	51.8	481	16 Q89YF1	Q89YF1 bacteroides
Q9ROT8	47.8	493	2 Q03657	Q03657 bacillus ci
Q9ROT8	46.4	484	16 Q97049	Q97049 streptococc
Q9ROT8	46.2	484	16 Q8DPC8	Q8DPC8 streptococc
Q9ROT8	46.0	488	16 Q8B696	Q8B696 streptococc

Query Match: 78.5%
Best Local Similarity: 75.4%
Matches: 361, Conserved: 48, Mismatches: 70, Indels: 0, Gaps: 0

Score: 2061; DB 2; Length 519;
Pred. No. 3,8e-134

QY 62 LGFEQKGVTRTKYKTSKELDAGISLHNRNOVYDVLNHRKAGADATEDYTAVERNPA 121
 DB 98 LGFEQKGVTRTKYKTSKELDAGISLHNRNOVYDVLNHRKAGADATEDYTAVERNPA 157
 QY 122 NRNOETSEEVQIAQWDFRPPRGNTYSDPKMWHYFDGADWDESKISRIKFRGEGKA 181
 DB 158 NRNOETSEEVQIAQWDFRPPRGNTYSDPKMWHYFDGADWDESKISRIKFRGEGKA 217
 QY 182 WDEVESENENYDYLWADYDHPDVVAETKKGIWYANELSLDGFRLDAVGHIDHEYL 241
 DB 218 WDEVESENENYDYLWADYDHPDVVAETKKGIWYANELSLDGFRLDAVGHIDHEYL 277
 QY 242 RDVQAVRQATGKEMFTVAEYQNNAGKLENTYKTSFNOSVDFVPLHFNLOAASSQGG 301
 DB 278 RDVQAVRQATGKEMFTVAEYQNNAGKLENTYKTSFNOSVDFVPLHFNLOAASSQGG 337
 QY 302 YDMRRLDGTVAVRHPEKATFVENHDTOPGQSLSTVQTFEKLAYAFILITRESGYPOV 361
 DB 338 YDMRRLDGTVAVRHPEKATFVENHDTOPGQSLSTVQTFEKLAYAFILITRESGYPOV 397
 QY 362 FYGDMYTGKTSPEKIPSLKDNIEPLIKARKEYAYGPOHDYIHDPVIGWTRGDSGA 421
 DB 398 FYGDMYTGKTSPEKIPSLKDNIEPLIKARKEYAYGPOHDYIHDPVIGWTRGDSGA 457
 QY 422 SGLAALITDPPGSKMVAAGLKNAGETWYDITGNRSDTYKISDGGGEFHVNDGSYSIY 480
 DB 458 SGLAALITDPPGSKMVAAGLKNAGETWYDITGNRSDTYKISDGGGEFHVNDGSYSIY 516

RESULT 2

QY 62 LGFEQKGVTRTKYKTSKELDAGISLHNRNOVYDVLNHRKAGADATEDYTAVERNPA 121
 DB 98 LGFEQKGVTRTKYKTSKELDAGISLHNRNOVYDVLNHRKAGADATEDYTAVERNPA 157
 QY 122 NRNOETSEEVQIAQWDFRPPRGNTYSDPKMWHYFDGADWDESKISRIKFRGEGKA 181
 DB 158 NRNOETSEEVQIAQWDFRPPRGNTYSDPKMWHYFDGADWDESKISRIKFRGEGKA 217
 QY 182 WDEVESENENYDYLWADYDHPDVVAETKKGIWYANELSLDGFRLDAVGHIDHEYL 241
 DB 218 WDEVESENENYDYLWADYDHPDVVAETKKGIWYANELSLDGFRLDAVGHIDHEYL 277
 QY 242 RDVQAVRQATGKEMFTVAEYQNNAGKLENTYKTSFNOSVDFVPLHFNLOAASSQGG 301
 DB 278 RDVQAVRQATGKEMFTVAEYQNNAGKLENTYKTSFNOSVDFVPLHFNLOAASSQGG 337
 QY 302 YDMRRLDGTVAVRHPEKATFVENHDTOPGQSLSTVQTFEKLAYAFILITRESGYPOV 361
 DB 338 YDMRRLDGTVAVRHPEKATFVENHDTOPGQSLSTVQTFEKLAYAFILITRESGYPOV 397
 QY 362 FYGDMYTGKTSPEKIPSLKDNIEPLIKARKEYAYGPOHDYIHDPVIGWTRGDSGA 421
 DB 398 FYGDMYTGKTSPEKIPSLKDNIEPLIKARKEYAYGPOHDYIHDPVIGWTRGDSGA 457
 QY 422 SGLAALITDPPGSKMVAAGLKNAGETWYDITGNRSDTYKISDGGGEFHVNDGSYSIY 480
 DB 458 SGLAALITDPPGSKMVAAGLKNAGETWYDITGNRSDTYKISDGGGEFHVNDGSYSIY 516

Query Match 74.2%; Score 1947; DB 16; Length 513;
 Best Local Similarity 71.8%; Pred. No. 2.8e-126;
 Matches 344; Conservative 47; Mismatches 88; Indels 0; Gaps 0;

DB 92 LGFEQKGVTRTKYKTSKELDAGISLHNRNOVYDVLNHRKAGADATEDYTAVERNPA 151
 QY 122 NRNOETSEEVQIAQWDFRPPRGNTYSDPKMWHYFDGADWDESKISRIKFRGEGKA 181
 DB 152 NRNOETSEEVQIAQWDFRPPRGNTYSDPKMWHYFDGADWDESKISRIKFRGEGKA 211
 QY 182 WDEVESENENYDYLWADYDHPDVVAETKKGIWYANELSLDGFRLDAVGHIDHEYL 241
 DB 212 WDEVESENENYDYLWADYDHPDVVAETKKGIWYANELSLDGFRLDAVGHIDHEYL 271
 QY 242 RDVQAVRQATGKEMFTVAEYQNNAGKLENTYKTSFNOSVDFVPLHFNLOAASSQGG 301
 DB 272 RDVQAVRQATGKEMFTVAEYQNNAGKLENTYKTSFNOSVDFVPLHFNLOAASSQGG 331
 QY 302 YDMRRLDGTVAVRHPEKATFVENHDTOPGQSLSTVQTFEKLAYAFILITRESGYPOV 361
 DB 332 YDMRRLDGTVAVRHPEKATFVENHDTOPGQSLSTVQTFEKLAYAFILITRESGYPOV 391
 QY 362 FYGDMYTGKTSPEKIPSLKDNIEPLIKARKEYAYGPOHDYIHDPVIGWTRGDSGA 421
 DB 392 FYGDMYTGKTSPEKIPSLKDNIEPLIKARKEYAYGPOHDYIHDPVIGWTRGDSGA 451
 QY 422 SGLAALITDPPGSKMVAAGLKNAGETWYDITGNRSDTYKISDGGGEFHVNDGSYSIY 480
 DB 452 SGLAALITDPPGSKMVAAGLKNAGETWYDITGNRSDTYKISDGGGEFHVNDGSYSIY 510

RESULT 3

QY 62 LGFEQKGVTRTKYKTSKELDAGISLHNRNOVYDVLNHRKAGADATEDYTAVERNPA 121
 DB 98 LGFEQKGVTRTKYKTSKELDAGISLHNRNOVYDVLNHRKAGADATEDYTAVERNPA 157
 QY 122 NRNOETSEEVQIAQWDFRPPRGNTYSDPKMWHYFDGADWDESKISRIKFRGEGKA 181
 DB 152 NRNOETSEEVQIAQWDFRPPRGNTYSDPKMWHYFDGADWDESKISRIKFRGEGKA 211
 QY 182 WDEVESENENYDYLWADYDHPDVVAETKKGIWYANELSLDGFRLDAVGHIDHEYL 241
 DB 212 WDEVESENENYDYLWADYDHPDVVAETKKGIWYANELSLDGFRLDAVGHIDHEYL 271
 QY 242 RDVQAVRQATGKEMFTVAEYQNNAGKLENTYKTSFNOSVDFVPLHFNLOAASSQGG 301
 DB 272 RDVQAVRQATGKEMFTVAEYQNNAGKLENTYKTSFNOSVDFVPLHFNLOAASSQGG 331
 QY 302 YDMRRLDGTVAVRHPEKATFVENHDTOPGQSLSTVQTFEKLAYAFILITRESGYPOV 361
 DB 332 YDMRRLDGTVAVRHPEKATFVENHDTOPGQSLSTVQTFEKLAYAFILITRESGYPOV 391
 QY 362 FYGDMYTGKTSPEKIPSLKDNIEPLIKARKEYAYGPOHDYIHDPVIGWTRGDSGA 421
 DB 392 FYGDMYTGKTSPEKIPSLKDNIEPLIKARKEYAYGPOHDYIHDPVIGWTRGDSGA 451
 QY 422 SGLAALITDPPGSKMVAAGLKNAGETWYDITGNRSDTYKISDGGGEFHVNDGSYSIY 480
 DB 452 SGLAALITDPPGSKMVAAGLKNAGETWYDITGNRSDTYKISDGGGEFHVNDGSYSIY 510

Query Match 74.2%; Score 1946; DB 2; Length 513;
 Best Local Similarity 72.0%; Pred. No. 3.5e-126;
 Matches 345; Conservative 44; Mismatches 90; Indels 0; Gaps 0;

QY 62 LGFEQKGVTRTKYKTSKELDAGISLHNRNOVYDVLNHRKAGADATEDYTAVERNPA 121
 DB 98 LGFEQKGVTRTKYKTSKELDAGISLHNRNOVYDVLNHRKAGADATEDYTAVERNPA 157
 QY 122 NRNOETSEEVQIAQWDFRPPRGNTYSDPKMWHYFDGADWDESKISRIKFRGEGKA 181
 DB 152 NRNOETSEEVQIAQWDFRPPRGNTYSDPKMWHYFDGADWDESKISRIKFRGEGKA 211
 QY 182 WDEVESENENYDYLWADYDHPDVVAETKKGIWYANELSLDGFRLDAVGHIDHEYL 241
 DB 212 WDEVESENENYDYLWADYDHPDVVAETKKGIWYANELSLDGFRLDAVGHIDHEYL 271
 QY 242 RDVQAVRQATGKEMFTVAEYQNNAGKLENTYKTSFNOSVDFVPLHFNLOAASSQGG 301
 DB 272 RDVQAVRQATGKEMFTVAEYQNNAGKLENTYKTSFNOSVDFVPLHFNLOAASSQGG 331
 QY 302 YDMRRLDGTVAVRHPEKATFVENHDTOPGQSLSTVQTFEKLAYAFILITRESGYPOV 361
 DB 332 YDMRRLDGTVAVRHPEKATFVENHDTOPGQSLSTVQTFEKLAYAFILITRESGYPOV 391
 QY 362 FYGDMYTGKTSPEKIPSLKDNIEPLIKARKEYAYGPOHDYIHDPVIGWTRGDSGA 421
 DB 392 FYGDMYTGKTSPEKIPSLKDNIEPLIKARKEYAYGPOHDYIHDPVIGWTRGDSGA 451
 QY 422 SGLAALITDPPGSKMVAAGLKNAGETWYDITGNRSDTYKISDGGGEFHVNDGSYSIY 480
 DB 452 SGLAALITDPPGSKMVAAGLKNAGETWYDITGNRSDTYKISDGGGEFHVNDGSYSIY 510

472 VNGSVSVWV 481
 481 CNGSVSVWV 490
 RESULT 7
 CDGT_BACSP STANDARD; PRT; 713 AA.
 ID CDGT_BACSP
 AC P30921
 DT 01-JUN-1993 (Rel. 26, Last sequence update)
 DT 01-JUN-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cyclomaldextrin glucanotransferase precursor (EC 2.4.1.19)
 DE (Cyclomaldextrin-glycosyltransferase) (CGTase).
 GN CGT.
 OS Bacillus sp. (strain 17-1).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CC NCBI_Taxid=1409;
 RN [1]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 28-44.
 RX MEDLINE=90257592; PubMed=2534600;
 RA Kaneko T., Song K.B., Hamamoto T., Kudo T., Horikoshi K.
 RT "Construction of a chimeric series of Bacillus cyclomaldextrin
 RT glucanotransferases and analysis of the thermal stabilities and pH
 RT optima of the enzymes."
 RL J. Gen. Microbiol. 135:3447-3457 (1989).
 CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
 CC of a 1,4-alpha-D-glucosidic bond.
 CC -1- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
 CC -1- SWEETIT: Monomer.
 CC -1- MISCELLANEOUS: CGTase may consist of two protein domains: THE ONE
 CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
 CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
 CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
 CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
 CC MALTOOLIGOSACCHARIDE PRODUCED.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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 CC
 CC EMBL: M28053; AAA22310.1;
 DR HSSP: P43379; 1CDG.
 DR InterPro: IPR006589; Alp_amy1_cat_sub.
 DR InterPro: IPR006048; Alpha_amy1_C.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR InterPro: IPR002044; CBD_4.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR InterPro: IPR007110; Ig_1like.
 DR InterPro: IPR002909; IPT_TIG.
 DR Pfam: PF00128; alpha-amy1ase; 1;
 DR Pfam: PF02806; alpha-amy1ase_C; 1;
 DR Pfam: PF00686; CBM_20; 1;
 DR Pfam: PF01833; TIG; 1;
 DR PRINTS: PR00110; ALPHAMYLASE.
 DR PRODOM: PD001568; CBD_4; 1.
 DR SMART: SM00642; Amyy; 1.
 DR SMART: SM00632; Amyy; 1.
 DR Transferrase; Glycosyltransferase; Calcium-binding; signal.
 FT SIGNAL 1 27
 FT CHAIN 1 27
 FT DOMAIN 28 713 CYCLOMALDEXTRIN GLUCANOTRANSFERASE.
 FT DOMAIN 28 165 A1.
 FT DOMAIN 166 229 B.
 FT DOMAIN 230 433 A2.
 FT DOMAIN 434 522 C.
 FT DOMAIN 523 609 D.
 FT DOMAIN 610 713 E.
 FT ACT_SITE 256 256 BY SIMILARITY.

FT ACT_SITE 284 284 BY SIMILARITY.
 FT ACT_SITE 355 355 BY SIMILARITY.
 FT METAL 54 54 CALCIUM 2 (BY SIMILARITY).
 FT METAL 56 56 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
 FT METAL 59 59 SIMILARITY).
 FT METAL 60 60 CALCIUM 2 (BY SIMILARITY).
 FT METAL 78 78 CALCIUM 2 (BY SIMILARITY).
 FT METAL 80 80 CALCIUM 2 (BY SIMILARITY).
 FT METAL 166 166 CALCIUM 1 (BY SIMILARITY).
 FT METAL 217 217 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
 FT METAL 226 226 SIMILARITY).
 FT METAL 260 260 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
 FT DISULFID 70 77 BY SIMILARITY).
 FT SEQUENCE 713 AA; 77389 MW; D13AEFC507F45E CRC64;
 Query Match 11.0%; Score 313; DB 1; Length 713;
 Best Local Similarity 24.7%; Pred. No. 8, 6e-15;
 Matches 135; Conservative 82; Mismatches 188; Indels 142; Gaps 29;
 19 DGLT-----WTKVANEANN--LSSLGITLMLP---AYKTSRSDYGVYDL 62
 67 DGTCTNRLYCGDMQGIINKINDGYLTGCVTAIWISQPVENISVINYSGVNTAHHG 126
 63 YDLSEFNQKGVRTKSTKAYLOIAOAAAGQYADVDFDKGGA--DGTENVDAVE 120
 127 YWADFCK---TNAYGTTIDFONLAAHAKIKITIDFANHSPASLDQPSFAENGK 183
 121 VNSPDNRQELISGYIOQAMTKPDPFGKNTYSEFKRWYHFGVDWDESKRLRYKRG 180
 184 LYNNGRRE--GGY-----TNTGHLNF--HNGGTGFS----- 211
 181 IGAADMEVDTEGNAYDYLM-VADLMDHPEVTELNKNGKYVTTNTIDGRDAVKHI 239
 212 -----TTENGIVKLVLDLNNHNSVDYTKAIKMWLD-LGIDGIRMDAVGEM 261
 240 KFSFPEMLSVRSQKQKPEFTYGEYMSYDINKL--HYITKIDGMEFPAPLANKFT 297
 262 PFGNQKFMATVANNY-KVFTFGE--WELGVNVSLENKHPANVSGLSDRPAKTRQ 318
 298 ASK--SGGAFDMRTMTNTL-----WKDPTLAVTFVDNHDTE--PGALQSWYDPMFK 347
 319 VKONTDMVGLKSMLSGASATDYAQMEDQ---VTFIDNHMERFFHNSANRKLREQ--- 371
 348 PLAYAFILTROEGPCYFGDYGYGIPOY-----NIDS-----LKSRIPL 387
 372 --ALAFILF--SRGVPAI---YGTBQVMSGSGNDPNRARISSFTTAYAYOVSKTLAPL 424
 388 LIARDVAYGTQHDYLDHSDIIGTWREGTE-----KFGSLALITDGGSGKRW 437
 425 KXSNPAIAYGTORRWANVDVLIYERKFGNNVAIVANRWNTASITGLVSLPAGS-- 482
 438 MYVGKHAKYFVYLTGN--RSDVTINSQDGE--FKVNGSVSVV--VPRKTVSTIAR- 492
 483 -----YTVLGLNGLNNTLTGSSGSASITLAAGGTAWQYTTATYAPITIGHV 531
 493 -PITTRP 498
 532 GPWMAKP 538
 RESULT 8
 AMYB_PABPO STANDARD; PRT; 1196 AA.
 ID AMYB_PABPO
 AC P21543;
 DT 01-MAY-1991 (Rel. 26, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-MAR-2004 (Rel. 42, Last annotation update)
 DE Beta/alpha-amy1ase precursor [includes: Beta-amy1ase (EC 3.2.1.2);
 DE Alpha-amy1ase (EC 3.2.1.1)].